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(57) Abstract

The present invention relates to peptides which exhibit potent anti-retroviral activity. The peptides of the invention comprise DP178 (SEQ ID:1) peptide corresponding to amino acids 638 to 673 of the HIV-1LAI gp41 protein, and fragments, analogs and homologs of DP178. The invention further relates to the uses of such peptides as inhibitory of human and non-human retroviral, especially HIV, transmission to uninfected cells.

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METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION

This is a Continuation-In-Part of Serial No. 08/360,107 filed December 20, 1994, which is a 5 Continuation-In-Part of Serial No. 08/255,208 filed June 7, 1994, which is a Continuation-In-Part of Serial No. 08/073,028 filed June 7, 1993, each of which is incorporated herein by reference in its entirety. This invention was made with Government support under Grant No. AI-30411-02 awarded by the National Institutes of Health. The Government has certain rights in the invention.

1. INTRODUCTION

15 The present invention relates, first, to DP178 (SEQ ID NO:1), a peptide corresponding to amino acids 638 to 673 of the HIV-1_{LAI} transmembrane protein (TM) gp41, and portions or analogs of DP178 (SEQ ID NO:1), which exhibit anti-membrane fusion capability, antiviral activity, such as the ability to inhibit HIV transmission to uninfected CD-4+ cells, or an ability to modulate intracellular processes involving coiledcoil peptide structures. Further, the invention relates to the use of DP178 (SEQ ID NO:1) and DP178 25 portions and/or analogs as antifusogenic or antiviral compounds or as inhibitors of intracellular events involving coiled-coil peptide structures. invention also relates to peptides analogous to DP107 (SEQ ID NO:25), a peptide corresponding to amino acids 558 to 595 of the HIV-1_{LAI} transmembrane protein (TM) gp41, having amino acid sequences present in other viruses, such as enveloped viruses, and/or other organisms, and further relates to the uses of such peptides. These peptides exhibit anti-membrane fusion capability, antiviral activity, or the ability to

modulate intracellular processes involving coiled-coil peptide structures. The present invention additionally relates to methods for identifying compounds that disrupt the interaction between DP178 and DP107, and/or between DP107-like and DP178-like peptides. Further, the invention relates to the use of the peptides of the invention as diagnostic agents. For example, a DP178 peptide may be used as an HIV subtype-specific diagnostic. The invention is demonstrated, first, by way of an Example wherein DP178 (SEQ ID:1), and a peptide whose sequence is homologous to DP178 are each shown to be potent, noncytotoxic inhibitors of HIV-1 transfer to uninfected CD-4+ cells. The invention is further demonstrated by Examples wherein peptides having structural and/or amino acid motif similarity to DP107 and DP178 are identified in a variety of viral and nonviral organisms, and in examples wherein a number of such identified peptides derived from several different viral systems are demonstrated to exhibit antiviral activity.

2. BACKGROUND OF THE INVENTION 2.1 MEMBRANE FUSION EVENTS

Membrane fusion is a ubiquitous cell biological process (for a review, see White, J.M., 1992, Science 258:917-924). Fusion events which mediate cellular housekeeping functions, such as endocytosis, constitutive secretion, and recycling of membrane components, occur continuously in all eukaryotic cells.

Additional fusion events occur in specialized cells. Intracellularly, for example, fusion events are involved in such processes as occur in regulated exocytosis of hormones, enzymes and neurotransmitters.

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Intercellularly, such fusion events feature prominently in, for example, sperm-egg fusion and myoblast fusion.

Fusion events are also associated with disease states. For example, fusion events are involved in the formation of giant cells during inflammatory reactions, the entry of all enveloped viruses into cells, and, in the case of human immunodeficiency virus (HIV), for example, are responsible for the virally induced cell-cell fusion which leads to cell death.

2.2. THE HUMAN IMMUNODEFICIENCY VIRUS

The human immunodeficiency virus (HIV) has been implicated as the primary cause of the slowly degenerative immune system disease termed acquired immune deficiency syndrome (AIDS) (Barre-Sinoussi, F. et al., 1983, Science 220:868-870; Gallo, R. et al., 1984, Science <u>224</u>:500-503). There are at least two distinct types of HIV: HIV-1 (Barre-Sinoussi, F. et al., 1983, Science 220:868-870; Gallo R. et al., 1984, Science 224:500-503) and HIV-2 (Clavel, F. et al., 1986, Science <u>233</u>:343-346; Guyader, M. <u>et al.</u>, 1987, Nature 326:662-669). Further, a large amount of genetic heterogeneity exists within populations of each of these types. Infection of human CD-4 Tlymphocytes with an HIV virus leads to depletion of the cell type and eventually to opportunistic infections, neurological dysfunctions, neoplastic growth, and ultimately death.

HIV is a member of the lentivirus family of retroviruses (Teich, N. et al., 1984, RNA Tumor Viruses, Weiss, R. et al., eds., CSH-Press, pp. 949-956). Retroviruses are small enveloped viruses that contain a diploid, single-stranded RNA genome, and

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replicate via a DNA intermediate produced by a virally-encoded reverse transcriptase, an RNA-dependent DNA polymerase (Varmus, H., 1988, Science 240:1427-1439). Other retroviruses include, for example, oncogenic viruses such as human T-cell leukemia viruses (HTLV-I,-II,-III), and feline leukemia virus.

The HIV viral particle consists of a viral core, composed of capsid proteins, that contains the viral RNA genome and those enzymes required for early replicative events. Myristylated Gag protein forms an outer viral shell around the viral core, which is, in turn, surrounded by a lipid membrane enveloped derived from the infected cell membrane. The HIV enveloped surface glycoproteins are synthesized as a single 160 Kd precursor protein which is cleaved by a cellular protease during viral budding into two glycoproteins, gp41 and gp120. gp41 is a transmembrane protein and gp120 is an extracellular protein which remains non-covalently associated with gp41, possibly in a trimeric or multimeric form (Hammarskjold, M. and Rekosh, D., 1989, Biochem. Biophys. Acta 989:269-280).

HIV is targeted to CD-4⁺ cells because the CD-4 cell surface protein acts as the cellular receptor for the HIV-1 virus (Dalgleish, A. et al., 1984, Nature 312:763-767; Klatzmann et al., 1984, Nature 312:767-768; Maddon et al., 1986, Cell 47:333-348). Viral entry into cells is dependent upon gp120 binding the cellular CD-4⁺ receptor molecules (McDougal, J.S. et al., 1986, Science 231:382-385; Maddon, P.J. et al., 1986, Cell 47:333-348) and thus explains HIV's tropism for CD-4⁺ cells, while gp41 anchors the enveloped glycoprotein complex in the viral membrane.

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2.3. HIV TREATMENT

HIV infection is pandemic and HIV associated diseases represent a major world health problem. Although considerable effort is being put into the successful design of effective therapeutics, currently no curative anti-retroviral drugs against AIDS exist. In attempts to develop such drugs, several stages of the HIV life cycle have been considered as targets for therapeutic intervention (Mitsuya, H. et al., 1991, FASEB J. 5:2369-2381). For example, virally encoded reverse transcriptase has been one focus of drug development. A number of reverse-transcriptasetargeted drugs, including 2',3'-dideoxynucleoside analogs such as AZT, ddI, ddC, and d4T have been developed which have been shown to been active against HIV (Mitsuya, H. et al., 1991, Science 249:1533-1544). While beneficial, these nucleoside analogs are not curative, probably due to the rapid appearance of drug resistant HIV mutants (Lander, B. et al., 1989, Science 243:1731-1734). In addition, the drugs often exhibit toxic side effects such as bone marrow suppression, vomiting, and liver function abnormalities.

which can inhibit viral entry into the cell, the earliest stage of HIV infection. Here, the focus has thus far been on CD4, the cell surface receptor for HIV. Recombinant soluble CD4, for example, has been shown to inhibit infection of CD-4* T-cells by some HIV-1 strains (Smith, D.H. et al., 1987, Science 238:1704-1707). Certain primary HIV-1 isolates, however, are relatively less sensitive to inhibition by recombinant CD-4 (Daar, E. et al., 1990, Proc. Natl. Acad. Sci. USA 87:6574-6579). In addition,

recombinant soluble CD-4 clinical trials have produced inconclusive results (Schooley, R. et al., 1990, Ann. Int. Med. 112:247-253; Kahn, J.O. et al., 1990, Ann. Int. Med. 112:254-261; Yarchoan, R. et al., 1989, Proc. Vth Int. Conf. on AIDS, p. 564, MCP 137).

The late stages of HIV replication, which involve crucial virus-specific secondary processing of certain viral proteins, have also been suggested as possible anti-HIV drug targets. Late stage processing is dependent on the activity of a viral protease, and drugs are being developed which inhibit this protease (Erickson, J., 1990, Science 249:527-533). The clinical outcome of these candidate drugs is still in question.

Attention is also being given to the development of vaccines for the treatment of HIV infection. HIV-1 enveloped proteins (gp160, gp120, gp41) have been shown to be the major antigens for anti-HIV antibodies present in AIDS patients (Barin, et al., 1985, Science 228:1094-1096). Thus far, therefore, these proteins seem to be the most promising candidates to act as antigens for anti-HIV vaccine development. To this end, several groups have begun to use various portions of gp160, gp120, and/or gp41 as immunogenic targets for the host immune system. See for example, Ivanoff, L. et al., U.S. Pat. No. 5,141,867; Saith, G. et al., WO 92/22,654; Shafferman, A., WO 91/09,872; Formoso, C. et al., WO 90/07,119. Clinical results concerning these candidate vaccines, however, still remain far in the future.

Thus, although a great deal of effort is being directed to the design and testing of anti-retroviral drugs, a truly effective, non-toxic treatment is still needed.

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3. SUMMARY OF THE INVENTION

The present invention relates, first, to DP178 (SEQ ID:1), a 36-amino acid synthetic peptide corresponding to amino acids 638 to 673 of the transmembrane protein (TM) gp41 from the HIV-1 isolate LAI (HIV-1_{LAI}), which exhibits potent anti-HIV-1 activity. As evidenced by the Example presented below, in Section 6, the DP178 (SEQ ID:1) antiviral activity is so high that, on a weight basis, no other known anti-HIV agent is effective at concentrations as low as those at which DP178 (SEQ ID:1) exhibits its inhibitory effects.

The invention further relates to those portions and analogs of DP178 which also show such antiviral activity, and/or show anti-membrane fusion capability, or an ability to modulate intracellular processes. involving coiled-coil peptide structures. The term "DP178 analog" refers to a peptide which contains an amino acid sequence corresponding to the DP178 peptide sequence present within the gp41 protein of HIV-1LMI, but found in viruses and/or organisms other than HIV-Such DP178 analog peptides may, therefore, correspond to DP178-like amino acid sequences present in other viruses, such as, for example, enveloped viruses, such as retroviruses other than HIV-1LAI, as well as non-enveloped viruses. Further, such analogous DP178 peptides may also correspond to DP178like amino acid sequences present in nonviral organisms.

The invention further relates to peptides DP107 (SEQ ID NO:25) analogs. DP107 is a peptide corresponding to amino acids 558-595 of the HIV-1_{LAI} transmembrane protein (TM) gp41. The term "DP107 analog" as used herein refers to a peptide which contains an amino acid sequence corresponding to the

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DP107 peptide sequence present within the gp41 protein of HIV-l_{LAI}, but found in viruses and organisms other than HIV-l_{LAI}. Such DP107 analog peptides may, therefore, correspond to DP107-like amino acid sequences present in other viruses, such as, for for example, enveloped viruses, such as retroviruses other than HIV-l_{LAI}, as well as non-enveloped viruses. Further, such DP107 analog peptides may also correspond to DP107-like amino acid sequences present in nonviral organisms.

Further, the peptides of the invention include DP107 analog and DP178 analog peptides having amino acid sequences recognized or identified by the 107x178x4, ALLMOTI5 and/or PLZIP search motifs described herein.

The peptides of the invention may, for example, exhibit antifusogenic activity, antiviral activity, and/or may have the ability to modulate intracellular processes which involve coiled-coil peptide structures. With respect to the antiviral activity of the peptides of the invention, such an antiviral activity includes, but is not limited to the inhibition of HIV transmission to uninfected CD-4⁺ cells. Additionally, the antifusogenic capability, antiviral activity or intracellular modulatory activity of the peptides of the invention merely requires the presence of the peptides of the invention, and, specifically, does not require the stimulation of a host immune response directed against such peptides.

The peptides of the invention may be used, for example, as inhibitors of membrane fusion-asociated events, such as, for example, the inhibition of human and non-human retroviral, especially HIV, transmission to uninfected cells. It is further contemplated that

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the peptides of the invention may be used as modulators of intracellular events involving coiled-coil peptide structures.

The peptides of the invention may, alternatively, be used to identify compounds which may themselves exhibit antifusogenic, antiviral, or intracellular modulatory activity. Additional uses include, for example, the use of the peptides of the invention as organism or viral type and/or subtype-specific diagnostic tools.

The terms "antifusogenic" and "anti-membrane fusion", as used herein, refer to an agent's ability to inhibit or reduce the level of membrane fusion events between two or more moieties relative to the level of membrane fusion which occurs between said moieties in the absence of the peptide. The moieties may be, for example, cell membranes or viral structures, such as viral envelopes or pili. "antiviral", as used herein, refers to the compound's ability to inhibit viral infection of cells, via, for example, cell-cell fusion or free virus infection. Such infection may involve membrane fusion, as occurs in the case of enveloped viruses, or some other fusion event involving a viral structure and a cellular structure (e.g., such as the fusion of a viral pilus and bacterial membrane during bacterial conjugation).

It is also contemplated that the peptides of the invention may exhibit the ability to modulate intracellular events involving coiled-coil peptide structures. "Modulate", as used herein, refers to a stimulatory or inhibitory effect on the intracellular process of interest relative to the level or activity of such a process in the absence of a peptide of the invention.

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Embodiments of the invention are demonstrated below wherein an extremely low concentration of DP178 (SEQ ID:1), and very low concentrations of a DP178 homolog (SEQ ID:3) are shown to be potent inhibitors of HIV-1 mediated CD-4⁺ cell-cell fusion (<u>i.e.</u>, syncytial formation) and infection of CD-4⁺ cells by cell-free virus. Further, it is shown that DP178 (SEQ ID:1) is not toxic to cells, even at concentrations 3 logs higher than the inhibitory DP-178 (SEQ ID:1) concentration.

The present invention is based, in part, on the surprising discovery that the DP107 and DP178 domains of the HIV gp41 protein non-covalently complex with each other, and that their interaction is required for the normal infectivity of the virus. This discovery is described in the Example presented, below, in Section 8. The invention, therefore, further relates to methods for identifying antifusogenic, including antiviral, compounds that disrupt the interaction between DP107 and DP178, and/or between DP107-like and DP178-like peptides.

Additional embodiments of the invention (specifically, the Examples presents in Sections 9-16 and 19-25, below) are demonstrated, below, wherein peptides, from a variety of viral and nonviral sources, having structural and/or amino acid motif similarity to DP107 and DP178 are identified, and search motifs for their identification are described. Further, Examples (in Sections 17, 18, 25-29) are presented wherein a number of the peptides of the invention are demonstrated exhibit substantial antiviral activity or activity predictive of antiviral activity.

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3.1. DEFINITIONS

Peptides are defined herein as organic compounds comprising two or more amino acids covalently joined by peptide bonds. Peptides may be referred to with respect to the number of constituent amino acids, i.e., a dipeptide contains two amino acid residues, a tripeptide contains three, etc. Peptides containing ten or fewer amino acids may be referred to as oligopeptides, while those with more than ten amino acid residues are polypeptides. Such peptides may also include any of the modifications and additional amino and carboxy groups as are described herein.

Peptide sequences defined herein are represented by one-letter symbols for amino acid residues as follows:

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A (alanine)
    R (arginine)
    N (asparagine)
    D (aspartic acid)
    C (cysteine)
    Q (glutamine)
20
    E (glutamic acid)
    G (glycine)
    H (histidine)
    I (isoleucine)
    L (leucine)
    K (lysine)
   M (methionine)
25
   F (phenylalanine)
   P (proline)
   S (serine)
   T (threonine)
   W
      (tryptophan)
   Y (tyrosine)
   V (valine)
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4. BRIEF DESCRIPTION OF THE FIGURES

Amino acid sequence of DP178 (SEQ ID:1) derived from HIVLA; DP178 homologs derived from HIV-1, pp. (DP-185; SEQ ID:3), HIV-1_{RF} (SEQ ID:4), and HIV-1_{MN} (SEQ ID:5); DP178 homologs derived from amino acid sequences of two prototypic HIV-2 isolates, namely, HIV-2_{rd} (SEQ ID:6) and HIV-2_{NDHZ} (SEQ ID:7); control peptides: DP-180 (SEQ ID:2), a peptide incorporating the amino acid residues of DP178 in a scrambled sequence; DP-118 (SEQ ID:10) unrelated to DP178, which inhibits HIV-1 cell free virus infection; DP-125 (SEQ ID:8), unrelated to DP178, also inhibits HIV-1 cell free virus infection; DP-116 (SEQ ID:9), unrelated to DP178, is negative for inhibition of HIV-1 infection when tested using a cell-free virus infection assay. Throughout the figures, the one letter amino acid code is used.

FIG. 2. Inhibition of HIV-1 cell-free virus infection by synthetic peptides. IC₅₀ refers to the concentration of peptide that inhibits RT production from infected cells by 50% compared to the untreated control. Control: the level of RT produced by untreated cell cultures infected with the same level of virus as treated cultures.

FIG. 3. Inhibition of HIV-1 and HIV-2 cell-free virus infection by the synthetic peptide DP178 (SEQ ID:1). IC₅₀: concentration of peptide that inhibits RT production by 50% compared to the untreated control. Control: Level of RT produced by untreated cell cultures infected with the same level of virus as treated cultures.

FIG. 4A-4B. Fusion Inhibition Assays. FIG 4A: DP178 (SEQ ID:1) inhibition of HIV-1 prototypic isolate-mediated syncytial formation; data represents the number of virus-induced syncytial per cell. FIG.

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4B: DP-180 (SEQ ID:2) represents a scrambled control peptide; DP-185 (SEQ ID:3) represents a DP178 homolog derived from HIV-1_{SF2} isolate; Control, refers to the number of syncytial produced in the absence of peptide.

- FIG. 5. Fusion inhibition assay: HIV-1 vs. HIV-2. Data represents the number of virus-induced syncytial per well. ND: not done.
- FIG. 6. Cytotoxicity study of DP178 (SEQ ID:1) and DP-116 (SEQ ID:9) on CEM cells. Cell proliferation data is shown.
- and maltose binding protein (MBP)-gp41 fusion proteins. DP107 and DP178 are synthetic peptides based on the two putative helices of gp41. The letter P in the DP107 boxes denotes an Ile to Pro mutation at amino acid number 578. Amino acid residues are numbered according to Meyers et al., "Human Retroviruses and AIDS", 1991, Theoret. Biol. and Biophys. Group, Los Alamos Natl. Lab., Los Alamos, NM. The proteins are more fully described, below, in Section 8.1.1.
 - FIG. 8. A point mutation alters the conformation and anti-HIV activity of M41.
- FIG. 9. Abrogation of DP178 anti-HIV activity. Cell fusion assays were carried out in the presence of 10 nM DP178 and various concentrations of M41 Δ 178 or M41P Δ 178.
 - FIG. 10. Binding of DP178 to leucine zipper of gp41 analyzed by FAb-D ELISA.
 - FIG. 11A-B. Models for a structural transition in the HIV-1 TM protein. Two models are proposed which indicate a structural transition from a native oligomer to a fusogenic state following a trigger event (possibly gp120 binding to CD4). Common

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features of both models include (1) the native state is held together by noncovalent protein-protein interactions to form the heterodimer of gp120/41 and other interactions, principally though gp41 interactive sites, to form homo-oligomers on the virus surface of the gp120/41 complexes; (2) shielding of the hydrophobic fusogenic peptide at the N-terminus (F) in the native state; and (3) the leucine zipper domain (DP107) exists as a homo-oligomer coiled coil only in the fusogenic state. The major differences in the two models include the structural state (native or fusogenic) in which the DP107 and DP178 domains are complexed to each other. In the first model (FIG. 11A) this interaction occurs in the native state and in the second (FIG. 11B), it occurs during the fusogenic state. When triggered, the fusion complex in the model depicted in (A) is generated through formation of coiled-coil interactions in homologous DP107 domains resulting in an extended α -helix. conformational change positions the fusion peptide for interaction with the cell membrane. In the second model (FIG. 11B), the fusogenic complex is stabilized by the association of the DP178 domain with the DP107 coiled-coil.

FIG. 12. Motif design using heptad repeat positioning of amino acids of known coiled-coils.

FIG. 13. Motif design using proposed heptad repeat positioning of amino acids of DP107 and DP178.

FIG. 14. Hybrid motif design crossing GCN4 and DP107.

FIG. 15. Hybrid motif design crossing GCN4 and DP178.

FIG. 16. Hybrid motif design 107x178x4, crossing DP107 and DP178. This motif was found to be

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the most consistent at identifying relevant DP107-like and DP178-like peptide regions.

FIG. 17. Hybrid motif design crossing GCN4, DP107, and DP178.

FIG. 18. Hybrid motif design ALLMOTI5 crossing GCN4, DP107, DP178, c-Pos c-Jun, c-Myc, and Flu Loop 36.

FIG. 19. PLZIP motifs designed to identify N-terminal proline-leucine zipper motifs.

isolate) enveloped protein gp41. Sequence search motif designations: Spades (*): 107x178x4; Hearts (*) ALLMOTI5; Clubs (*): PLZIP; Diamonds (*): transmembrane region (the putative transmembrane domains were identified using a PC/Gene program designed to search for such peptide regions).

Asterisk (*): Lupas method. The amino acid sequences identified by each motif are bracketed by the respective characters. Representative sequences chosen based on 107x178x4 searches are underlined and in bold. DP107 and DP178 sequences are marked and

in bold. DP107 and DP178 sequences are marked, and additionally double-underlined and italicized.

FIG. 21. Search results for human respiratory syncytial virus (RSV) strain A2 fusion glycoprotein F1. Sequence search motif designations are as in FIG. 20.

FIG. 22. Search results for simian immunodeficiency virus (SIV) enveloped protein gp41 (AGM3 isolate). Sequence search motif designations are as in FIG. 20.

FIG. 23. Search results for canine distemper virus (strain Onderstepoort) fusion glycoprotein 1. Sequence search motif designations are as in FIG. 20.

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FIG. 24. Search results for newcastle disease virus (strain Australia-Victoria/32) fusion glycoprotein F1. Sequence search motif designations are as in FIG. 20.

FIG. 25. Search results for human parainfluenza 3 virus (strain NIH 47885) fusion glycoprotein F1. Sequence search motif designations are as in FIG. 20.

FIG. 26. Search results for influenza A virus (strain A/AICHI/2/68) hemagglutinin precursor HA2. Sequence search designations are as in FIG. 20.

FIG. 27A-D. Respiratory Syncytial Virus (RSV) peptide antiviral and circular dichroism data. FIG. 27A-B: Peptides derived from the F2 DP178/DP107-like region. Antiviral and CD data. FIG. 27C-D: Peptides derived from the F1 DP107-like region. Peptide and CD data.

Antiviral activity (AV) is represented by the following qualitative symbols:

"-", negative antiviral activity;
"+/-", antiviral activity at greater than
100µg/ml;

"+", antiviral activity at between 50-100µg/ml; "++", antiviral activity at between 20-50µg/ml; "+++", antiviral activity at between 1-20µg/ml; "++++", antiviral activity at <1µg/ml.

CD data, referring to the level of helicity is represented by the following qualitative symbol:

"-", no helicity;

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"+", 25-50% helicity;

"++", 50-75% helicity;

"+++" 75-100% helicity.

IC₅₀ refers to the concentration of peptide necessary to produce only 50% of the number or syncytial relative to infected control cultures

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containing no peptide. IC₅₀ values were obtained using purified peptides only.

FIG. 28A-B. Respiratory syncytial Virus (RSV) DP178-like region (F1) peptide antiviral and CD data. Antiviral symbols, CD symbols, and IC₅₀ are as in FIG. 27A-D. IC₅₀ values were obtained using purified peptides only.

FIG. 29A-B. Peptides derived from the HPIV3 P1 DP107-like region. Peptide antiviral and CD data. Antiviral symbols, CD symbols, and IC₅₀ are as in FIG. 27A-D. Purified peptides were used to obtain IC₅₀ values, except where the values are marked by an asterisk (*), in which cases, the IC₅₀ values were obtained using a crude peptide preparation.

FIG. 30A-B. Peptides derived from the HPTV3

F1 DP178-like region. Peptide antiviral and CD data.

Antiviral symbols, CD symbols, and IC₅₀ are as in FIG.

27A-D. Purified peptides were used to obtain IC₅₀

values, except where the values are marked by an

asterisk (*), in which cases, the IC₅₀ values were obtained using a crude peptide preparation.

FIG. 31. Motif search results for simian immunodeficiency virus (SIV) isolate MM251, enveloped polyprotein gp41. Sequence search designations are as in FIG. 20.

FIG. 32. Motif search results for Epstein-Barr Virus (Strain B95-8), glycoprotein gp110 precursor (designated gp115). BALF4. Sequence search designations are as in FIG. 20.

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FIG. 33. Motif search results for Epstein-Barr Virus (Strain B95-8), BZLF1 trans-activator protein (designated EB1 or Zebra). Sequence search designations are as in FIG. 20. Additionally, "@" refers to a well known DNA binding domain and "+" refers to a well known dimerization domain, as defined

by Flemington and Speck (Flemington, E. and Speck, S.H., 1990, Proc. Natl. Acad. Sci. USA 87:9459-9463).

FIG. 34. Motif search results for measles virus (strain Edmonston), fusion glycoprotein F1. Sequence search designations are as in FIG. 20.

FIG. 35. Motif search results for Hepatitis B Virus (Subtype AYW), major surface antigen precursor S. Sequence search designations are as in FIG. 20.

FIG. 36. Motif search results for simian Mason-Pfizer monkey virus, enveloped (TM) protein qp20. Sequence search designations are as in FIG. 20.

FIG. 37. Motif search results for Pseudomonas aerginosa, fimbrial protein (Pilin). Sequence search designations are as in FIG. 20.

price 38. Motif search results for Neisseria gonorrhoeae fimbrial protein (Pilin). Sequence search designations are as in FIG. 20.

FIG. 39. Motif search results for Hemophilus influenzae fimbrial protein. Sequence search designations are as in FIG. 20.

FIG. 40. Motif search results for Staphylococcus aureus, toxic shock syndrome toxin-1. Sequence search designations are as in FIG. 20.

FIG. 41. Motif search results for Staphylococcus aureus enterotoxin Type E. Sequence search designations are as in FIG. 20.

FIG. 42. Motif search results for Staphylococcus aureus enterotoxin A. Sequence search designations are as in FIG. 20.

FIG. 43. Motif search results for Escherichia coli, heat labile enterotoxin A. Sequence search designations are as in FIG. 20.

FIG. 44. Motif search results for human cfos proto-oncoprotein. Sequence search designations are as in FIG. 20.

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FIG. 45. Motif search results for human lupus KU autoantigen protein P70. Sequence search designations are as in FIG. 20.

FIG. 46. Motif search results for human zinc finger protein 10. Sequence search designations are as in FIG. 20.

FIG. 47. Measles virus (MeV) fusion protein DP178-like region antiviral and CD data. Antiviral symbols, CD symbols, and IC_{50} are as in FIG. 27A-D. IC values were obtained using purified peptides.

FIG. 48. Simian immunodeficiency virus (SIV) TM (fusion) protein DP178-like region antiviral data. Antiviral symbols are as in FIG. 27A-D not tested.

FIG. 49A-C. DP178-derived peptide antiviral The peptides listed herein were derived from the region surrounding the HIV-1 BRU isolate DP178 region (e.g., gp41 amino acid residues 615-717).

In instances where peptides contained DP178 point mutations, the mutated amino acid residues are shown 20 with a shaded background. In instances in which the test peptide has had an amino and/or carboxy-terminal group added or removed (apart from the standard amidoand acetyl- blocking groups found on such peptides), such modifications are indicated. FIG. 49A: column to the immediate right of the name of the test peptide indicates the size of the test peptide and points out whether the peptide is derived from a one amino acid peptide "walk" across the DP178 region. The next column to the right indicates whether the test peptide contains a point mutation, while the column to its right indicates whether certain amino acid residues have been added to or removed from the DP178-derived amino acid sequence. FIG 49B: column to the immediate right of the test peptide name

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indicates whether the peptide represents a DP178 truncation, the next column to the right points out whether the peptide contains a point mutation, and the column to its right indicates whether the peptide contains amino acids which have been added to or removed from the DP178 sequence itself. FIG. 49C: The column to the immediate right of the test peptide name indicates whether the test peptide contains a point mutation, while the column to its right indicates whether amino acid residues have been added to or removed from the DP178 sequence itself. as defined in FIG. 27A-D, and IC50 values were obtained using purified peptides except where marked with an asterisk (*), in which case the IC₅₀ was obtained using a crude peptide preparation. 15

FIG. 50. DP107 and DP107 gp41 region truncated peptide antiviral data. IC_{50} as defined in FIG. 27A-D, and IC_{50} values were obtained using purified peptides except where marked with an asterisk (*), in which case the IC_{50} was obtained using a crude peptide preparation.

FIG. 51A-B. Epstein-Barr virus Strain B95-8 BZLF1 DP178/DP107 analog region peptide walks and electrophoretic mobility shift assay results. The peptides (T-423 to T-446, FIG. 51A; T-447 to T-461, FIG. 51B) represent one amino acid residue "walks" through the EBV Zebra protein region from amino acid residue 173 to 246.

The amino acid residue within this region which corresponds to the first amino acid residue of each peptide is listed to the left of each peptide, while the amino acid residue within this region which corresponds to the last amino acid residue of each peptide is listed to the right of each peptide. The

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length of each test peptide is listed at the far right of each line, under the heading "Res".

"ACT" refers to a test peptide's ability to inhibit Zebra binding to its response element. "+" refers to a visible, but incomplete, abrogation of the response element/Zebra homodimer complex; "+++" refers to a complete abrogation of the complex; and "-" represents a lack of complex disruption.

FIG. 52A-B. Hepatitis B virus subtype AYW major surface antigen precursor S protein DP178/DP107 analog region and peptide walks. 52A depicts Domain I (S protein amino acid residues 174-220), which contains a potential DP178/DP107 analog region. In addition, peptides are listed which represent one amino acid peptide "walks" through domain I. 52B depicts Domain II (S protein amino acid residues 233-291), which contains a second potential DP178/DP107 analog region. In addition, peptides are listed which represent one amino acid peptide "walks" through domain II.

5. <u>DETAILED DESCRIPTION OF THE INVENTION</u>

Described herein are peptides which may exhibit antifusogenic activity, antiviral capability, and/or the ability to modulate intracellular processes involving coiled-coil peptide structures. The peptides described include, first, DP178 (SEQ ID NO:1), a gp41-derived 36 amino acid peptide and fragments and analogs of DP178.

In addition, the peptides of the invention described herein include peptides which are DP107 analogs. DP107 (SEQ ID NO:25) is a 38 amino acid peptide corresponding to residues 558 to 595 of the HIV-1_{LAI} transmembrane (TM) gp41 protein. Such DP107 analogs may exhibit antifusogenic capability, antiviral activity or an ability to modulate

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intracellular processes involving coiled-coil structures.

Purther, peptides of the invention include DP107 and DP178 are described herein having amino acid sequences recognized by the 107x178x4, ALLMOTI5, and PLZIP search motifs. Such motifs are also discussed.

Also described here are antifusogenic, antiviral, intracellular modulatory, and diagnostic uses of the peptides of the invention. Further, procedures are described for the use of the peptides of the invention for the identification of compounds exhibiting antifusogenic, antiviral or intracellular modulatory activity.

While not limited to any theory of operation, the following model is proposed to explain the potent anti-HIV activity of DP178, based, in part, on the experiments described in the Examples, infra. HIV protein, gp41, DP178 corresponds to a putative α helix region located in the C-terminal end of the gp41 ectodomain, and appears to associate with a distal site on gp41 whose interactive structure is influenced by the leucine zipper motif, a coiled-coil structure, referred to as DP107. The association of these two domains may reflect a molecular linkage or "molecular clasp" intimately involved in the fusion process. It is of interest that mutations in the C-terminal α helix motif of gp41 (i.e., the D178 domain) tend to enhance the fusion ability of gp41, whereas mutations in the leucine zipper region (i.e., the DP107 domain) decrease or abolish the fusion ability of the viral protein. It may be that the leucine zipper motif is involved in membrane fusion while the C-terminal α helix motif serves as a molecular safety to regulate the availability of the leucine zipper during virusinduced membrane fusion.

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On the basis of the foregoing, two models are proposed of gp41-mediated membrane fusion which are schematically shown in FIG. 11A-B. The reason for proposing two models is that the temporal nature of the interaction between the regions defined by DP107 and DP178 cannot, as yet, be pinpointed. Each model envisions two conformations for gp41 - one in a "native" state as it might be found on a resting The other in a "fusogenic" state to reflect conformational changes triggered following binding of gp120 to CD4 and just prior to fusion with the target cell membrane. The strong binding affinity between gp120 and CD4 may actually represent the trigger for the fusion process obviating the need for a pH change such as occurs for viruses that fuse within 15 intracellular vesicles. The two major features of both models are: (1) the leucine zipper sequences (DP107) in each chain of oligomeric enveloped are held apart in the native state and are only allowed access to one another in the fusogenic state so as to form 20 the extremely stable coiled-coils, and (2) association of the DP178 and DP107 sites as they exist in gp41 occur either in the native or fusogenic state. 11A depicts DP178/DP107 interaction in the native state as a molecular clasp. On the other hand, if one assumes that the most stable form of the enveloped occurs in the fusogenic state, the model in FIG. 11B can be considered.

When synthesized as peptides, both DP107 and DP178 are potent inhibitors of HIV infection and fusion, probably by virtue of their ability to form complexes with viral gp41 and interfere with its fusogenic process; e.g., during the structural transition of the viral protein from the native structure to the fusogenic state, the DP178 and DP107

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> peptides may gain access to their respective binding sites on the viral gp41, and exert a disruptive influence. DP107 peptides which demonstrate anti-HIV activity are described in Applicants' co-pending application Serial No. 08/264,531, filed June 23, 1994, which is incorporated by reference herein in its entirety.

As shown in the Examples, infra, a truncated recombinant gp41 protein corresponding to the ectodomain of gp41 containing both DP107 and DP178 domains (excluding the fusion peptide, transmembrane region and cytoplasmic domain of gp41) did not inhibit HIV-1 induced fusion. However, when a single mutation was introduced to disrupt the coiled-coil structure of the DP107 domain -- a mutation which results in a total loss of biological activity of DP107 peptides -the inactive recombinant protein was transformed to an active inhibitor of HIV-1 induced fusion. transformation may result from liberation of the potent DP178 domain from a molecular clasp with the 20 leucine zipper, DP107 domain.

For clarity of discussion, the invention will be described primarily for DP178 peptide inhibitors of HIV. However, the principles may be analogously applied to other viruses, both enveloped and nonenveloped, and to other non-viral organisms.

5.1. DP178 AND DP178-LIKE PEPTIDES

The DP178 peptide (SEQ ID:1) of the invention corresponds to amino acid residues 638 to 673 of the transmembrane protein gp41 from the HIV-1LAI isolate, and has the 36 amino acid sequence (reading from amino to carboxy terminus):

NH2-YTSLIHSLIEESQNQQEKNEQELLELDKWASLWNWF-COOH (SEQ ID:1)

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In addition to the full-length DP178 (SEQ ID:1) 36-mer, the peptides of the invention may include truncations of the DP178 (SEQ ID:1) peptide which exhibit antifusogenic activity, antiviral activity and/or the ability to modulate intracellular processes involving coiled-coil peptide structures. Truncations of DP178 (SEQ ID:1) peptides may comprise peptides of between 3 and 36 amino acid residues (i.e., peptides ranging in size from a tripeptide to a 36-mer polypeptide), as shown in Tables I and IA, below. 10 Peptide sequences in these tables are listed from . amino (left) to carboxy (right) terminus. "X" may represent an amino group (-NH2) and "Z" may represent a carboxyl (-COOH) group. Alternatively, "X" may represent a hydrophobic group, including but not limited to carbobenzyl, dansyl, or T-butoxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (FMOC) group; or a covalently attached macromolecular group, including but not limited to a lipid-fatty acid conjugate, polyethylene glycol, carbohydrate or peptide group. Further, "Z" may represent an amido group; a T-butoxycarbonyl group; or a covalently attached macromolecular group, including but not limited to a lipid-fatty acid conjugate, polyethylene glycol, carbohydrate or peptide group. A preferred "X" or "Z" macromolecular group is a peptide group.

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TABLE I DP178 (SEO ID: 1) CARBOXY TRUNCATIONS

```
X-YTS-Z
   X-YTSL-Z
   X-YTSLI-Z
   X-YTSLIH-Z
   X-YTSLIHS-Z
   X-YTSLIHSL-Z
   X-YTSLIHSLI-Z
   X-YTSLIHSLIE-Z
   X-YTSLIHSLIEE-Z
   X-YTSLIHSLIEES-Z
   X-YTSLIHSLIEESQ-Z
   X-YTSLIHSLIEESQN-Z
   X-YTSLIHSLIEESQNQ-Z
   X-YTSLIHSLIEESQNQQ-Z
   X-YTSLIHSLIEESQNQQE-Z
   X-YTSLIHSLIEESQNQQEK-Z
    X-YTSLIHSLIEESQNQQEKN-Z
   X-YTSLIHSLIEESQNQQEKNE-Z
   X-YTSLIHSLIEESQNQQEKNEQ-Z
   X-YTSLIHSLIEESQNQQEKNEQE-Z
    X-YTSLIHSLIEESQNQQEKNEQEL-Z
    X-YTSLIHSLIEESQNQQEKNEQELL-Z
    X-YTSLIHSLIEESQNQQEKNEQELLE-Z
    X-YTSLIHSLIEESQNQQEKNEQELLEL-Z
    X-YTSLIHSLIEESQNQQEKNEQELLELD-Z
    X-YTSLIHSLIEESQNQQEKNEQELLELDK-Z
    X-YTSLIHSLIEESQNQQEKNEQELLELDKW-Z
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    X-YTSLIHSLIEESQNQQEKNEQELLELDKWA-Z
    X-YTSLIHSLIEESQNQQEKNEQELLELDKWAS-Z
    X-YTSLIHSLIEESQNQQEKNEQELLELDKWASL-Z
    X-YTSLIHSLIEESQNQQEKNEQELLELDKWASLW-Z
    X-YTSLIHSLIEESQNQQEKNEQELLELDKWASLWN-Z
    X-YTSLIHSLIEESQNQQEKNEQELLELDKWASLWNW-Z
    X-YTSLIHSLIEESQNQQEKNEQELLELDKWASLWNWF-Z
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The one letter amino acid code is used.

Additionally,

"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (FMOC) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

TABLE IA DP178 (SEQ ID:1) AMINO TRUNCATIONS

```
X-NWF-Z
                                                    X-WNWF-Z
                                                   X-LWNWF-Z
                                                  X-SLWNWF-Z
                                                 X-ASLWNWF-Z
                                                X-WASLWNWF-Z
                                               X-KWASLWNWF-Z
                                              X-DKWASLWNWF-Z
                                             X-LDKWASLWNWF-Z
                                            X-ELDKWASLWNWF-Z
                                           X-LELDKWASLWNWF-Z
                                          X-LLELDKWASLWNWF-Z
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                                         X-ELLELDKWASLWNWF-Z
                                        X-QELLELDKWASLWNWF-Z
                                       X-EQELLELDKWASLWNWF-Z
                                      X-NEQELLELDKWASLWNWF-Z
                                    X-KNEQELLELDKWASLWNWF-Z
                                   X-EKNEQELLELDKWASLWNWF-Z
                                  X-QEKNEQELLELDKWASLWNWF-Z
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                                 X-QQEKNEQELLELDKWASLWNWF-Z
                                X-NQQEKNEQELLELDKWASLWNWF-Z
                               X-QNQQEKNEQELLELDKWASLWNWF-Z
                              X-SQNQQEKNEQELLELDKWASLWNWF-Z
                             X-ESQNQQEKNEQELLELDKWASLWNWF-Z
                            X-EESQNQQEKNEQELLELDKWASLWNWF-Z
                           X-IEESQNQQEKNEQELLELDKWASLWNWF-Z
                          X-LIEESQNQQEKNEQELLELDKWASLWNWF-Z
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                         X-SLIEESQNQQEKNEQELLELDKWASLWNWF-Z
                        X-HSLIEESQNQQEKNEQELLELDKWASLWNWF-Z
                       X-IHSLIEESQNQQEKNEQELLELDKWASLWNWF-Z
                      X-LIHSLIEESQNQQEKNEQELLELDKWASLWNWF-Z
                     X-SLIHSLIEESQNQQEKNEQELLELDKWASLWNWF-Z
                    X-TSLIHSLIEESQNQQEKNEQELLELDKWASLWNWF-Z
                   X-YTSLIHSLIEESQNQQEKNEQELLELDKWASLWNWF-Z
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The one letter amino acid code is used.

Additionally,

"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

The peptides of the inventi n also include DP178like peptides. "DP178-like", as used herein, refers, first, to DP178 and DP178 truncations which contain one or more amino acid substitutions, insertions and/or deletions. Second, "DP-178-like" refers to peptide sequences identified or recognized by the ALLMOTI5, 107x178x4 and PLZIP search motifs described herein, having structural and/or amino acid motif similarity to DP178. The DP178-like peptides of the invention may exhibit antifusogenic or antiviral activity, or may exhibit the ability to modulate intracellular processes involving coiled-coil peptides. Further, such DP178-like peptides may possess additional advantageous features, such as, for example, increased bioavailability, and/or stability, or reduced host immune recognition.

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HIV-1 and HIV-2 enveloped proteins are structurally distinct, but there exists a striking amino acid conservation within the DP178-corresponding regions of HIV-1 and HIV-2. The amino acid conservation is of a periodic nature, suggesting some conservation of structure and/or function. Therefore, one possible class of amino acid substitutions would include those amino acid changes which are predicted to stabilize the structure of the DP178 peptides of the invention. Utilizing the DP178 and DP178 analog sequences described herein, the skilled artisan can readily compile DP178 consensus sequences and ascertain from these, conserved amino acid residues which would represent preferred amino acid substitutions.

The amino acid substitutions may be of a conserved or non-conserved nature. Conserved amino acid substitutions consist of replacing one or more amino acids of the DP178 (SEQ ID:1) peptide sequence with amino acids of similar charge, size, and/or

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hydrophobicity characteristics, such as, for example, a glutamic acid (E) to aspartic acid (D) amino acid substitution. Non-conserved substitutions consist of replacing one or more amino acids of the DP178 (SEQ ID:1) peptide sequence with amino acids possessing dissimilar charge, size, and/or hydrophobicity characteristics, such as, for example, a glutamic acid (E) to valine (V) substitution.

Amino acid insertions may consist of single amino acid residues or stretches of residues. insertions may be made at the carboxy or amino terminal end of the DP178 or DP178 truncated peptides, as well as at a position internal to the peptide. Such insertions will generally range from 2 to 15 amino acids in length. It is contemplated that insertions made at either the carboxy or amino terminus of the peptide of interest may be of a broader size range, with about 2 to about 50 amino acids being preferred. One or more such insertions may be introduced into DP178 (SEQ.ID:1) or DP178 truncations, as long as such insertions result in peptides which may still be recognized by the 107x178x4, ALLMOTI5 or PLZIP search motifs described herein, or may, alternatively, exhibit antifusogenic or antiviral activity, or exhibit the ability to modulate intracellular processes involving coiled-coil peptide structures.

Preferred amino or carboxy terminal insertions are peptides ranging from about 2 to about 50 amino acid residues in length, corresponding to gp41 protein regions either amino to or carboxy to the actual DP178 gp41 amino acid sequence, respectively. Thus, a preferred amino terminal or carboxy terminal amino acid insertion would contain gp41 amino acid sequences found immediately amino to or carboxy to the DP178 region of the gp41 protein.

Deletions of DP178 (SEQ ID:1) or DP178 truncations are also within the scope of the invention. Such deletions consist of the removal of one or more amino acids from the DP178 or DP178-like peptide sequence, with the lower limit length of the resulting peptide sequence being 4 to 6 amino acids. Such deletions may involve a single contiguous or greater than one discrete portion of the peptide sequences. One or more such deletions may be introduced into DP178 (SEQ.ID:1) or DP178 truncations, as long as such deletions result in peptides which may still be recognized by the 107x178x4, ALLMOTI5 or PLZIP search motifs described herein, or may, alternatively, exhibit antifusogenic or antiviral activity, or exhibit the ability to modulate intracellular processes involving coiled-coil peptide structures.

DP178 analogs are further described, below, in Section 5.3.

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5.2. DP107 AND DP107-LIKE PEPTIDES

Further, the peptides of the invention include peptides having amino acid sequences corresponding to DP107 analogs. DP107 is a 38 amino acid peptide which exhibits potent antiviral activity, and corresponds to residues 558 to 595 of HIV-1_{LAI} transmembrane (TM) gp41 protein, as shown here:

 $\mathrm{NH_{2}} ext{-}\mathrm{NNLLRAIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ-COOH}$ (SEQ ID:25)

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In addition to the full-length DP107 (SEQ ID:25) 38-mer, the peptides of the invention may include truncations of the DP107 (SEQ ID:25) peptide which exhibit antifusogenic activity, antiviral activity and/or the ability to modulate intracellular processes

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involving coiled-coil peptide structures. Truncations of DP107 (SEQ ID:25) peptides may comprise peptides of between 3 and 38 amino acid residues (i.e., peptides ranging in size from a tripeptide to a 38-mer polypeptide), as shown in Tables II and IIA, below. Peptide sequences in these tables are listed from amino (left) to carboxy (right) terminus. "X" may represent an amino group (-NH $_2$) and "Z" may represent a carboxyl (-COOH) group. Alternatively, "X" may represent a hydrophobic group, including but not limited to carbobenzyl, dansyl, or T-butoxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (FMOC) group; or a covalently attached macromolecular group, including but not limited to a lipid-fatty acid conjugate, polyethylene glycol, carbohydrate or peptide group. Further, "2" may represent an amido group; a T-butoxycarbonyl group; or a covalently attached macromolecular group, including but not limited to a lipid-fatty acid conjugate, polyethylene glycol, carbohydrate or peptide group. A preferred "X" or "Z" macromolecular group is a peptide group.

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TABLE II DP107 (SEQ ID:25) CARBOXY TRUNCATIONS

X-NNL-Z X-NNLL-Z X-NNLLR-Z X-NNLLRA-Z X-NNLLRAI-Z X-NNLLRAIE-Z X-NNLLRAIEA-2 X-NNLLRAIEAQ-Z X-NNLLRAIEAQQ-Z X-NNLLRAIEAQQH-Z X-NNLLRAIEAQQHL-Z 10 X-NNLLRAIEAQQHLL-Z X-NNLLRAIEAQQHLLQ-Z X-NNLLRAIEAQQHLLQL-Z X-NNLLRAIEAQQHLLQLT-Z X-NNLLRAIEAQQHLLQLTV-Z X-NNLLRAI EAQQHLLQLTVW-Z X-NNLLRAI EAQQHLLQLTVWQ-Z X-NNLLRAIEAQQHLLQLTVWQI-Z X-NNLLRAI EAQQHLLQLTVWQIK-Z X-NNLLRAIEAQQHLLQLTVWQIKQ-Z X-NNLLRAIEAQQHLLQLTVWQIKQL-Z X-NNLLRAIEAQQHLLQLTVWQIKQLQ-Z X-NNLLRAIEAQQHLLQLTVWQIKQLQA-Z X-NNLLRAIEAQQHLLQLTVWQIKQLQAR-Z X-NNLLRAIEAQQHLLQLTVWQIKQLQARI-Z X-NNLLRAIEAQQHLLQLTVWQIKQLQARIL-Z X-NNLLRAIEAQQHLLQLTVWQIKQLQARILA-Z X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAV-Z X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAVE-Z X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAVER-Z X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAVERY-Z X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAVERYL-Z 25 X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAVERYLK-Z X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAVERYLKD-Z X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ-Z

The one letter amino acid code is used.

Additionally,

"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (FMOC) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

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"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

TABLE IIA DP178 (SEO ID:25) AMINO TRUNCATIONS

```
X-KDQ- Z
                                                    X-LKDQ- Z
                                                   X-YLKDQ- Z
  5
                                                  X-RYLKDQ-
                                                            Z
                                                 X-ERYLKDQ-
                                                            Z
                                                X-VERYLKDQ- Z
                                               X-AVERYLKDQ- Z
                                              X-LAVERYLKDQ- Z
                                             X-ILAVERYLKDQ-
                                                            Z
                                            X-RILAVERYLKDQ-
                                                            Z
 10
                                          X-ARILAVERYLKDQ- Z
                                         X-QARILAVERYLKDQ- Z
                                        X-LQARILAVERYLKDQ- Z
                                       X-QLQARILAVERYLKDQ- Z
                                      X-KQLQARILAVERYLKDQ- Z
                                     X-IKQLQARILAVERYLKDQ-
                                                            Z
                                    X-QIKQLQARILAVERYLKDQ- Z
                                   X-WQIKQLQARILAVERYLKDQ- Z
15
                                  X-VWQIKQLQARILAVERYLKDQ- Z
                                 X-TVWQIKQLQARILAVERYLKDQ- Z
                                X-LTVWQIKQLQARILAVERYLKDQ-
                               X-QLTVWQIKQLQARILAVERYLKDQ-
                                                           2
                             X-LQLTVWQIKQLQARILAVERYLKDQ- Z
                            X-LLQLTVWQIKQLQARILAVERYLKDQ- Z
                           X-HLLQLTVWQIKQLQARILAVERYLKDQ-
                                                           Z
                          X-QHLLQLTVWQIKQLQARILAVERYLKDQ-
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                         X-QQHLLQLTVWQIKQLQARILAVERYLKDQ- Z
                        X-AQQHLLQLTVWQIKQLQARILAVERYLKDQ- Z
                       X-EAQQHLLQLTVWQIKQLQARILAVERYLKDQ- Z
                      X-IEAQQHLLQLTVWQIKQLQARILAVERYLKDQ- Z
                     X-AIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ-
                    X-RAIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ-
                   X-LRAIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ- Z
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                  X-LLRAIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ- Z
                 X-NLLRAIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ- Z
                X-NNLLRAIEAQQHLLQLTVWQIKQLQARILAVERYLKDQ- Z
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The one letter amino acid code is used.

Additionally,

"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

The peptides of the inv ntion also include DP107-"DP107-like", as used herein, refers, like peptides. first, to DP107 and DP107 truncations which contain one or more amino acid substitutions, insertions and/or deletions. Second, "DP-107-like" refers to peptide sequences identified or recognized by the ALLMOTI5, 107x178x4 and PLZIP search motifs described herein, having structural and/or amino acid motif similarity to DP107. The DP107-like peptides of the invention may exhibit antifusogenic or antiviral activity, or may exhibit the ability to modulate intracellular processes involving coiled-coil Further, such DP107-like peptides may peptides. possess additional advantageous features, such as, for example, increased bioavailability, and/or stability, or reduced host immune recognition.

HIV-1 and HIV-2 enveloped proteins are structurally distinct, but there exists a striking amino acid conservation within the DP107-corresponding regions of HIV-1 and HIV-2. The amino acid conservation is of a periodic nature, suggesting some conservation of structure and/or function. Therefore, one possible class of amino acid substitutions would include those amino acid changes which are predicted to stabilize the structure of the DP107 peptides of the invention. Utilizing the DP107 and DP107 analog sequences described herein, the skilled artisan can readily compile DP107 consensus sequences and ascertain from these, conserved amino acid residues which would represent preferred amino acid substitutions.

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The amino acid substitutions may be of a conserved or non-conserved nature. Conserved amino acid substitutions consist of replacing one or more amino acids of the DP107 (SEQ ID:25) peptide sequence with amino acids of similar charge, size, and/or

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hydrophobicity characteristics, such as, for example, a glutamic acid (E) to aspartic acid (D) amino acid substitution. Non-conserved substitutions consist of replacing one or more amino acids of the DP107 (SEQ ID:25) peptide sequence with amino acids possessing dissimilar charge, size, and/or hydrophobicity characteristics, such as, for example, a glutamic acid (E) to valine (V) substitution.

Amino acid insertions may consist of single amino acid residues or stretches of residues. insertions may be made at the carboxy or amino terminal end of the DP107 or DP107 truncated peptides, as well as at a position internal to the peptide. Such insertions will generally range from 2 to 15 amino acids in length. It is contemplated that insertions made at either the carboxy or amino terminus of the peptide of interest may be of a broader size range, with about 2 to about 50 amino acids being preferred. One or more such insertions may be introduced into DP107 (SEQ.ID:25) or DP107 truncations, as long as such insertions result in peptides which may still be recognized by the 107x178x4, ALLMOTI5 or PLZIP search motifs described herein, or may, alternatively, exhibit antifusogenic or antiviral activity, or exhibit the ability to modulate intracellular processes involving coiled-coil peptide structures.

Preferred amino or carboxy terminal insertions are peptides ranging from about 2 to about 50 amino acid residues in length, corresponding to gp41 protein regions either amino to or carboxy to the actual DP107 gp41 amino acid sequence, respectively. Thus, a preferred amino terminal or carboxy terminal amino acid insertion would contain gp41 amino acid sequences found immediately amino to or carboxy to the DP107 region of the gp41 protein.

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Del tions of DP107 (SEQ ID:25) r DP178 truncations are also within the scope of the invention. Such deletions consist of the removal of one or more amino acids from the DP107 or DP107-like peptide sequence, with the lower limit length of the resulting peptide sequence being 4 to 6 amino acids. Such deletions may involve a single contiquous or greater than one discrete portion of the peptide sequences. One or more such deletions may be introduced into DP107 (SEQ.ID:25) or DP107 truncations, as long as such deletions result in peptides which may still be recognized by the 107x178x4, ALLMOTI5 or PLZIP search motifs described herein, or may, alternatively, exhibit antifusogenic or antiviral activity, or exhibit the ability to modulate intracellular processes involving coiled-coil peptide structures.

DP107 and DP107 truncations are more fully described in Applicants' co-pending U.S. Patent Application Ser. No. 08/374,666, filed January 27, 1995, and which is incorporated herein by reference in its entirety. DP107 analogs are further described, below, in Section 5.3.

5.3. DP107 and DP178 ANALOGS

Peptides corresponding to analogs of the DP178, DP178 truncations, DP107 and DP107 truncation sequences of the invention, described, above, in Sections 5.1 and 5.2 may be found in other viruses, including, for example, non-HIV-1_{LAI} enveloped viruses, non-enveloped viruses and other non-viral organisms.

The term "analog", as used herein, refers to a peptide which is recognized or identified via the 107x178x4, ALLMOTI5 and/or PLZIP search strategies discussed below. Further, such peptides may exhibit antifusogenic capability, antiviral activity, or the

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ability to modulate intracellular processes involving coiled-coil structures.

Such DP178 and DP107 analogs may, for example, correspond to peptide sequences present in TM proteins of enveloped viruses and may, additionally correspond 5 to peptide sequences present in non enveloped and nonviral organisms. Such peptides may exhibit antifusogenic activity, antiviral activity, most particularly antiviral activity which is specific to the virus in which their native sequences are found, or may exhibit an ability to modulate intracellular processes involving coiled-coil peptide structures.

DP178 analogs are peptides whose amino acid sequences are comprised of the amino acid sequences of peptide regions of, for example, other (i.e., other than HIV-1_{LAI}) viruses that correspond to the gp41 peptide region from which DP178 (SEQ ID:1) was derived. Such viruses may include, but are not limited to, other HIV-1 isolates and HIV-2 isolates. DP178 analogs derived from the corresponding gp41 peptide region of other (<u>i.e.</u>, non $HIV-1_{LAI}$) HIV-1isolates may include, for example, peptide sequences as shown below.

NH2-YTNTIYTLLEESQNQQEKNEQELLELDKWASLWNWF-COOH (DP-185; SEQ 25 ID:3);

NH2-YTGIIYNLLEESQNQQEKNEQELLELDKWANLWNWF-COOH (SEQ ID:4);

NH2-YTSLIYSLLEKSQIQQEKNEQELLELDKWASLWNWF-COOH (SEQ ID:5). 30

SEQ ID:3 (DP-185), SEQ ID:4, and SEQ ID:5 are derived from $HIV-1_{SF2}$, $HIV-1_{RF}$, and $HIV-1_{MN}$ isolates, respectively. Underlined amino acid residues refer to those residues that differ from the corresponding position in the DP178 (SEQ ID:1) peptide. One such

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DP178 anal g, DP-185 (SEQ ID:3), is described in the Example presented in Section 6, below, where it is demonstrated that DP-185 (SEQ ID:3) exhibits antiviral The DP178 analogs of the invention may also include truncations, as described above. Further, the analogs of the invention modifications such those described for DP178 analogs in Section 5.1., above. It is preferred that the DP178 analogs of the invention represent peptides whose amino acid sequences correspond to the DP178 region of the gp41 protein, it is also contemplated that the peptides of the invention may, additionally, include amino sequences, ranging from about 2 to about 50 amino acid residues in length, corresponding to gp41 protein regions either amino to or carboxy to the actual DP178 amino acid sequence.

Striking similarities, as shown in FIG. 1, exist within the regions of HIV-1 and HIV-2 isolates which correspond to the DP178 sequence. A DP178 analog derived from the HIV-2_{NIHZ} isolate has the 36 amino acid sequence (reading from amino to carboxy terminus):

NH2-LEANISQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-COOH (SEQ ID:7)

Table III and Table IV show some possible truncations of the HIV-2_{NUHZ} DP178 analog, which may comprise peptides of between 3 and 36 amino acid residues (i.e., peptides ranging in size from a tripeptide to a 36-mer polypeptide). Peptide sequences in these tables are listed from amino (left) to carboxy (right) terminus. "X" may represent an amino group (-NH₂) and "Z" may represent a carboxyl (-COOH) group.

Alternatively, "X" may represent a hydrophobic group, including but not limited to carbobenzyl, dansyl, or T-butoxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (FMOC) group; or a

covalently attached macromolecular group, including but not limited to a lipid-fatty acid conjugate, polyethylene glycol, carbohydrate or peptide group. Further, "Z" may represent an amido group; a T=butoxycarbonyl group; or a covalently attached macromolecular group, including but not limited to a lipid-fatty acid conjugate, polyethylene glycol, carbohydrate or peptide group. A preferred "X" or "Z" macromolecular group is a peptide group.

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TABLE III

HIV-2_{NDZ} DP178 analog carboxy truncations.

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X-LEA-Z
   X-LEAN-Z
   X-LEANI-Z
   X-LEANIS-Z
  X-LEANISQ-Z
   X-LEANISQS-Z
   X-LEANISQSL-Z
   X-LEANISQSLE-Z
    X-LEANISQSLEQ-Z
    X-LEANISQSLEQA-Z
    X-LEANISQSLEQAQ-Z
   X-LEANISQSLEQAQI-Z
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    X-LEANISQSLEQAQIQ-Z
    X-LEANISQSLEQAQIQQ-Z
    X-LEANISQSLEQAQIQQE-Z
    X-LEANISQSLEQAQIQQEK-Z
    X-LEANISQSLEQAQIQQEKN-Z
    X-LEANISQSLEQAQIQQEKNM-Z
    X-LEANISQSLEQAQIQQEKNMY-Z
   X-LEANISQSLEQAQIQQEKNMYE-Z
    X-LEANISQSLEQAQIQQEKNMYEL-Z
    X-LEANISQSLEQAQIQQEKNMYELQ-Z
    X-LEANISQSLEQAQIQQEKNMYELQK-Z
    X-LEANISQSLEQAQIQQEKNMYELQKL-Z
    X-LEANISQSLEQAQIQQEKNMYELQKLN-Z
    X-LEANISQSLEQAQIQQEKNMYELQKLNS-Z
    X-LEANISQSLEQAQIQQEKNMYELQKLNSW-Z
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    X-LEANISQSLEQAQIQQEKNMYELQKLNSWD-Z
    X-LEANISQSLEQAQIQQEKNMYELQKLNSWDV-Z
    X-LEANISQSLEQAQIQQEKNMYELQKLNSWDVF-Z
    X-LEANISQSLEQAQIQQEKNMYELQKLNSWDVFT-Z
    X-LEANISQSLEQAQIQQEKNMYELQKLNSWDVFTN-Z
    X-LEANISQSLEQAQIQQEKNMYELQKLNSWDVFTNW-Z
    X-LEANISQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z
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The one letter amino acid code is used.

Additionally,

"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (FMOC) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

TABLE IV HIV-2_{NHZ} DP178 analog amino truncations.

X-NWL-Z X-TNWL-Z X-FTNWL-Z X-VFTNWL-Z X-DVFTNWL-Z X-WDVFTNWL-Z X-SWDVFTNWL-Z X-NSWDVFTNWL-Z X-LNSWDVFTNWL-Z X-KLNSWDVFTNWL-Z X-QKLNSWDVFTNWL-Z X-LQKLNSWDVFTNWL-Z 10 X-ELQKLNSWDVFTNWL-Z X-YELQKLNSWDVFTNWL-Z X-MYELQKLNSWDVFTNWL-2 X-NMYELQKLNSWDVFTNWL-Z X-KNMYELQKLNSWDVFTNWL-Z X-EKNMYELQKLNSWDVFTNWL-Z X-QEKNMYELQKLNSWDVFTNWL-Z 15 X-QQEKNMYELQKLNSWDVFTNWL-Z X-IQQEKNMYELQKLNSWDVFTNWL-Z X-QIQQEKNMYELQKLNSWDVFTNWL-Z X-AQIQQEKNMYELQKLNSWDVFTNWL-Z X-QAQIQQEKNMYELQKLNSWDVFTNWL-2 X-EQAQIQQEKNMYELQKLNSWDVFTNWL-Z X-LEQAQIQQEKNMYELQKLNSWDVFTNWL-Z X-SLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z 20 X-QSLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z X-SQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z X-ISQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z X-NISQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z X-ANISQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z X-EANISQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z X-LEANISQSLEQAQIQQEKNMYELQKLNSWDVFTNWL-Z

The one letter amino acid code is used.

Additionally,

"X" may represent an amino group, a hydrophobic group, including but not limited to carbobenzoxyl, dansyl, or T-butyloxycarbonyl; an acetyl group; a 9-fluorenylmethoxy-carbonyl (FMOC) group; a macromolecular carrier group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

"Z" may represent a carboxyl group; an amido group; a T-butyloxycarbonyl group; a macromolecular carrier
group including but not limited to lipid-fatty acid conjugates, polyethylene glycol, or carbohydrates.

DP178 and DP107 analogs are recognized or identified, for example, by utilizing one or more of the 107x178x4, ALLMOTI5 or PLZIP computer-assisted search strategies described and demonstrated, below, in the Examples presented in Sections 9 through 16 and 19 through 25. The search strategy identifies additional peptide regions which are predicted to have structural and/or amino acid sequence features similar to those of DP107 and/or DP178.

The search strategies are described fully, below, 10 in the Example presented in Section 9. While this search strategy is based, in part, on a primary amino acid motif deduced from DP107 and DP178, it is not based solely on searching for primary amino acid sequence homologies, as such protein sequence homologies exist within, but not between major groups of viruses. For example, primary amino acid sequence homology is high within the TM protein of different strains of HIV-1 or within the TM protein of different isolates of simian immunodeficiency virus (SIV). 20 Primary amino acid sequence homology between HIV-1 and SIV, however, is low enough so as not to be useful. It is not possible, therefore, to find peptide regions similar to DP107 or DP178 within other viruses, or within non-viral organisms, whether structurally, or 25 otherwise, based on primary sequence homology, alone.

Further, while it would be potentially useful to identify primary sequence arrangements of amino acids based on, for example, the physical chemical characteristics of different classes of amino acids rather than based on the specific amino acids themselves, such search strategies have, until now, proven inadequate. For example, a computer algorithm designed by Lupas et al. to identify coiled-coil propensities of regions within proteins (Lupas, A., et al., 1991 Science 252:1162-1164) is inadequate for

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identifying protein regions analogous to DP107 or DP178.

Specifically, analysis of HIV-1 gp160 (containing both gp120 and gp41) using the Lupas algorithm does not identify the coiled-coil region within DP107. It does, however, identify a region within DP178 beginning eight amino acids N-terminal to the start of DP178 and ending eight amino acids from the C-terminus. The DP107 peptide has been shown experimentally to form a stable coiled coil. A search based on the Lupas search algorithm, therefore, would not have identified the DP107 coiled-coil region. Conversely, the Lupas algorithm identified the DP178 region as a potential coiled-coil motif. However, the peptide derived from the DP178 region failed to form a coiled coil in solution.

A possible explanation for the inability of the Lupas search algorithm to accurately identify coiled-coil sequences within the HIV-1 TM, is that the Lupas algorithm is based on the structure of coiled coils from proteins that are not structurally or functionally similar to the TM proteins of viruses, antiviral peptides (e.g. DP107 and DP178) of which are an object of this invention.

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The computer search strategy of the invention, as demonstrated in the Examples presented below, in Sections 9 through 16 and 19 through 25, successfully identifies regions of proteins similar to DP107 or DP178. This search strategy was designed to be used with a commercially-available sequence database package, preferably PC/Gene.

A series of search motifs, the 107x178x4, ALLMOTI5 and PLZIP motifs, were designed and engineered to range in stringency from strict to broad, as discussed in this Section and in Section 9, with 107x178x4 being preferred. The sequences

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> identified via such search motifs, such as those listed in Tables V-XIV, below, potentially exhibit antifusogenic, such as antiviral, activity, may additionally be useful in the identification of antifusogenic, such as antiviral, compounds, and are intended to be within the scope of the invention.

Coiled-coiled sequences are thought to consist of heptad amino acid repeats. For ease of description, the amino acid positions within the heptad repeats are sometimes referred to as A through G, with the first position being A, the second B, etc. The motifs used to identify DP107-like and DP178-like sequences herein are designed to specifically search for and identify such heptad repeats. In the descriptions of each of the motifs described, below, amino acids enclosed by brackets , i.e., [], designate the only amino acid residues that are acceptable at the given position, while amino acids enclosed by braces, i.e., {}, designate the only amino acids which are unacceptable at the given heptad position. When a set of bracketed or braced amino acids is followed by a number in parentheses i.e., (), it refers to the number of subsequent amino acid positions for which the designated set of amino acids hold, e.g, a (2) means "for the next two heptad amino acid positions".

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The ALLMOTIS is written as follows:

 $\{CDGHP\}-\{CFP\}(2)-\{CDGHP\}-\{CFP\}(3)-$ (CDGHP)-{CFP}(2)-{CDGHP}-{CFP}(3)- $\{CDGHP\}-\{CFP\}(2)-\{CDGHP\}-\{CFP\}(3) \{CDGHP\}-\{CFP\}\{2\}-\{CDGHP\}-\{CFP\}\{3\} \{CDGHP\}-\{CFP\}(2)-\{CDGHP\}-\{CFP\}(3)-$

Translating this motif, it would read: "at the first (A) position of the heptad, any amino acid residue except C, D, G, H, or P is acceptable, at the next two (B,C) amino acid positions, any amino acid residue except C, F, or P is acceptable, at the fourth 35 heptad position (D), any amino acid residue except C,

D, G, H, or P is acceptable, at the next three (E, F, G) amino acid positions, any amino acid residue except C, F, or P is acceptable. This motif is designed to search for five consecutive heptad repeats (thus the repeat of the first line five times), meaning that it searches for 35-mer sized peptides. It may also be designed to search for 28-mers, by only repeating the initial motif four times. With respect to the ALLMOTI5 motif, a 35-mer search is preferred. Those viral (non-bacteriophage) sequences identified via such an ALLMOTI5 motif are listed in Table V, below, at the end of this Section. The viral sequences listed in Table V potentially exhibit antiviral activity, may be useful in the the identification of antiviral compounds, and are intended to be within the scope of the invention. In those instances wherein a single gene exhibits greater than one sequence recognized by the ALLMOTI5 search motif, the amino a cid residue numbers of these sequences are listed under "Area 2", Area 3", etc. This convention is used for each of the Tables listed, below, at the end of this Section.

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The 107x178x4 motif is written as follows:

[EFIKLNQSTVWY]-{CFMP}(2)-[EFIKLNQSTVWY]-{CFMP}(3)-[EFIKLNQSTVWY]-{CFMP}(2)-[EFIKLNQSTVWY]-{CFMP}(3)-[EFIKLNQSTVWY]-{CFMP}(2)-[EFIKLNQSTVWY]-{CFMP}(3)-[EFIKLNQSTVWY]-{CFMP}(2)-[EFIKLNQSTVWY]-{CFMP}(3)-

Translating this motif, it would read: "at the first (A) position of the heptad, only amino acid residue E, F, I, K, L, N, Q, S, T, V, W, or Y is acceptable, at the next two (B,C) amino acid positions, any amino acid residue except C, F, M or P is acceptable, at the fourth position (D), only amino acid residue E, F, I, K, L, N, Q, S, T, V, W, or Y is acceptable, at the next three (E, F, G) amino acid positions, any amino acid residue except C, F, M or P is acceptable. This motif is designed to search for

four c nsecutive h ptad repeats (thus the repeat f the first line four times), meaning that it searches for 28-mer sized peptides. It may also be designed to search for 35-mers, by repeating the initial motif five times. With respect to the 107x178x4 motif, a 28-mer search is preferred.

Those viral (non-bacteriophage) sequences identified via such a 107x178x4 motif are listed in Table VI, below, at the end of this Section, with those viral (non-bacteriophage) sequences listed in Table VII, below at the end of this Section, being preferred.

The 107x178x4 search motif was also utilized to identify non-viral procaryotic protein sequences, as listed in Table VIII, below, at the end of this Section. Further, this search motif was used to reveal a number of human proteins. The results of this human protein 107x178x4 search is listed in Table IX, below, at the end of this Section. The sequences listed in Tables VIII and IX, therefore, reveal peptides which may be useful as antifusogenic compounds or in the identification of antifusogenic compounds, and are intended to be within the scope of the invention.

The PLZIP series of motifs are as listed in FIG.

19. These motifs are designed to identify leucine zipper coiled-coil like heptads wherein at least one proline residue is present at some predefined distance N-terminal to the repeat. These PLZIP motifs find regions of proteins with similarities to HIV-1 DP178 generally located just N-terminal to the transmembrane anchor. These motifs may be translated according to the same convention described above. Each line depicted in FIG. 19 represents a single, complete search motif. "X" in these motifs refers to any amino acid residue. In instances wherein a motif contains

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two numbers within parentheses, this refers to a variable number of amino acid residues. For example, X (1,12) is translated to "the next one to twelve amino acid residues, inclusive, may be any amino acid".

Tables X through XIV, below, at the end of this Section, list sequences identified via searches conducted with such PLZIP motifs. Specifically, Table X lists viral sequences identified via PCTLZIP, P1CTLZIP and P2CTLZIP search motifs, Table XI lists viral sequences identified via P3CTLZIP, P4CTLZIP, P5CTLZIP and P6CTLZIP search motifs, Table XII lsts viral sequences identified via P7CTLZIP, P8CTLZIP and P9CTLZIP search motifs, Table XIII lists viral sequences identified via P12LZIPC searches and Table XIV lists viral sequences identified via P23TLZIPC search motifs The viral sequences listed in these tables represent peptides which potentially exhibit antiviral activity, may be useful in the identification of antiviral compounds, and are intended to be within the scope of the invention.

The Examples presented in Sections 17, 18, 26 and 27 below, demonstrate that viral sequences identified via the motif searches described herein identify substantial antiviral characteristics. Specifically, the Example presented in Section 17 describes peptides with anti-respiratory syncytial virus activity, the Example presented in Section 18 describes peptides with anti-parainfluenza virus activity, the Example presented in Section 26 describes peptides with anti-measles virus activity and the Example presented in Section 27 describes peptides with anti-simian immunodeficiency virus activity.

The DP107 and DP178 analogs may, further, contain any of the additional groups described for DP178, above, in Section 5.1. For example, these peptides

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> may include any of the additional amino-terminal groups as described above for "X" groups, and may also include any of the carboxy-terminal groups as described, above, for "2" groups.

Additionally, truncations of the identified DP107 and DP178 peptides are among the peptides of the invention. Further, such DP107 and DP178 analogs and DP107/DP178 analog truncations may exhibit one or more amino acid substitutions, insertion, and/or deletions. The DP178 analog amino acid substitutions, insertions 10 and deletions, are as described, above, for DP178-like peptides in Section 5.1. The DP-107 analog amino acid substitutions, insertions and deletions are also as described, above, for DP107-like peptides in Section 5.2.

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Tables XV through XXII, below, present representative examples of such DP107/DP178 truncations. Specifically, Table XV presents Respiratory Syncytial Virus F1 region DP107 analog carboxy truncations, Table XVI presents Respiratory Syncytial Virus F1 region DP107 analog amino truncations, Table XVII presents Respiratory Syncytial Virus F1 region DP178 analog carboxy truncations, Table XVIII presents Respiratory Syncytial Virus F1 region DP178 analog amino truncations, Table XIX 25 presents Human Parainfluenza Virus 3 F1 region DP178 analog carboxy truncations, Table XX presents Human Parainfluenza Virus 3 F1 region DP178 analog amino truncations, Table XXI presents Human Parainfluenza Virus 3 F1 region DP107 analog carboxy truncations and Table XXII presents Human Parainfluenza Virus 3 F1 region DP107 analog amino truncations. Further, Table XXIII, below, presents DP107/DP178 analogs and analog truncations which exhibit substantial antiviral activity. These antiviral peptides are grouped 35 according to the specific virus which they inhibit,

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including respiratory syncytial virus, human parainfluenza virus 3, simian immunodeficiency virus and measles virus.

TABLE V

ALLMOTIS SEARCH RESULTS SUMMARY

FOR ALL VIRAL (NON-BACTERIOPHAGE) PROTEINS

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PCGENE	ALLMOTIS	(All Virgin (na betierloghages)		li		7		- 1		
CULKANE	PAGITIE	YRUS	7	41.0	3		34	7	700.4	
PINK TRVPS	POTENTIAL IN KD PROTEIN	TOBACCO RATTLE VIAUS (STRAIN PSO)	6				1000	1		1
PIGE TRYST	POTENTIAL IN KD PROTEIN	TOBACCO RATTLE VIRUS (STRAIN SYN)	2	10.5	2		7	1		· ::
DOVEN CHES	SS 8 KD PROTEIN	HERPES SDIPLEX VIRUS (TYPE 6 / STRAIN UGANDA-1101)	2							:
PAAMT MOVAM	DELTA ANTICEN	HEPATITIS DELTA VIRUS (ISOLATE AMERICAN)		201-80			1			:
ושאשו ושאאו		HEPATITIS DELTA MINUS (ISOLATE DING)	**/							:
PAAMT MOVIT	DELTA ANTIGEN (ALPHA ANTIGEM)	HEPATITIS DELTA YTHUS (ISOLATE ITALIAN)	7	100					•	
PAANT HOVE!	DELTA ANTIGEN	HEPATITIS DELTA VIRUS (ISOLATE LERANON-I)	7							:
PAAMT HOWAL	DELTA ANTIGEN	INEPATITIS DELTA VIRUS (ISOLATE JAPANESE AI-1)		8					1	:
PAAM MOVAD	DELTA ANTIGEN	HEPATITIS DELTA VIRUS (ISOLATE JAPANESE NI-1)	7	B						
PAANT HOWIA	DELTA ANTIGEN	HEPATITIS DELTA VIKUS (ISOCATÉ MAURU)	=	<u>₹</u>						
PAANT HOYSI	DELTA ANTIGEN	HEPATITIS DELTA VIRUS (ISOLATE JAPANESE S-1)	£:	2 8						
PANT NOVS	DELTA ANTIGEN	INEPATITIS DELTA VIRUS (ISOLATE JAPANESE 5-1)	ş	≅ ₹						!
PANT IDVWO	DELTA ANTIGEN	HEPATITIS DELTA VIAUS (ISOLATE WOORCINCK).	1.4	100-144	-				j	
PATCH FONTIA	ANTITHOUGH HIS HOMOLOG	FOWEPOX VIRUS (ISOLATE IP-434)	11-110							:
PATH VACCV	IN KD A. TYPE INCLUSION PROTEIN	VACCINIA VIRUS (STRAIN WR)	18.87	430-564	130-425					:
PATI! VARV		VARIOLA VIRUS	413-525	\$95-165	171-621					
PATTI MEVIT	ALTHA TRANS-INDUCING PACTOR	HERPES SIMPLEX YIRUS (TYPE.I)	304.345							
L	AL PHA TRANS CHOICENS PACTOR	HEAPES SDAPLEX VIRUS (TYPE I)	102-139	304-345						
L	AL PHA TRANS DEDICTING FACTOR	EQUINE MERPES VIXUS TYPE I (STRAIN ABAP)	101-101	764-33						
L	PLEATURE ALTYPE INCLUSION PROTEIN	VACCINIA VIRUS (STRAIN COPENHAGEN)	79-134	19.763						
L	PLITATIVE A-TYPE DAT USION PROTEIN	VACCINIA VIRUS	76-134					,		
L	AL PHA TRANS-INDUCING PACTOR	WARICELLA-ZOSTER VIRUS (STRAIN DUNIAS)	396-361	195.420						
L	PLITATIVE A-TYPE INCLUSION PROTEIN	VACCINIA VIRUS	21-32 22-32							
1	AL PHA TRANS-INDUCING PROTEIN (VIAW61)	HERPES SOURCEX VOLUS (TYPE 2)	616-96	324.311						
1_	AL PHA TILANS DIGUCING PROTEIN (YANNES)	HERPES SIMPLEX VIRUS (TYPE 1)	111-122	134-381						
L	ALMA TILMS-INDUCING PROTEIN	BOVINE HEAPESVIAUS TYPE !	191.256							
1_	ALMA TILANS INDUCTING PROTEIN	EQUINE HELDESVIRUS TYPE I	241-239							_:
PATEN YZVD	ALTHA TAMBINDUCING PROTEIN (VARICELLA-ZOSTER VIRUS (STRAIN DUNIAS)	206-252							:
PATI COUPX	A-TYPE DICLUSION PROTEIN	COWTOX VIRUS.	14.57	425-526	112-366	\$72-439	66-603	1106-1150		:
PRD4.3 EBV	PROTEIN BOLF1	EPSTEIN-BARK VIRUS (STRAIN BPS-8)	161-06							
PBRL1 EBV	TRANSCRUTTION ACTIVATOR BRLF!	EPSTEIN-BARK VIRUS (STRAIN B95-8)	180-187					-		; ;
ICOA! POVBA	COAT PROTEIN VP	POLYONGAVIRUS BK	101.141							
PCOAT POWER	COAT PROTEIN VP.	POLYOMAYTRUS BK	107-141							:
PCOA! POWA	COAT PROTEIN VPI	HAMSTER POLYONAVIRUS	159-195							
PCOAL SV40	COAT PROTEIN VP	SDAIAN VIRUS 40	19:16					-	1	
HCOA1 BFDV	COAT PROTED VP2	RUDGERIGAR FLEDGLING DISEASE VIRUS	<u>=</u>				-		-	
PCOA1 POVBA	COAT PROTEIN VP2	POLYOMAYTHUS BK (STRAIN AS)	3	113						:
PCOA1 POYBK	COAT PROTEIN VP2	POL YOMAYTRUS BK	\$	13.35						:
PCOAL POYBO	COAT PROTEIN VP2	BOYINE POLYOMAVIRUS	2	2					İ	
PCOAL POWIA	COAT PROTEIN VP2	HAMSTER POLYONAVIRUS	=	Z .						:
PCOAL POVIC	COAT PROTEIN VP3	POCYOMAYTHUS IC	3	. W.						:
PCOAL POYLY	COAT PROTEIN VP2	LYNDHOTHOPIC POLYGMAVIAUS	-	20.30						
PCON, POWO	COAT PROTEIN VP2	MOUSE POLYOMAVIRUS (STRAIN))	=							
PCOA3 POVACA	COAT PROTEIN VP2	MOUSE POLYGMAVIRUS.	=	<u>=</u>						
PCOAL POWAC	COAT PROTEIN VP2	MOUSE POLYOMAVIRUS	=======================================	33.18						-
PCOAJ POWAR	COAT PROTEIN VP2	INDUSE POLYOMAVIRUS	2							.1
MON SVE	COAT PROTEIN VP3	SDGAN VIRUS 40	7	236-362	<u>=</u>					
PCOAT ABANW	COAT PROTEIN	ABUTELON MOSAIC VIRUS (ISOLATE WEST INDIA	2.0							-
PCOAT ACLSV	COAT PROTEIN	APPLE CHEOROTIC LEAF SPOT VIRUS	=							
PCOAT AEDEV	COAT PROTEDI VPI	AEDES DENSONUCLEOSIS VIXUS	2							
POOKT ALCV	COAT PROTEIN	AATICHOKE MOTTLED CRINKLE VIRUS	2	100-134						
SCOAT BLRV	COAT PROTEN	BEAN LEAFROLL VIRUS	19-12)					_		
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COAT PROTEIN	PCOAT BYDY!	COATPROTECT	AABLEY YELLOW DWALF VIRUS				-			!
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COAT MOTING CALLITOWING NAMES WILLIAM NAMES WASHED	PCOAT BYDY	COAT PROTEIN	BALLEY YELLOW DWALF VIALIS		100,000	-	-			
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COAT FACTER CLAIF GOVER VILLY 11-11 11	PCDAT CAN'N	COAT PROTEIN	CALLIFLOWER MOSAIC VIRUS	3		-				
COAT PROTEIN CARANTERN (SULE) 11-11 11	PCDAT CAMMI	COATPROTEIN	CALL IFLOWER MOSAIC VIRUS		_		-			
COAT PROTEIN CONTEA DELOYING 111-118 1	POONT CAMPS	COAT PROTEIN	CARNATION MOTTLE VIRUS	=		1	 			_
COAT FROTTEN CLANATION ETCRED ENG VALUE 1912 1913	PCOAT CAUM	COAT PROTEIN	FOUNDER CHI ORDITIC NIDITLE VIRUS	2		+	-			
ACASA LATERY NAME VALAGETICA BOTA ALA CILLO VILLS COLT BOTTEN	PCOAT COAN	COAT PROTEIN	CANALTION STORED RING VIRUS	2 ·						!
PALONG LOAD FROTEN CASSAVA LATEAT VIRUS 19111	PCOAT CERV	PROBABLE COAT PROTEIN	SARANGCHIA BIRSARIA CIRORELLA VIRUS I	20.00		1			<u> </u> -	: : i-
COAT PROTECT COAT	PCOAT CANTI	NAJOR CAPSID PROTEIN	CARCELON CONT.	197-331		+				-
COAT PROTEIN CULTABER MISSAIC WILLS 113-111	KOAT CLYK	COAT PROTEIN	CASSACA LA TENT VIBUS	167-231		1			-	
COAT PROTEIN CUCLOBER NOSAIC VRUS 113-181 113-18	PCOAT CLYN	COAT PROTEIN	CASSACE LICENSE	133-117		1			<u> </u>	<u>.</u>
COAT PROTEIN CUCLOBER MOSACY VILLS	COAT CAME	COATPROTEIN	COCONIDER MODELS	15)-11)		-	-		-	
COAT FROTEIN CUCCAGER MOSACY YRUS 115-181	MO YOU	COAT PROTEIN	COLORBEA RICEAST CORTS	133-183				1	-	:
19.181 1	SWO LYON	COAT PROTEIN	COCUMBER RIVERS VITE	193-187					-	:
COAT PROTEIN CUCKABER NEGACIS VIRUS 111-181	PCOAT OWO	COAT PLOTEIN	COCONGER MOSAIC VIEWS	133-187				\downarrow	ļ	-
COAT PAOTEN CUCUMBER NEGOSIS VIRUS 111-161 COAT PAOTEN CUCUMBER NEGOSIS VIRUS 111-161 COAT PAOTEN CTRUS TASTEZA VIRUS 111-101 COAT PAOTEN CLOPEN PROCESS 111-101 COAT PAOTEN CLOPEN PROCESS 111-101 COAT PAOTEN CLOPEN PROCESS 111-101 COAT PAOTEN FELNE CALKIVARUS 111-101 COAT PAOTEN ALLIES STRAK VIRUS 111-101 COAT PAOTEN ALLIES STRAK VIRUS 111-101 COAT PAOTEN POOTAT PAOTEN 111-101	MOAT CHAM.	COAT PROTEIN	CUCUMBER ANGENT TINGS	133-107						:
COAT PROTEIN CUCLMBEA PECADOS VIRUS 18-219 COAT PROTEIN CITAGO STRAITE A VIRUS 18-219 COAT PROTEIN CITAGO STRAITE A VIRUS 18-219 COAT PROTEIN ECCRLANT VIRSAIC VIRUS 18-219 COAT PROTEIN ECCRLANT VIRSAIC VIRUS 18-219 COAT PROTEIN FELNE CALCIVRUS 18-180 18-180 COAT PROTEIN MALES STRAK VIRUS 18-181 18-181 COAT PROTEIN PARATICA STRAK VIRUS 18-181 18-181 COAT PROTEIN PARATICA STRAK VIRUS 18-181 18-181 COAT PROTEIN <td>200</td> <td>COAT PROTEIN</td> <td>CUCUMBER MOSARC VIRUS</td> <td>100</td> <td></td> <td></td> <td></td> <td></td> <td></td> <td>ļ</td>	200	COAT PROTEIN	CUCUMBER MOSARC VIRUS	100						ļ
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COAT PROTEIN ELOPE CLACKVRIUS 131-464 164-400 151-464 164-400 161-164 164-400 161-164 164-400 161-164 164-400 161-164 164-400 161-164		COAT MOTEN	CLOVER YELLOW MOSAIC VIRUS	2.0						1-1
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COAT PAOTEN SELECTOR	POUR POUR	COAT PROTEIN	PELING CALCIVIANO	\$19.53	169-403	-				-
PROBABLE COAT PROTEIN FROWOAT MOSAIC VRUS FEET		COAT PROTEIN	SELINE CALICIVINOS	100		-483		1	1	-
CAPTER PROTECT CAPT	200	PROBABILE COAT PROTEIN	FIGWORT MOSAIC VIRUS	86.130				1		1
CAPSID PROTECH TITULA BLUESCENT VIRUS 51-15	3	COAT PROTEIN	FOXTAR MOSAIC VIRUS	200				4		1
COAT PROTECH STANDAR GALLES VINUS 11-45 11-45	NA PARTY	CAPSED PROTEIN	TIPLE A DESCRIT VINUS	201.00						1
COAT PROTECH CAPTO PROTECH 13-70 215-310	PCOAT BY23	CAPSID PROTEIN	STATE THE COLUMN VALUE	\$ -				1	1	-
COAT PROTEIN MALES STREEK VINUS 117.21	PCDAT BAY	CANSID PROTEIN	CALLO INDESCRIPTION OF THE PROPERTY OF THE PRO	11.70	255-309	1		1		-
COAT PROTEIN WALES STREAK VRUS 111-221	MONT LSV	COAT PROTEIN	MALTE CTRICK VIRUS	3.74	121-21	+		1	-	-
COAT PAOTEIN MALES STRACK VIRLIS 110-221 110-221 110-221 110-221 110-221 120-221	PCOAT METV	COAT PROTEIN	MALES CEREAL VINE	111-231		1	1	1	-	-
COAT PASTEN MAJE STREAK VIRUS 110-121	POOAT MSYK	COAT PLOTEIN	TALLY CTREAK YRUS	117-221		1	+	1	-	1
COAT PAGTERN COAT PAGTERN 10-119 144-410	PCOAT MSWY	COAT MOTEIN	WAIDS STREAM VINE	117-231		1		-	-	-
COAT MOTERN BOTTHE SOUTH PARYOTHUS 180-14 444-440 COAT MOTERN V?	POOAT MEVS	COAT PROTEIN	CHONTOGLOSSUM ICHGSPOT VIRUS	<u>2</u>		1	-		-	
COAT PROTEIN V22 CANING PALVOVRUS 49-131	PCOAT ONSY	COAT PAOTEIN	BOYING PARYOVIRUS	1004	444-480	1	-	-		
COAT MOTERN YT PEA EAULY BROWNEND VIRUS 15-114	PCOAT PAYED	COAT PROTEIN VP2	CANINE PARVOVINUS	37.33	+		-	-		-
COAT MOTEIN POPLAN MOSAIC VRUS 1641 1621 1621 1622 1623	POORT PAYOR	COAT PROTEIN VF!	PEA EARLY BROWNING VIRUS	=	+	+		-		
COAT PROTEIN PEPFER MED MOTTLE VINUS 104-131 151-191 151	PCOAT PEBV	COAT PROTEIN	POPLAR MOSAIC VIRUS	3	+	+		-		-
COAT PROTEIN POTATO VIRUS 19-73 131-731 131-73	PCOAT POPMY	COAT MOTEIN	PEPPER MILD MOTTLE VIRUS	= =	+		1	-		
COAT PLOTED 190-214	PCOAT PPAYS	COAT PROTEIN	PATATO VIRUS	=	721-32	+	+	\downarrow		-
COAT PROTEIN LASPELLY BUSHY DWALE VIRUS 1044 144-179 144	PCOAT PYSP	COAT PROTEIN	MOTATO VELLOW MOSAIC VIRUS	190-224	1	+		-		L
COAT PROTEIN TAB CLOVEN PECHOTIC MOSALC VIRUS 111-306 7 COAT PROTEIN 14-10 11-120	POSAT PYNOV	COAT PROTEIN	TOTAL OFFICE OF STATE VIRUS	10-44	140-199	1		+	+	
V COAT PROTEIN 14-11 11-120	VOLT PADY	COAT PROTEIN	SOURCE SOURCE STORY OF THE	171-306			1		1	
New Johnson Company of the Company o	PCOAT ROAD	COAT PROTEIN	Size states Walls	34-61		Ş		+		
COAT MUTAIN	VEAT LEV	COAT PROTEIN	SCHOOL CAR CINE	190-324						
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1000	CALL DE COURSE	CANTEL THE LALIDE WALLES I TAN LANGLED WRITE	813		7000	Т	Т	Ţ	Τ	1
TON SALE	CONTRACTOR	A LEAGUE FINE FAMILE LAND MARKEY VINCE								Ī
1004 TOO?	COAT MOTEN	SOTREAM CALOROTIC MOTILE VIRUS	170-100					1		
PCOAT STIN'I	COAT PROTEIN	SATELLITE TOBACCO MECROSIS WRUS I	2.2					1		
PCOAT, STIMT	COATPROTEIN	SATELLITE TOBACCO NECROSIS VIRUS 1	116-72							į
PCOAT_TAMV	GENOME POLYPROTEIN	TAMARILO MOSAIC VIRUS	7.55							
PCOAT_TAV	COAT PROTEIN	TOMATO ASPERMY VIRUS	14-48							
PCOAT, TISSVE	COAT PROTEIN	TOMATO BUSHY STUNT VIRUS	1.33	470						
PCOAT TBSVC	COAT PROTEIN	TOMATO BUSKY STUNT VIRUS	44-38	186134						
PCOAT TCV	COAT PROTEIN	TURNIP CALNKLE VIRUS	13.46							
PCOAT TONY	COAT PROTEIN	TOMATO COLDEN MOSAIC VIRUS	186-270				!- !			
PCOAT THOMY	COAT PROTEIN	TOBACCO MILD GREEN MOSAIC VIRUS	103.139							:
PCOAT TAV	COAT PROTES	TOBACCO MOSAIC VIRUS	103:139							
PCOAT THYON	COAT PROTEIN	TOBACCO MOSAIC VIRUS	103-137							
COAT TANCO	COATPROTEN	TOBACCO MOSAIC VIRUS	76-138							İ
PCOAT THYOA	COAT PROTEIN	TOBACCO MOSAIC VIRUS	103-137				Ī	-		
PODAT TAMER	COAT PROTEIN	TOBACCO MOSAIC WRUS	101-117							
PODAT TAMB	COAT PROTEIN	TOBACCO MOSAIC VIRUS	101.117							
1 TAN	COAY DECITIVE	TOBACCO LECENIC VIBILS	101.113							Ī
1000	Cost seconds									
COAL PARTY	CONTROLLIN	TOBACCO MODAIC VINOS								
POWE THATO	COAT PROTEDY	IDBACCO MOSAIC VIRUS	103-137							
COAT TAYER	COAT PROTEIN	TOBACCO KATTLE VIKUS	8							
POONT TRYTIC	COAT PROTEDI	TOBACCO RATTLE VIRUS	69-103							
PCOAT TYDYA	COAT PROTED!	TOBACCO YELLOW DWANT VIRUS	1.36					-		
POOKT TYNON	COAT PROTEIN	TURNIP YELLOW MOSAIC VIRUS	41.75							
PODAT TYNAA	COAT PROTEIN	TURNIP YELLOW MOSAIC VIRUS	41-75							!
PCDAT WCAYO	COAT PROTEIN	WHITE CLOVER MOSAIC VIRUS	163.197							
POOR HOBGS	CONT. ANTICEN	GROUND SQUILLEL HEPATITIS VIRUS	94-135							
PORA HOBVE	COAS ANTIGEN	HEPATITIS B VIRUS	111-140							
POOKA WHY!	CORE ANTIGEN	WOODCHUCK REPATITIS VIRUS I	43-106							
PCORA WINI	COAL ANTICEM	WOODCHUCK HEFATIBIS VIRUS 8	h1.106					 - 		
PD250_ASPB7		AFRICAN SWINE PEVER VIRUS	194-232							
PDYG1 ADEQ1	EAALY E2A DMA-BINDING PROTEIN	HUMAN ADENOVIRUS TYPE 3	:01-336						:	
POPEL ADEBS	BALLY ELA CHA-BINDING PROTEIN	KURIAN ADENOVIRUS TYPI: 9	291-134				-		:	
PONB! EBV	MAJOR DWA-BINDING PROTEIN	EPSTEIN-BARA VIRUS	215-253	116.752	234.1071	10;3:30AR		!	:	
PONB! HOLIVA	MAJOR DNA-BRIDDIO PROTEDI	HUMAN CYTONEGALOVIRUS	116-372	1013-1014						
PONB! HSVI!	MAJOR DIVA-BRIDING PROTEIN	HERPES SIGNLEX VIRUS	187-591	019:005	769.80)	0919-6101				
POYOL HOVE	2.3	HERPES SIMPLEX VIAUS	943-594	140.00	164-803	011-601				
POROL HSVIK	MAJOR DRA-BINDING PROTEIN	HERPES SINITLEX VIRUS	155.404	UT9-145	78-80)	1079.1140				
PONEI HSVB1		BOVINE IERPESVIRUS TVPE. I	152.501	169-661	1041-1131					
	MAJOR DNA-BINDENG PROTEIN	EQUINE IGAPESVIAUS TYPE I	233-314				i İ		:	
l	MAJOR DNA-BINDING PROTEIN	EQUINE HERPESVIAUS TYPE. I	117-454	1107-1148						
1 1	MAJOR DNA-BINDING PROTEIN	herpesyrus sainiiri		130-167	506-517	131.707				
	MAJOR DNA-BINDING PROTEIN	murine cytoaregalovirus	584-612	417.1175						
POMBI FORMS	ALLIOR DIVA-BRIDING PROTEIN	SINIAM CYTOMEGALOVIRUS	535-562							
POKSI VZVD	MAJOR DNA-BRYDING PROTEIN	Varicella-20ster virus	613.650	1043-1037				-		
PORT ASPIC	DRIA LICASE	AFLICAN SWINE FEVER VIRUS	73.10¢							
POPIL! VACCE	DNA LIGASE	VACCINIA VIRUS	393-436							:
POME VACEV	DWA LIÔASE	VACCIMIA YIRUS	195.416							
PONU VARV	DNA LIGASE	VAUOLA VIRUS	395.436							
POPOL ADEST	DNA POLYMEDASE	MUMAN ADENOVIRUS TYPE 2	667.743							
POPOL ADERS	DHA POLYNEAASE	HUMAN ADENOVIRUS TYPE S	667.743							
POPOL ADED?	DNA POLYMERASE	HUMAN ADENOVIRUS TYPE 1	133.600							

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PCCENE						3	ľ	Ī		•
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Г		TONIOPOXYIRUS	٦	97:-19						:
SPOL OFF	DHA POLYNERASE		247-284							:
POPOL CHANG		CIN DRELLA VIRUS I	247-264	٦			-			
DPOL CIMPI			٦	7	=======================================					: .
DPOL FOWPY		GALOVIRUS (STRAIN AD164)	3.3	20.00						:
TOPOL HOWA			-	İ			İ	1	İ	
POPOL MODE										· · · ·
DPOL MEDIC		IAI DUCK ISOLATE \$3	٦				j		!	
POPOL HOSOW		COCKET SOURCE STEPATITIS VIRUS	35	٦						:
POPOL HOROS	DNA POLYNGRASE				25.32					!_
POPCIL HORIGE	DRIA POLYNERASI	PE AYWI	201-135							:
POPOL, HOTOVY	DNA POL'THERASE	9	201-235							; <u>+</u>
POPOL HOBYZ	DNA POLYACIASE	APN 13)	\$11.550							
DOC HEVII	DHA POLYAZIASE	KGELOTTI	311-559							: :
POPOL MSVIA	DNA POLYNEMASE	THE PROPERTY OF THE PROPERTY OF THE ARM POST	311:33							1.
POPOL HSVIK	DNA POLYNEJASE		31:53							i.
POPOL HEVIS	DNA POLYNGIASE		212.560							نـ
MACE MSV21	DNA POLYNGRASE	COUNTY SIMPLEA VIRUS (1175 47 6150)	494.578					١		:
POPOL HSVEB	DNA POLYNERASE	EQUING MEMORS VINOS 1116 (STICKIES CATEISH VIRUS)	191	370.346	401-415	304-348	20.00			<u>:</u>
POPOL HSVII	DHA POLYNERASE	ICTALURID PRINCES TINGS I COMMISSION MICROSIS VIRUS	***							į.
POPOL NOVAC	DNA POLYNERASE	AUTOGRAPH CALIFORNICA ROCERON I COM	(19:69)	270-618	128-462					j
POPCE VACOC	DNA POLYNCEASE	VACCINIA VIIIUS (S INAIR COLECTIONS)	(3)-6(3)	770-811	178-162					
AND AND	DNA POLYMERASE	VACCINGA VIXUS (STRAIN WR)	626.60	769-817	197-48					1
VALV	DNA POLYNERASE	VALIDIA VIIUS	3.5							
OVEN TOTAL	DNA POLYNERASE	VALCELLA-EOS IER VIROS (BIRON DOMES)	200							i
POPOL WAY	DNA POLYNGIASE	WOODCHUK PEPATITIS VINUS	180							
PDPGL WHV59	DNA POLYNGIASE	WOODCALL TO SEE STATE WESTS	100-007							<u> </u>
PDPOL WHY?	DKA POLYNGRASE	WOODCHING ASSAULTS VIRUS B	219-330							: -
POPOL WAY	DNA POLYNGRASE	WOODCHAFT HERAFITTS VIRUS & (POLCTIOUS CLONE)	196-331							!
POPOL WHIVE	DRA POLYNERASE	LICENTITIES VIBILITY CONTINUE ATVIN	201-235							-
POPON NOTON		TOTAL TOTAL TOTAL TOTAL TARE I (STRAIN ABA)	133-169							į
POUT HISVED		IOSPHATE MOCLEOIDANI ICADIA CARDES CARDEN CTRAIN 111	139-223							!
POUT HEYSA	DEOXYUNDOR S-TRIPHOSPHATE NUCLEUTIDORY	ACCESSION AND AND AND AND AND AND AND AND AND AN	197-141							
PEIA ADBAI	SARLY BIA 37 KD PROTEIN	AND ADDROVABLE TYPE 40	162-166							1
FEIBL ADGA		AND AND ADDRESS OF TARE 2	10)-133				-			į.
PEIBS ADREC	71	THE AND ADDRESS TYPE 5	10)-133				1			ļ
PEIBS ADESS	ELB PROTEIN, SMALL T-ANTICEN	WEAN APPROVISES TYPE (1	161-14							ļ
PEIDS ADEI2	BIB PROTEIN, SMALL T-ANTICEN	LABLAN ADENOVIUS TYPE 40	100-134							1
PEIRS ADEM	BID PROTEIN, SMALL T-ANTIVEN	MINAMA ADENOVIRUS TYPE 41	180					\downarrow		ļ
PEIRS ADEAL	BIS PROTED, SAALE I-ANIMAN	LOUISE ADENOVIRUS TYPE I	2					1		ļ
PEIRS ADDAI	ISIB PLOTER, SPALL 1-AN INCA	HEDALAN ADEMOVIRUS TYPE 2	2			-	1			L
PESIA ADOM		MIDALN'S ADENOVIRUS TYPE 3	5				1	1		Ĺ
PEST ADERS		MUNICH ADENOVINUS TYPE \$				1	1			_
PESIA ADESS		HUBLAN ADENOVIRUS TYPE I	7			1				L
PEDIA ADEO?	EALT IS 13.3 FOR FOLLING	HAMAN ADENOVIRUS TYPE 15	2				1			L
PELM ADESS	EVILY D'AU IN CATONYOLES	HABAKN ADENOVIRUS TYPE 15	200			1	1			Ļ
PESS ADESS	TALLY IN THE CONTROL OF THE CONTROL	HIDAAN ADENOVIRUS TYPE 1	3			1				
FEAT ADENT	PROBABLE EACHT SALL ED PROTEIN	HUMAN ADEMOVIAUS TYPE S	3			1	ŀ			
PEALL ADERS		EPSTEIN-BARA VINUS (STRAIN 895-4)				-		L		
PEAR DV	EALT AT MEN PAINT	SPSTEDICACLA VIDUS (STRAIN BH)-1)								L
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PCCENE	ALLMOTTS	All Virues (as bacteriophages)								
FILENAME		VMAUS	ARTA!	ABEAL	ABEAJ	7777	45.64.5	ANTAL	1442	PKI (
PEN PER		FLEND SPLEEN FOCUS-FORMONG VIRUS	341-378					-		
PENY, TREPY	ENV POLYPROTEIN PRECURSOR	FRIEND SPLEEDI FOCUS-FORMING VIRUS	341.376							:
PEN AVER	ENV FOLYPROTEIN	s viaus	470-472							_
PENV AVIDA	ENV POLYPROTEIN		247927							
PEN BAEYN		BABOOH ENDOGENOUS VIRUS (STILATIN M.T)	N-7061			П				i
PEN BING		BOYINE IMMINIODEFICIENCY VIRUS (ISOLATE 194)		П		23610	I			!
PENV BIVE	ENV POLYPROTEIN PRECURSOR	BOVINE INDIRINGOEFICIENCY VIRUS (ISOLATE 117)	٦	<u>=</u>	18 18 18 18 18 18 18 18 18 18 18 18 18 18 18 1	72.00	359-639	ž:		
PDW BLVA	BAY POLYMOTEIN	BOVINE LEUKEMIA VIRUS (AMERICAN ISOLATE PLK)	304.178							
PENV BLVAU	ENV POLYPROTEIN	BOVINE LEUKEANA VIRUS (AUSTRAL IAN ISOLATE)	2				1	T		:
PCM BLVAV	ENV POLYTROTEIN	BOVINE LEUKEMIA VIRUS (AMERICAN INDLATE VEM)	2				1			•
PENV BLVB1	ENV FOLYPROTEIN	BOYING LEUKEANA VIRUS (BELGIUM ISOLATE LINUS)	204.379							:
PENV BLVBS	ENV POLYPROTEDI	BOYINE LEUXEMIA VIRUS (DELGRAFISOLATE LBS))	2				-		į	:
PENV BLVI		BOVING LEUKEMIA VIRUS (JAPANESE ISRLATE NLV.1)	١.	;			- <u>-</u> ! i			
PENY CABVC		CAPRINE ARTHRITIS ENCEMIALITIS VIRUS (STRAIN CORK)			751-715	£				:
PENY CAEVO		CAPRIME ARTHURITIS ENCEMIALITIS VIRUS (STRAIN G63)	اء	27.75	74.71)	843.393				: :
PERV ELAVI		EQUING INFECTIOUS ANEAIIA VIRUS (CLONE P) 2-1)				\$61.74				
PENV EIAV2	ENY POLYPROTEIN PLECUASOR	EQUING INTECTIOUS ANEAUA VIRUS (CLONE P.) 2-2)				656.402		~		
PENY EIAYS	ENV POLYPROTEIN PRECURSOR	EQUINE INSECTIOUS ANEAUA VIRUS (CLONE P13-3)	39.76	436-525	159.591	651.716				!
PEN ELAYS	ENV POLYPROTEIN PRECURSOR	EQUINE INFECTIOUS ANEXIA VIRUS (CLONE P) 2-3)		431-536	\$40.544	699-669		-		
PENV ELAVO	DAY POLYPRÖTEN PRECURSOR	EQUINE INFECTIOUS ANEAUA VIRUS (CLONE 1349)				651.716				
PENV ELAVE		EQUINE INTECTIOUS ANEALIA VIRUS (CLONE CL22)	19.76		139-593	651.716		4		
PENY ELAVW	ENY POLYPROTEIN PRECURSOR					651.714				
PENY ELAYY	ENV POLYPROTEIN PRECURSOR	EQUING INFECTIOUS ANEALIA VIRUS (ISOLATE WYONING)	38-36	115-513	165.645	651-716				:
ושט שטו	ENV POLYPROTTIN PRECURSOR		\$ \$55.08	\$61.606						
PENY FINE		PELINE DIGAUNCOEPICIENCY WRUS (ISOLATE PETALUNIA)	09-01-0	35.35						1
PENY FINED	ENVELOPE POLYPROTEIN PRECLASOR	FELDAE DOACNODEFICIENCY VIRUS (150CATE SAN DIEGO)	117-19	7 X						! !
PEN TYTE	ENVELOPE POLYPROTEIN PRECURSOR		60-121	849.EM	314.755					i
PEN TWG	DIV POLYPROTEIN PLECURSOR	FELDIR LEUKEMAA PROVIAUS (CLONE CFE-4)	697.509	541-395						
PEN TING	ENV POLYMOTERY PRECURSOR	1)		343-536						
IEN THE	ENV POLYPROTEIN PRECURSOR	A-81)	П	362-396						
PENV PLVSA	ENV POLYPROTEIN PRECUASOR	RAIN SAIMA)	415-517							
PEN TOUN	ENV POLYPROTEIN	HUNGAY SPUBARETROVIRUS	1	П	121-355	\$61.693	\$64-903			:
PENV TSVQA	ENV POLYPROTEIN PRECURSOR	DNER-AUNSTEIN)		162-596						 !
PEN FSVGB	DAY POLYMOTED PRECURSOR	FELINE SARCOMA VIRUS (STRAIN GA)	П	343-576						
PEN ISVEN	DAY FOL YPROTEIN PRECURSOR		٦	25.5						 !
PENV PSVST		IN SMYDER-THEREIN)	П				1			İ
A GALV	ENV POLITICAL PRECORSOR	GEBOT AT LEUKEMA VIKUS	T	787-621			1	Ī		
PENY HILLIA	DAY NOT YOUTEN	SOLATE		Ī			T	1		<u> </u>
MI TH AGA	DAY POLYPROTEIN	HUMAN T-CELL LEUKEMIA VIRUS TYPE I (ISOLATE A(T-2)	100		Ī					
PEN HILVS		HUMAN T-CELL LEUKEMIA VIRUS TYPE II	111.117							İ
PEN HVIAL	ENVELOPE FOL YPROTEIN GP166 PRECURSOR	I (ARVZSP2 ISOLATE	697-393 6	117-219	766-845		-			
PENV AVIBI			105-594 6	810-019	167-443					
PENV HVIBE	ENVELOPE POLYPROTEIN OP 146 PAECURSOR		300-519 K	П	162-010					
PEN HVIBN		E)				763-111				
PENV HVIBA		HUNCH BOADHOOFFICIENCY VIRUS TYPE I (BAU ISOLATE)						2		
PEN WIC		ATE)	142-176 \$	909-015		179.055				
PEN WIEL		П				764-829				
PENY HVIRE		╗	1		767-436					
PEN HVIH		_	7	П			-	Ì		İ
PERV HVID		Т	I	1	٦	2				
PBV HVIR	ENVELOPE POLYPROTEIN OPIGG PRECURSOR	HUMAN DOMUNDOEFICIENCY VIRUS TYPE I (FICSF ISOLATE)	335.763	35.56	Ž.	200	1	1		7

POCENE	ALLMOTIS	AR VIDAM (14) DOCUMENT (15)		145	1980	Į			117.44	
TALLET OF THE PARTY		VAUS	221-99		2.53	1	1	1		
SULVA.	& POLYTROTEIN	MAKAN BORNOLE KIENCI VINCE INTELICIONALI INCLATE	Γ	20.58	611.714	170-825				
		Т	Γ	Γ	185-141					
ANIMA MAINA		J	T	ī	617.713	710.04				
PENV KVIDO	THE WALL AND THE PARTY OF THE PARTY OF THE COMMON AND THE COMMON A	1	9	1						
				464 464	101.107	327-138				
EN HVINS	ENVELORE PACIFICATION CONTROL MODERNIA CONTROL	1	20.4			1777				
PENY HVIND	EMELOTE FOLTTROICE OF THE TANK	7	136-370	146-140						
ENY HYIOT	ENTEROPE POLYPROTEIN CPHO PILLUNSON		505.574	610-712	167.143					
ERV HVIPV	ENVELOPE FOLYPROTEIN GPIGG PLECURSON	Θ	344.378	(0 3 -(06	619-721	776-851				
MILAN AND		Γ	494-305	101-101	756-130					
1	ENAME OF POLYTROTEIN CPIES PLECURSOR	Ţ	11.14	194-550	407-306	763-637				
		J		100,100	411.312	361.034				
ENV MAISO	ENVELOPE CONTRACTOR CO	٦	cor-ic			W. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1.				
	ENGLOPE FOLTMUIEM CTION ACCOUNTS	2	50.5	84 C-140						
L	ENVELOPS POLYPROTEIN GP160 PRELUKAUM	I (MANA MANAGERICANCY WRITS TYPE I (WAUS 150LATE)	127-361	419-514	102-201	2011				
L	ENVELOPS FOL YPROTEIN GP140 PRECURSOR	FORMAN DESCRIPTION OF THE PARTY OF THE STATE	25-28	145-205	10-104	764-831				
١	ENVELOPE FOL YPROTEIN CP 140 PRECURSOR	HOLLAN BONDANCE PARTY CONTROL ATEL 1901 ATEL 1	231-292							
١	EXAMEN AND PARK VARIOTEIN COME PARCURSOR			107 707	16.404	744-840				
١	CAN CANADA CONTRACTOR OF CANADA CONTRACTOR C		130-02			411.510	274.431		L	
	ENVELOPE FOL L'ANDIENN OF THE BERGING ON		/RF-947	17.5						
PENV HVIZB	ENVELOPE POLYTROLEIN OF INCLUSION	ğ	\$21.594	612-471	71.7					
Ļ	ENVELOPE POLYPROTEIN OF 160 PRECURSOR	_	447-481	\$10.395	617-680					İ
1	ENVELOPE POLYPROTEDN OP 166 PRECURSOR	L	\$12.501	619.309						
١	ENVELOPE POLYPROTEDY OPING PRECURSOR	Ţ	701.484	187-104		L				
	TO SECURSOR	HUMAN BARNODEFICIENCY VIRUS TYPE Z (1300-A) B DITT			87.85		L	L		
١	THE SAME WAS A STREET AS IN DEFCURSOR	3								
ENV HYZGI		INDIAN BOARMOOFICIENCY VIRUS TYPE 2 (ISOLATE NIH-Z)	121-32	607-017						L
PENV HYSKE	ENTERON POLYTRONEN UP 190 FACUS ON THE	CHANGE THAT PROPERTIENCY VIRUS TYPE 3 (ISOLATE ROD)	311.394	118.70						L
DAY HYZRO	ENVELOPE POLYPROTEIN CP160 PALCUASON	101	442.476	305-390	17:20					
HENV KYZSI	ENVELOPE POLYPROTEIN GP160 PLECURSOR	MUNICAL INCOME CONTROL OF STATE SELIST	526-586	614-700						
PENV HY25B		1	147-611	305-590	413.702					
l	ENVELOPE POLYTROTEIN GP146 PRECURSOR		367-432	465-527						į
١	ENV POLYPROTEIN PLECURSOR	SELIC	\$\$ 7 [0]	23:465			_			
l	ENV POLYPROTERN PRECURSOR	BANA WINE	13:535	117.571						
	THAY BOY YOU OF THE PRECURSOR		107.76	411.572						
ł	ENCY BAN YOR OTEN PRECIDED ROAT FOL YPRO	JUNE LEUKENIA VIAUS HOULA		197.19						
	SALES AND CONTRACT OF SALES CO			1				L		
PEN MEVAV	ENV FOLITROI EN FRECHESCO		2			1			L	L
, Lavo	DAY FOLLTRUITS TRECORDS		Ž							 -
PERV MENTS	DAY POLYTHOLDIN PRESENTAN	19)	ž	2			1			Ĺ
PENV NO. VITE	ENV POLYPROTEIN PRECURSOR	FRIED ANTENE LEUKENIA VIRUS (180LATE PVC-211)	S20-564	ž			1			
BY MAY	IDAY POLYPROTEIN PRECURSOR	LALAR CARACTER FIRE VIRUS	504.551	943-507						ļ.
PERV MALVHO	ENV POLYTROTER PRECURSOR	CHOTTEN AND THE DESTREAM ATRUS	26-03	104-131						<u>:</u>
DEN MANE	DAY POLYMOTEDY	AIR IST WOMEN TO THE CAME AND A CHARLES AND THE CAME AND A CHARLES AND THE CAME AND A CHARLES AND THE CAME AN	303.5M	244-400						-
DAY M. VACO	74	MOLCAR FROMME LEGICAL TRAIN	30.50	20.12						;
ON PT AND	ENV POLYMOTERN PRECURSOR	I	407.540	15.10	L	L			j	_ <u> </u>
	TOWN BOX YOU OF EN PRECURSOR	No. Cont.						_		_
	SAN AND VARIOTIES	MOUSE MARIARY TURIOR VIRUS (STRAIN BRE)								
NO.	The second of th	MOUSE MARGIARY TURIOR VIRUS (STRAIN GR)								_
ישל אפון	DAY TOLITABLE IN	SDAAN MASON-PFIZER VIRUS	2			1		-	<u> </u>	: !
150 VOV	EXV POLYTRUIEN	FBI MURDIE OSTEOSARCOMA VIRUS				111				
PENY MISTER		DAYNG LENTINGELS (STRAIN SA-CAN'Y)	₹.	22.43			ļ	-		::-
PEN CHIVIS	ENV POLYPROTEIN PRECURSOR	SALECTED LINE CELL FOCUS: NOUCING VIAUS	464.538	365.574					ļ	•
PEN INOV		SALISONES ON BEN EOCISC FORMON VIRUS	142-176							:
PON RSTV	ENV POLYPROTEIN PRECURSOR	CAUSANT METERS OF SECTION AND	<u>-</u>	101-140	134-205	20.55	ş	1		;
NO AU	ENV POLYTROTEIN	SDAIAN POART VINCE LITTER A PLANT IN IN	3	5.53	116-121	\$60-706	5	1	1	-¦.
100		SBOLAN FORMAT VINCE (1978) SERVEN CALLED ATER	1	127153	107-(3-5)	-	_			
TEL ME AND		The state of the s								

272.00										
FILE NAME	PROTEIN	All Virging (se besterdehafer)	7	Т			П	lī	li	
PERV SIVAG	PACEL DES POR VERDITERA CELLA SERVINECIA	COURT WAS PROPERTY WAS VIOLET AND A SECTION	J	T	3	1444	4854	147.86	738	AREAL.
PEN SIVA		SORAN INGRODING KIRKET TIKUS (AUST INCKTE)		T						İ
PENV SIVAT		SOAN BARDODE FICENCY VIRUS (TVC.) 1604 ATEX	244.700	217	000		98.26			-
PEN SIVEZ	DAVILOPE FOLYPROTEIN GP146 PILECURSOR	CHINE INCOMEDITION OF THE STATE	T	7	70.53	10,07		1		-
PENV SIVOB		STATION INDIGNODEFICIENCY VIRUS (ISOLATE CAL)	I	1			1			
PENV TIVAL		STATIAN TANDACOEFICIENCY VIRUS (TANIA)-13 (SOLATE)	Т	\$.5	521.611	1	177.00	Ì	-	:
PENY STAND		STATAM INDICATOR FIGURACY VINUS (FIRALS) ISOLATE)	Τ	ī	100		+			:
PENY SIVICE	EMPLIANT POLYPROTEIN OPIN PLECUMION	SIMIAM INDIREMEFICIENCY VIRUS (KAW ISOLATE)	Ĺ	Т	12.5	İ		Ī	İ	
PEN STAR		STATION INDICINOCERCIENCY VIRIUS (K 74 (SOLATE)	Ī	!	671.714		-	-	!	
PEN SINS		SBRAN BORDNOOFFICIENCY VIRUS (F236/SNRM ISOLATE)	466-508	314	25.35	13.22	-	-	i	
PEN SWS		SOMAN DORINODEFICIENCY VIRUS (PRINGCI) ISOLATE)	470-513	Γ	E:33	11.846]		;
TENY SOUNE	DAY FOLYPROTEIN PRECURSOR	SOUTHABL MONKEY RETROVINUS (SAIRV-II)	400-464					Ī	İ	
PEN SAVI		SINIAN ARTHOUTAUS SAV.1	409.475						-	•
MOV VIEV	ENV POLYPROTEIN PRECURSOR	MISHA LEMINIRUS (STRATIN 1514)	Γ	22.2	637.740	173.603			Ì	
אטע אניאו	ENV POLYPROTEIN PRECURSOR	VISNA LENTIVIRUS (STRAIN ISI4/CLONE LVI-IKSI)	24:2	=====================================	643.746	710.114	-		-	•
TENY VILVA	ENV FOLTPROTTIN PRECURSOR	MSNA LEMTIVIRUS (STRAIN 1514/CLONE LVI-1KSZ)	21-42	- F	105.741	117:11	+		: 	
PENDA AVILA	EULA ONCOCENE PROTEIN	AVIAN ERYTIMODLASTOSIS VIRUS (STRAIN ES4)	071.90					Ī	İ	
PETF FOUR	EARLY TRANSCLUPTION FACTOR TO KED SUBLINIT	FOWILD X VIRUS (STRAIN FP.1)	527.061	100			 -	İ		
MIT SWA	EARLY TRAMSCRIPTION FACTOR 10 KD SUBURIT	SHOPE FIBROXIA VIRUS (STRAIN KASZA)	17.71	Γ	110.517			T	Ī	•
אינע אנע אנע אנע	EARLY TRANSCRIPTION FACTOR 70 KD SUBLINIT	YACCIMA VIRUS (STRAIN COPENIAGEN)	17:03	Γ			-		İ	:
MITTI VACCV	EARLY TRANSCRIPTION FACTOR TO RD SUBLINIT	VACCINIA VIRUS (STRAIN WR)	17:12	10.10 10.10			+	İ	İ	:
TETT VACC	EALLY TRANSCRIPTION FACTOR IS NO SUBURIT	VACCIMIA VIRUS (STRAIN COPENHAGEN)	13.01	12.2G				İ	İ	1
VETT 2 VARV	ILABLY TRANSCRIPTION FACTOR 12 KD SUBURIT		13.47	17.70				İ	-	:
PEXON HOWA	ALKALINE EXONUCLEASE	HUNLAN CYTOMEGALOVIRUS (STRAIN AD169)	11.0				 	Ť		
PETON HEVER	ALEALINE EXONUCLEASE	EQUINE HEADES VIRUS TYPE 1 (STRAIN ABAP)	12.40					İ	İ	:
PETON PRVN		PSEUDORABIES VIRUS (STRAIN NIA-1)	e :-					İ		:
PETON VZVD	ALKALINE EXOMICLEASE	VAUCELLA-ZOSTER VIRUS (STRAIN DURIAS)	109-157	143.183				Ţ	İ	:
PFIB2 ADEAB	41.4 KD FIDER PROTEIN		182-233				 	İ	j	:
77.82 ADE41	ALAKD FIBER PROTEIN		162-233							:
PFIDE ADEON	FIRENCYEN		156-194				-	İ	Ì	:
19 AD 17	FINER PROTEIN		176-210					Ť	İ	!
WIEW ADEA	FIBER PROTEIN		101-151					T	Ì	
MBP ADEL	FIBER PROTEIN	1	320-366				-	Ť	Ť	• • • • • • • • • • • • • • • • • • • •
77 GP ADCB3			101-215	363.638			T		Ť	
PFOST MSVFR		MA VIRUS	131-169				-	İ	Ì	-
703 AVBAX	PANA TANKE GOOM PROTEIN		151-601				 	İ	İ	!
2000			155-193					<u> </u>		j.
POAG AVEVI	GAG POLYMOTER	AVIAN EMPORTACIONE MAIN EV.	<u></u>							
POAG AVEV2	GAO POLYPROTEDI	Claren venice	*	1						
POAG AVBAC	QUO POLYMOTEIN					1				
PGAO AYDAD			1 2 0	1	1	1	+		j	-
POAG AVISU				1			1	1	j	İ
POAO AVISY			1 2	T	T	Ť	+	1	j	İ
POAG BIVOS	GAG POLYPROTEIN (PS3)	SOLATE 1061		Ť		1	1	1		Ì
POAG_ELAYY	GAG POLYPROTED	T	81:118	1			+	1	1	İ
PGAG_FTVPE	GAG POLYMOTEIN	ALLINIA).	16.10	T	Ī		+	1		1
POAG FTVSD		DIEGO	36-110	T		†		+	1	
POAD PIYTS		CY VIRUS (ISOLATE TAIS)	76-110	T	T	Ť		t	1	-
POAD PLY			496-533	T			+	\dagger	1	Ī
POAG FOAMY			134-184 39	191-425	039-60	607-615	-	\dagger	\dagger	Ī
POAD PENIED	GAG POLYPROTEIN	FELINE SARCOMA VIRUS (STRAIN MCDONOUGH)	488-534	Г	Г		1	\dagger		İ
								1		7

TOTAL MARK TO TO			37.04							1
									L	ĺ
	GAG POLYPROTED		193-444							
	CAN IN VALOITED		Γ	74.370						1
П	CAG POLYPROTEDY	Τ	Γ	11:50						1
T	CAC POL YPEGIEIN	T	Γ	347-734						1
	GAG POL VPBOTEIN	Τ	Ī	351.136						
Ī	OLO BOL VEROTRIN		Ī	20:13						!
T	CALCAST ASSOCIATION	T	I	200						; ;
T	CAN VALOREDA	T		20.55					ļ	1
I	AU TOUR STATE OF	Ţ	T	303.134					ا	_
	GAU PALITRUISM	T	T	100			L			<u>:</u>
	GAO POL TRADIEIR	3	T	200						_
	GAG POLYPROTED		20.00							
	GAO POLYPROTEIN			205-339						
	GAG FOLYPROTEIN	1504	16138	192-126						
Γ	GAG FOL TPROTEIN	MANAN DONOTHER PARTY TOTAL TOTAL SOLATE)	2.2	(11:412						ĺ
I	GAG POLYTROTEIN	Γ	101-04	293-376						1
I	OAS BOY VOROTEDA	T	Γ	202.376						-
T	CALCAST CONTROL		T	×1.136		_				<u> </u>
T	CALL TOTAL CONTRACTOR	HUMAN BOADWOOFICIENCY VIRUS TYPE I (IUMAT 130CA15)								
1	CAU PALTYAVIEN	51	, , , ,							
٦	DAG FOLTFRUIE	HIMAN DARMODEFICIENCY VIRUS TYPE I (WAUS 1SOLATE)	267.762					-		
	GAG POLYPLOTED	₹1	17.112					+		L
	GAG POLYPROTEIN	LA DA AN MACHINGE FICIENCY VIRUS TYPE 2 (ISOLATE SBLISY)	192-126							 -
		LANGETT BETTE ACTORT BINAL A-PARTICLE	93-121	Š			-			 -
Γ		TOWNS IN THE ACTION AS A REPORT A SAN THE RESERVENCE AS A SAN THE RESERVENCE A	67.103							
		MOUPE IN INVALOR CONTRACTOR AND AND AND AND AND AND AND AND AND AND	16133	118113						ļ
	RETROYMUS ATLATED GAG FOL YPROTEIN	MOUSE INTRACTOR AND ADDRESS OF THE PARTY.	- 85 Se							
Ī	GAG POLYPROTEIN	SPEET FULNIONAL ADENOMINATION OF THE SPEET AND INC.	13:13	061-951						-
5	DAO POLYPROTEIN	MOUSE HAMMART TOWNS VINCE (STEEL)	=	24.180						1
OWN OF THE	DAG POLYPROTEIN	MOUSE MANANAN I UNION WAS IN	237:260							
VAN DAN	OAD POLYPROTEIN	STATAN MASON-PRIZER VINUS	1						1	ļ
200	GAO POLYPAOTER	ROUS SALCONA VIRUS (STRAIN PRACUE C.)	561.50	15.00						ļ
TOWO POWER	MAIOR COAT PROTEIN	SACCHANONYCES CELEVISIAE VIRUS L'A (SUVELIN)	100	1	×4.15					-
TONO XVIII	MITORY YEAR	SDOAN FOAMY VIRUS (TYPE I)	2.60	100	100		Ŀ			· •
1000 St. 10	CAN POLYPROTED	SINGLAN FOAMY VIRUS (TYPE) / SIRAIN EAS)	10.136		L		Ц			-;-
POAG STATE	CAR POLYPROTEIN	STRAIN DONNODEFICIENCY VIAUS (ACMISS ISOCALE)	106.160						4	-
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	DAD POLYPROTEIN	STAGAN BANANDOEF KLIENLY VANCE (NOW) 1900 N. L.		5.60	L	L	Ц			1
PONO SILVE	DAG POL YPROTEIN	SDAAN DOAMODEFICIENCY VIXUS (BOLATE AURI) CLOTE				-				<u> </u>
NAME OF THE PARTY	DAD FOLVFROTTIN	SPEAN ROAMODE FICENCY VIRUS (170-1 ISOLA 12)	101.31							!
2000	DAD POLYTROTTIN	CHOWANCE INSCINOUS CHANCE AND ATTEMPT	15.70	32.52	111-317	L			-	
200	GAG POLYPROTERY	SDAAM INDAMPOOLITIERAL TIROS (13047-15 05)	15.5						1	:
200	GAG FOL TPROTEIN	SECTION SALCONA VIRUS	82.22	27.5%		Н				+
11000	PROPARI & HELICASE	MEMPES SDOTLEA VIRUS (1172 1) 31 PAIN !!	464.502	1212		H				+
	PACHASI E VELICASE	HERDES SEAPLEX VINUS (TVTE 27.5) EALIN MUSA	8	3	(F#4)					
THE POYEN	INCOME BIGILICALE	HEAPESVIRUS SASKIRI (STRAIN II)		10.07						
NOT HOLD	PACCE AND IN LIVE IN LASE	VANCELLA-20STER VIRUS (STILAIN DUMAN)								
MELL VZVO	AND AND AND AND AND AND PRECURSOR	BOVING CORONAVIRUS (STIAM F13)				-				j
PEDA CAR	: 12	BOVING CORONAVIRUS (STILAIN LY-131)					L			
PHEAL CALLY	DECACOL CONTROL BOTTODA OR PRECIDENCE	BOYDE CORONAVIRUS (STILAIN NEBUS)		\downarrow	1				L	
HEA CABA		BOVING CORONAVINUS (STRAIN QUEBEC).	787-65		1	-			L	_
MENA CYBQ	MENA COLUTINATE BY LEASE FOR THE COL	HUNKAN CORONAVIRUS (STRAIN OC43)	ž			-	-			Ľ
PIEMA CYNOC	SENACOLUTRON-ESTERASES ACCOUNT	INSTUDICA A VIRUS (STRAIN MAICHINES)	Î		\downarrow	-		-	L	
PHENA MAK	HOSAGOLUTINIA PRECONCIA	INFLUENZA A VIRUS (STRAIM ABANGKOKUM)			1	-				
PIEMA IABAN	HEXAOGLUTING PRECUSOR	INFI 1/FNZA A VTRUS (STRAIN ABUDGENGARMOKKAIDO/I/T) 178-49	378.474							

			-			-	-	[-
PCGENE	АТТИОШЬ	All Wrone (se betterophism)	Т	AREA? AREA?	Т	AREA O AREAS APEAS	48842	7.04
MON WOR	HENADOLITONN PRECURSOR	ENZA A VIRUS (STRAM ACHICKENALABANAVIMS)	75-56		П	1-1		; ;
PIEDA MCKO	HEMAGGUITHM PRECURSOR		104-142 175	115.471 494.528				-
MENA MORP		1143)		187-533				1:: ::-
ı	MENTACCLUTININ PLECURSOR	√ 1370′		487.533	-		1	
1	HEMADOLUTEM PRECURSOR		7	Z				
1 1	HEMAGGLUTP/THECURSOR	3	Т	131.440	1		1	
PHEMA LADA!	HEMACOLUTININ PRECURSOR		T					ļ
1	HEMADOLUTININ PRECURSOR	T	7	402.347	-	1	\ 	1
1	HENAGOLUTBAN PRECURSOR	INFLUENZA A VIRUS (STRAIN ADDICE/ALBERTA/IVA)	100	54.50	-			1
1	HEMAGOLUTIMIN PLECURSOR	14/44/	Ţ		-		-	İ
MENA MOC	MEMORAL DINING THE CONSUM	Τ	T	317.473		-		
1	REMANDED INTO THE CONSOL		T _e		+			Ī
1.	MEMORAL LIMIN PRECORDER		164-440			-	-	
THE PARTY OF THE P	MENANCE INTROM SERVICES SON		164-440		-			
1	NEWACCH UTTOON PRECURSOR	T	364.440				-	
ı	HEMACOLUTINON PRECIDESOR		364-440	_	-			
ı	HEMAGOLUTINGN PRECURSOR	Γ	354-440					
ı	HEMADOLUTINGN PRECURSOR		97790				_	
L	HEMAGGLUTDON PRECURSOR		179-471	104-551				
PHENA MONI	HEMAGGLUTDEN PLECIASOR		21.35					
PHEDAIA, IADIAZ	HEMAGGLUTININ PRECURSOR		380-436					
	HEMADOLUTINAN PRECURSOR		21.55					
ı	HEMAGGLUTDEN PLECURSOR	(9//10/	171-454					
	HEMAGGLUTDON PLECURSOR		S-18					
	HEMAGGLUTDON PRECURSOR	1,63)	360-4%					
ı	HEMAGGLUTRON PLECURSOR		25-021					
H	HEMAGGLUTDON PLECURSOR.	श	177.477			-		j
П	HEMAGOLUTINE PRECURSOR	ĝ	178-454		+			
1	HEMAGOLUTINIM PRECUTSOR	T	174.47)	1	-	-	+	i
	HEMAOGLUTHM PRECURSOR	INTLUENZA A VIKUS (STRAIN AGGILLASTRAKHANZZZZZ)	177.476	+	1	1	1	1
1	HEMACCALUTININ PRECURSOR	11411	Τ	144.444 461.119				1
MENA MICE	HENACOCO I INTO PRECONSOR	Τ	Т	Τ	-			İ
PIGNA LANCO	NEWAGGLITTERN PRECURSOR	Π	Γ	Τ	-			
MEMA INDE	HEMAGGLUTININ PRECURSOR	NGLUENZA A VIRUS (STRAIN AEQUINEDETROITIIMA)	П	501-517				
MENA INPO	HEMANGULITIWHI PRECURSOR	-1	179-455	-				
PPENA LAIRCE	HEMADGLUTBON PRECURSOR	I	178-435				-	
MENA WAX	HEMARKELUTININ PRECURSOR	INTEREST A VIEW (SIRAIN ARMINERARY INCAVINS)	113.146	110.484		-		1
MENTA IAIR	MENANCE INTOM PRECINEDS	Τ	Τ	Т			-	
PHONA TARON	MEMAGGLUTTHON PRECURSOR	Γ	135-455	-				
PIENA IMPON	HEMAGGLUTHIN PRECURSOR,	(9/	П	П				
PIEMA IADON	HEMANGOLUTION PRECUNSOR.	٥	112-146 360-	360-484 303-333				
PIEMA IMOR	NESTA COLUTION PRECURSOR		113-146 360-	360-484 503-537				
PHENA MARO	HEMAGGLUTININ PRECURSOR		179-455			_		
	HEMAGGLUTININ PRECURSOR		П	П				i
1	HEMAGGLUTININ PRECURSOR	_	٦	٦				
	HEMACOLUTININ PRECURSOR	Ę	7	160-414 501-537				-
	HENALOGLÚTBITN PRECURSOR	\$	33.43		1		1	
MENA WITO	HENALOGE UTENIN PRECURSOR	INTLUENZA A YIKUS (STRAIN AFQUINE/TOXI)	\$ 1.00 m	1	.		1	
MEDIA LANGE	HEDGADOLUTININ PRECUISOR		1					

PCCENE	ALLAGORS	Appl (so becteriopinger)	AREAL	ABEAL ABEAL	1	TOTAL	1		
THE HAME		VARIOR AND AND AND AND AND AND AND AND AND AND		103.547					
	HENLAGOR LITTONIA PALECURIDOR		376.476	25-52					
THE PARTY	ANTI-LANCE LITTERIAL PRECIENCE.		Τ	506.548	L				
PODA MAIL	AND AND AND AND AND AND AND AND AND AND								
MOW INTER	STATE OF THE PARTIES OF				_	_			İ
SALE TANK	VELLACOS LITROS PRECURSOR	Π.	757 931						
2	HEMACCLITININ PLECUASOR	TOROGE IN I	180-456						
Service Services	MENACCE LITTERN PRECURSOR		100.454						
1	VENTACCI LITERIA PRECURSOR								
١	THE WAS STREET FOR THE SOR		1	167.61					į
١	LELLA COLLINATA PRECURSOR	EDENAT			-				
ı	Carried Indian post Rich	Т		700					į
١	MEMACALO LIMENT PROCESSION OF THE CASE	KE/32 [MA]		200	-	-			
HEMA INFIL	MDAACCLUITMIN THELCHACK			100		-			
HENA INUE	HEMACOLUTINEN PRECURSON					\ 			<u> </u>
MENA IARUD	HEMADOLUTION PRECURSOR	_		-	+	-			
HEMA IMSES	MEMAGGLUTING PRELIMENT		_	200	1		ļ		<u>.</u>
	HEMAGOLUTININ PRECUSOR	MAILENZA A VIRUS (STRAIN ASSTARLINGWICTORIANS 19415)	27.146	32.05		+			<u>.</u>
1	HEMACOLUTININ PRELUASOR	INFLIENZA A VIRUS (STRAIN ATURKEYARELANDVI) 14/13)	3.5	36.35		-			_
-	MEMAGGLUTERIN PRECURSOR	MELLENZA A VIRUS (STRAIN ATTURKEY MINNESOTANDA)	2	1	<u> </u>	-			
	HEMAGOLUTBON PILICUISON	INSTITUTE A VIBUS (STRAEN ACTURKEY/ONTALION 1) 2/66)	193-470	25.50		1			<u>.</u>
. 1	HEMADOLUTIMIN PILECUIDOR	ACTION A VIEW (STRAIN A/TURKE Y/ONT ARIOW (1841)	75.	693.540		-			
	HEMADOLUTION PRECURSOR	THE LOCKET A CHAIR (CTRAIN A/TURK EY/OREON/TI)	ş	374-476		1			
	HEMAOCEUTING PRECURSOR	TRELIENCA A MASIA RETRAIN ACTURE EYAVISCONSINUMS	373-472	487-539	-	1	1		:
PIEMA IATEW	HEMAGGLUTININ PLECURSOR	INCLUSION A VACABLE PARTIES AND AMERICALISTRAL (AACHOOT)	= :: :::						ļ
	HENADOLUTEYIN PRECURSOR	INCLUENCA A VIRUS (3) INCLUENCE AND TARROLUCIONES A SECURITARIA DE LA COMPANIO (1772)	387-486			i			:
1_	HEMAGGLUTTININ PRECURSOR	TRELEGICA A VIALE (STEEL)	176-478	304-348	-				į
PIEMA LAUSS	HENYOCKLITININ PRECURSOR	DOPLOENCA A VINUS (STEAM AAACTORIAATAS)	100						!
PER WY	HEMADOLUTININ PRECURSOR	INTLUENCA A VINCE (CTB AND AAVIR SON, SAILTHUS)	113-471	505-547					+
MENA LAWE	HENAGOLUTBAN PRECURSOR	COLUMN A TABLE SERVICE OLD AND AND AND AND AND AND AND AND AND AN	370-016						!
PIEMA IAZOD	HEMACOLUTININ PRECUISOR	DALUENCA A VINCE (STRANG AS WINDAMOND KONGALITS)	364.440			<u> </u>			اِ
DAN MZIG	HEMAGGLUTEVIN PRECURSOR	INTUCACA A CASING ASTRAIN ASTRAIGNON CONCUINTS)	364.40		-	1			:
HEM LAZM	HENCAGOL UTININ PRECUISOR	INTEGRACE A VINCE (STREET, STR	179.478	175-90:					!
EMA IAZIN	HEMADOLUTINAN PRECURSOR	THE LUBRICA A VINCE SCHOOL ASSESSMENT FREE SEY! 17%)	199.478	204-347					1
THE WENT	REMADOLUTION PRECURSOR	INTLUENCA A VIEW CORANA ASSUME A SECTION	310.4%						ļ
PHENA WZUK	HELLAGOLUTINGN PRECURSOR	AND INCOME A VIEW STRAIN PREISING IA?	311-433		$\frac{1}{1}$	+	\downarrow	1	!
HENA MIN	HENAGOLUTININ PRECUISOR	PART (PARTA & MALIS (STRAIN IMBORNAS)	378-463		1				<u>.</u>
PIESKA BIBBO	HEMAGGLUTHMIN PRECURSOR	THE LEWIS & VIELTS (STRAIN DEDICHAND/211/82)	366-471			1	1		1
PICENT PARDY	MEMACOLUTERN PARCURSON	THE LEWIS A VIRUS (STRAIN BAIONG KONGOLIS)	381-463		-				
PHENA INTHO	HEMADOLUTININ PRECUISOR	PARTITIONE A BYRUS (STRAIN BAEE/40)	1073		+	1	1		
ENA INDLE	HEMACGLUTBYIN PRECURSOR	MELLIENZA B VIRUS (STIAM BAKARYLAND/39)	13-461		-		1		
HENA MIND	HEMADOLUTINEN PLECURSON	INGLIENZA B VIRUS (STILLIN BACENTHIS-4-04)	7		+	1	-		-
PREDA DONG	ADMAGGLUTINGS PRELUMON	DISTURNZA B VTRUS (STLAM BYOREOOWATO)	3		-	$\left \cdot \right $	-		
HELY DOOR	ADMAGLE UTINGS TALL MACON	DATLUENZA B VIRUS (STRAIN BASINGAPORE/222/79)				 			
PERT DES	MEMACACULI IMIN PACCINESTR	DATLUENZA B VIRUS (STRAIN BAUSSIVICORS)	-		 	+			
PHENA DOUS	PENADULUININ PRECISOR	DIFLUENZA B VIRUS (STRAIN BWICTORIANA)	\$			-			
HEMA BOW	MENACOLUMBI PRECUNSOR	INTLUENZA B VIAUS (STRAIN BAYICTONA/2/17)				+			
HELL DOW	PENADOR UTININ PILEUNASCH	INTITIDICA C VIRUS (STRAIN CCALIFORNIA/74)	5		-		-		<u>.</u>
PIEDIA INCCA	SEMAGOLUTININ PRECURSOR	INFLIENZA C VIRUS (STRAIN CENGLANDANIA)	\$			-	1		
PERM DICEM	HEMAOGLUTININ PRECURSOR	INSTITENZA Č VIZUS (STRAIN CONEAT LAKES) 1677/H)	63:50 53:00 53:00 53:00 53:00 53:00 53:00 53:00 53:00 53:00 53:00 54:00 56:00		+		1	-	L
PHEDALA DINCOLL	Ž	INFILIENZA C VIRUS (STRAIN CAPYODOVIA))	3		+	+		-	
HEDAL BACHT	MENADOLUTRIN	INFLLENZA C VIRUS (STRAPH CHOHANNESBURG/UM)	<u>=</u>		-	1	-		L
			***	-	_	-			

1000	ALLANOLD	AR Virtues (no horizriophages)	1	ī	T	T		1	I	
	THE PARTY OF THE PARTY IN CO.	P. 10. 10. 10. 10. 10. 10. 10. 10. 10. 10]	420	J	4	441	1	1	1
	MENACOLO INFORMACIONAL	MALUCACA CAIXOS (31 KAIR UNISSISSATIVO)	7. Care	1	1	1				
ALDER HAND	MEMORALDI IMIN		X	1	1	1				
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	PENALUKA HININ PRELUKKOR		471-378	1	1					
THEMAN INC.		INFLUENCA C VIRUS (STRAIN CHICABELINGN ISE)	471-579	1	1					ĺ
THEMA INC.	MEASURES VINUS (STRAIM MALLE)	INSTRUCTOR C VIRUS (STRAIN CHORDEDING/1991)	471-359		1					i
PILIPA INC. IA	MENANCKI UTININ TRECURSOR	INTELLERZA C VIRUS (STRAIN CTAYLODI 11)447	431-359		1					į
PLEASE LA LA	MENANCE IN THE CASON	INTLUENZA C VIRUS (STRAIN CYANIAGATA/10/11)	471-539							
THE PERSON NAMED IN	PERCOCAL DISTRIBUTION OF THE PERCOCALINITION	MEASLES VIRUS (STRAIN EDMONSTON)	46-90		1	j				
MANA MAN	MENANCE INTERNATIONAL PRINCIPLE AND A CO.	MEASURE VIRUS (STRAIN HALLE)	8.4		1					-
TIENES PIENES	NEWACCO I HIN-MUNCHING ASE	MEASUES VIRUS (STRAIN IP.).CA)	19-91							
	HEMA COLUI DITHANEURAMINEDASE	MEASLES VIRUS (STRAIN YAMADATA-I)	46-87							
MENA MORO!	PEDALOCE UTTNIN-YEUTAKINDASE	MUMO'S VIRUS (STRAIN SEL-I	34-99							
MENA MUNDA	POWGGLUTDW-MEURANMOASE	MANDS VIRUS (STRAIN AIIYAHARA VACCINE)	14-90		H	l	ľ			
HENA MARIN	HEMAN COLUMNAME LIKANOMEDASE	MUNUS VIRUS (STRAIN RW)	24-50	ŀ	-		-			
PIENA MADOS	HEMAOQLUTDAN-HEURANMDASE	MUNDS VIRUS (STILAIN SEL)	34-99	-	-					Ī
HEMA NOVA	HEMAGGLITIMIN-NEURAHINIDASE		23.4	417.579						İ
PHENA YOUR	NEMACCLUT BITH-MEURANIMIDASE	NEWCASTLE DISEASE VIRUS (STRAIN BEALDETTE CAS)	\$	-		l				i
PERMA NOVO	HEMACOLUTININ-YEURAAMMOASE	NEWCASTLE DISEASE VIRUS (STRAIN D26/14)	3:1	-	t	T		Ī	-	İ
HEAL HOVE	HEMAGGLUTININ-HEURAMINDASE	NEWCASTLE DISEASE VIRUS (STRAIN MIYADERAJSI)	<u> </u>	\mid		T				İ
PHEMA NOVO	HEMAGGLUTDATH-YEURANDHODASE	NEWCASTLE DISEASE VIRUS (STRATH QUEENSLANDING)	13:	-		-				İ
PHENA, MOVTO	HEMA OCLUTIND - MEURANDMIDASE	NEWCASTLE DISEASE VIRUS (STRAIN TEXAS G B./41)	1	-	-		Ī		T	
MENA NOV	HEMAOGLITHM MEURAMINIDASE	NEWCASTLE DISEASE VIRUS (STRAIN UE STEAR)	=		\mid	T				
PHEDALA PHODY	HEDAAOGLUTTHRA-MEUTAMENTDASE	PHOCINE DISTEMPER VIRUS	19.73	+	I	T		1		Ī
PERTY PIET	HEMACCLUT PAN MELPLANINIDA SE	HUMAN PARADOLLIENZA I VIRUS (STRAD) WASHINGTON/16571	44.10	-	-	T		Ť		1
1.	HEMAGGLUTTIMINH-MELTINAMINEDASE		347.381			\dagger	1			
L	HENAGGLUTORINARIONASE	(STRAIN TOSHIBA)	247.281	\dagger		1				
1	HEMAGGELUTERINAMINADASE		11.01		\dagger	1				
L	HEDLAGGLUTDRIN-MEUTAARDASE	(STRAIN MR 47415)	T.	104.431	\parallel	Ť	İ		1	
١.	HEMA GOLUT DATH MELTINAMINEDASE	ŝ	Γ	10,10	\dagger	\dagger				
PHENA, PUNT		Τ	Τ	194-428	$\frac{1}{1}$		1			Ī
HEDA MIHU			Γ	104.42	\dagger	İ			T	
PHEDAL, PUNY		T	Γ	194-429	╁	\dagger	1	T		
PHEDICA PISHEN	HENCACOLUTERIN-MEURA-MONTO A SIE		Γ	194-428	-	t	T	T		Ī
	HEMADCLUTEMHARURAAMIDASE	Ē	Γ	104.428	\mid	T	T	Ī		ĺ
	HEMADOLUT PITH-MEUTAMPHIDASE	47.A 4A VIRUS (STRAIN TOSHIDA)	25.0	-	-		-		T	İ
1	HEMADOLUTION PRECURSOR		166-214 236-290	£						
PHODA KINDK	MENAGOR UTDAM - MEULAAM MIDASE	(SETE O)								1
PREMA RINGE	NEWALKALUI ININ-NBURAMINIDASE	MMDENTEST VIRUS (STRAIN L)	T	191-225	1					
PLENT COME	INCREASED INTERPRETATION OF THE PARTY OF THE		27:10	1	1	1		j		
PICMA REMIN	HENAGGE UTDRINGERANDASE		211.6	1	1	+	1	1	j	İ
PHENA SOUN	SENADOLITHMANICMANIMASE		201	+	+	1	1			
PIEMA COCK	NEMACCI LITTION-NET LIBANDASE		9116	1	+	1	1	1		İ
PHEMA SVAI	MENA COLLINGA, NET RAARMIDASE			+	+	+		1	İ	į
PHEMA IVS	HOWACCE UPPERANCEMENTALES	STRAIN WILL	1		1	+		1		ĺ
PIEMA SVSLN		MAXAM		+	+	\dagger	1	1	1	-
PIEMA VARV	HEMA OCI, UTIMIN PRECURSOR		17.71	-	1	†	1	1	1	Ī
HEXD ADER	PEMPENTOWAL HEXON-ASSOCIATED PROTEIN	ARUS TYPE 2	8134	+	\parallel	\dagger	†	1	1	
PIEZO ADERS			\$0.04	-	\dagger	t	-	1	1	
PHEXA ADRECT			107		\parallel	t	1	†		
PHEXY ADEM	HEXIDA-ASSOCIATED PROTEIN		V(-)	+	+	+	\dagger	1	1	
MEXI ADEO	HEXINAASSOCIATED PROTEIN	AND ISTANA ADENOVISUS TYPE			\downarrow	t	1	†	1	Ī
					1	$\left \right $	1	1	1]

PCGENE	ALLMOTIS	AB VICTOR (se succession)		र रज्ञ	3	191	0			
Ä	PROTEIN	N ADDROVIRUS TYPE 12								
	TEAN.		67.1%							
HEX9 ADE41			\$3-103							
HOX9 ADEC	200		601-19							
HEXY ADEM		C Service of the Serv	341-336	433-467 5	20,424					
HEX ADER			136-136	-						
PACK ADENI	HOXON PROTEIN		103-152	408-449	351-587					
HELK ADE40			304.335	135-389						
MET ADEA			20:34	313-419	344-338	203-739				
1000		/AUS TYPE 3	120,101	433-489						
	·									
HOLD COWTA		(N)		017.00						
PERM ASSEV	· mentene		1							
PIBING CALIVA	TACIES.	(I I)	27.50							
THE CAN'S	INCLUSION BOOT MATRIX TRUITER	_	7.7	-						
BAP CAMPC	INCLUSION BODY MATTLE PROTEIN		1-44	12-45						
BIA CAMO		CALE NO DAME MOSAIC VIRUS (STRAIN FIDC)	1.11	176-419						
BLO CAMVE	INCLUSION BODY MATRIX PROTEIN	AM)	-11	378-419						
PIBLO CAMVI	INCLUSION BODY MATTLY PROTEIN		1.17	378-419						
THE CHAM	INCLUSION BOOT MATRIX PROTEIN		1.1	374-419						
	INCLUSION BOOY MATRIX PROTEIN	BOURG)	1	378-419						
	INCLUSION BOOT MATTUX PROTEIN		111							
ì	INCLUSION BOOY MATRUX PROTEIN	CANALINA ELITADO MESO MESOS DE LA PARTIDA DE DESCRIPCIONES DE LA PARTIDA	_	372-406						
1	DACLUSION BODY MATRUX PROTEIN		3	132.179						
VOOR SARIY	INCLUSION BOOY MATRIX PROTEIN		ž.	190-324	491-332					1
1	PROBABLE PROCESSING AND TRANSPORT PROTEIN		100							
l	PROCESSING AND TRANSPORT PROTEIN	I	395301							1
1	PROCESSING AND TRANSPORT PROTEIN	HERDES SOCIETY VIKUS (TTPE 1/3 I IANIF ATTENDED)	174.162							
l	PROCESSIONS AND TRANSPORT PROTEIN	HELVES SDOTLEX VINUS (1175 17 STROUT)	464-500							1
١	PROBABLE PROCESSING AND TRANSPORT PROTEIN		25.55							
l	PROBABLE PROCESSING AND TRANSPORT PROTEIN	GRUESVAUS 1778 I (ISOUALE RYSSAN)	₩. <u>;</u>	201-305						1
l	PROBABLE PROCESSING AND TRANSPORT PROTEIN	KERPESYTIUS SADVIJU (STRAM 11)	21139	Г	147.2					_
	PROBABLE PROCESSING AND TRANSPORT PROTEINA	ARRING CYTORGUALOVINOS (STRAIN SHALIT)	28.53	20.50						
1	PROBABLE PROCESSING AND TRANSPORT PROTEIN	PARLIDOLABRES VIROS (STRAIN INLIANAS CINCOLAS	F0.224							1
HOP HEVB!	THANS ACTING TRANSCUPTIONAL PROTEIN ICPO	BOVING NEXT SYLVES LIVE I (STRAIN 1977)	190-324							1
PICO MSVBK	TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICPO	BOVING MEN ESVINGS LIVE : (** TO A DE CA)	1023-1054							1
PICK NSWA	TRANS-ACTING TRANSCRIPTIONAL ACTIVATOR PR	MANUELS DISEASE MANUEL VINCENCY CONTRACTOR	20-026							1
HON YZYD	TRANSLACTING TRANSCUPTIONAL PROTEIN ICH	VALUE LA-LOSTEN VINCE (STRAIN ADIÉM)	145.02							1
MEAS HONYA	TRANSCRIPTIONAL REGULATOR REAL HUMBLOO	LEADER CALIFORNIA TITLE I / STRADN 37)	241-275							1
POEAS HISVII	TRANSCRUTIONAL REGULATOR REAL	COLUMN LIPE DE CYTELIS TYPE I (STRAIN ABAP)	163:316							\downarrow
PIEGO HEVED	TRANSCIE TIONAL REGULATOR LESS NOMICO	VARICELLA POSTER VIRUS (STRAIN DUMAS)	195-229	36.30		1			1	1
PIEAS VZVD	TANKOUTTONAL ALCOLATOR LESS FISHERS	EFYLINE MEMPESVIAUS TYPE 4 (STRAIN 1942)	2.2						ļ	1
PIEM HSVE4	DOCTIAND EALT FROIDS CON	FOLINE HERPESVIKUS TYPE I (STRAIN ABAP)	2						ļ	-
PEH HIVED	DOCEDIATE CALLY PROTEIN CON	HERPESYRUS SARON (STRAIN II)	2			1		1		ļ
PEG HSVSA	DOCEMATE LANGE TO THE PARTY OF	HEBITAN CYTONEGALOVINUS (STRADN ADION)	3			\downarrow				L
PERS HOWA	MTFOIREIGHE FROIEN IN	HUMAN CYTOMEGALOVIRUS (STRAIN AD169)	3				-			L
PIRIT NOWA	NYPOTHE FIGURE PROJECT TO ANGROUPING PROF		200				1		ļ	L
PKABL PSYRY	TYLOSTIE PROTEIN KIRKASE I KANGORATIO PROT		2			1	1	1		L
PKABL MEVAB	TYROSOG PROTEIN KANASA INOMININA	_	2	263.20		\downarrow	1		L	l
PKAKT MAVAT	AKT KDASE TRANSLOGGING THE ANSTORAGIO PROT		3	200			1			L
PICFES PSYGA	TYROSDIE TROTEIN KIPASE I MANSFOLATIO PROT		2			1	1		L	\mid
PICTOR TIVER	TALOSOMEMICIES		22.53	638-479		1	1	\downarrow		ļ

Trigged Scripts (SALE TANDED SCRIPT)	978.552	1111100016	All Wester (no hacterise hates)								
Through Excitational Properties 144	T P HAME		YRUS		П	П	П	48543	REAL		IVIII.LI
Principal RAMS AMSACH AMSOC REPORT READ	KFTS FUSIV	KINASE TLANSFORKING PROT	FUTNAMI SARCONIA VIRUS	П		П	П				;
Principate Bayes	PKITH AMBPV	THY SEDIME KONASE	AMSACTA MODREI ENTOMOPOXVIRUS	47.81							:
Principace English	KE CAK	THYLODINE KOKASE	CAPAIPOXVIRUS (STRAIN KS-I								
Principate EAALE PRINCES SERVES VARIES (TITELAN FED) 90-114	KITH COV	THYLODINE KINASS	EPSTEIN-BALL VIRUS (STRAIN B95-1)		431-472						:
Principate (NAME PRINCES SAME EX VALIG (TYPE 1 STRANK (CL)	PKITH MSVII	THYNADOME KIMASE	HERPES SECRECK VIRUS (TYPE I / STRAIN I 1)	90-134						j	•
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		FELINE LEUKEMIA PROMINUS FTT	163-437					1		İ
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	LANCE ROCKERS PROTECT	CANINE DISTEMBER VIRUS (STRATH ONDERSTEPOORT)	11.174	118-811	200-051			Ì		i
	Land Inches Parities	CHANDIPURA VIRUS (STRATM 1613514)	10.44	121.300						
	CALL FOR ABOUT BE	BOYING CORONAVIRUS (STRAIN F15)	149.363							
	COLUMN SOUTH	BOYINE CORONAVIBUS (STRAIN ACEDUS)	10.00							
	MINISTER SECTION	CANTHE ENTERIC CORONAVIRUS (STRAIM K178)	165-127					Ì		
200	And contact and the	HEMAN CORCHAVIRUS (STRAIN OC43)	116.313							:
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PHCAP MOPES	MUCL EDCAPSID PROTEIN	MOPELA VIRUS	55.TB	\$.E			-		
PICA MAD	MACLED CAPSED PLÓTERA	MARRY VIRUS (STILARY SAL-1)	214.33	3					
TICAN MORNI	MUCLED CAPAD PROTEIN	MACAPS VIRUS (STRADY MIYALIARA VACCINE)	214-355						
MCAD MY	MUCLEOCAPSID PROTEIN	PROSPECTIFIL VAUS	1:1	27.0	111.341				-
WCA HINC	MUCL FOCAPSIO PROTEIN	HERIAN PARAMELUENZA I VIBUS (STRAIN CIM)		441.510					
THE PERSON	MUCTEDCAPSID PROTEIN	HABIAN PARAINTLIENZA I VIRUS ISTRATY WASHINGTONIESTY	_	441.510					
WAY WAY	MCCCAND MOTEN	HAGAN PARAINFLLENZA 3 VIRUS (STRAIN TOSSUBA)	214.34	14.33					:
PHCAP PURE	NACH EGCAPSID PROTEIN	MAKAN BABANAT MENER TATAN	9	F		İ		<u> </u>	
PKA PAR	MUCH ECCAPSID PROFEIN	MATCH DAD AND LINES AT LIBERT SON THE STRAIN		2	3	169.491			
PHCAP PICHE	MUCLEOCAPSID PROTEIN	IRRIAN PARAMETERS A 48 TABLE SERVICE (11)		2					
PHCAP PIARY	PACLEDCAPIN PROTEIN	PICKODE ABOVECIS					-		
PACAD PIRTY	MUCLEOCAPSID PROTEIN	PIRY VIRUS		916					
PHCAP PUBBL	MICLEOCAPSIO PROTEIN	PURDIALA VIRUS (STRAIN HALLMAS RI)			:::				
THE PUBMS		PUTDAALA VIRUS ISTRATIN SOTRANIO!	=	6.15				i	
THEAD PYN	MUCLEOCAPSID PROTEIN	PREUNIONIA VIRUS OF ANCE	10.00	24.00	18:38		-		
THE MAY	PACLECCATIO PROTEIN	AARIES VIRUS (STAALY AVO!)	133.103						:
PHCAP SENS	MUCLEOCASID PROTEIN	SEMBAI VARUS (STRAIN Z / HOST AIUTANTS)	111.111	141.00				1	
MCAP SENE	MUCLEDCA/SID PROTEIN	SENDAI VIRUS (STRAIN ENDERS)	11.33	100					
PICAS MORE		SENDAI VIAUS (STRAIN Z)	211.373	10.00				-	
PHCAL SECUL		SEOUL VIRUS (STRAIN SR-11)	=	5.74	- FE				:
אכיר פאין			215-267	173-406				İ	-
PACAL STRIV		W NET VIAUS	113-144					İ	: : i
PICAP TACY	MUCLEOCAPSID PROTEIN	TACAURE VIRUS	¥.6₹	230.364				İ	1
PNCAP TOSV			27.70						<u>.</u>
MCAP TSWYB		CPMIJAR	20.50			-		İ	-
PHCAP TSWNH	MCLEOCAPSID PROTEIN	ISOLATE)	3.28						-
THE PARTY	MUCLEOCANSID PROTEIN	WILT YAUS (STRAIN L.)	79.120					Ī	:
THE WORL	MULEUCAYSID PROJEIN		31.102						:
A CHANGE	MULEUCATIO PROJEIN	7	266-323						İ
THE VEHICLE	MCLECCASIO MOTEIN			249-325					-
PICAP YSVID	PACH FOCASID PROTEIN	VESTITA A STORATION VIAUS (SEAD) THE INDIANA / STRAIN CO	5						
PHCAP VSVSJ		VESICIA AR STONIATITIS VIRUS ISTRAIN SAN HAND		1				j	-
PHEF HYZBE	NEGATIVE FACTOR	E BEN	=		\dagger		j	j	į
PHEF HYZDI	NEGATIVE FACTOR	ŀ	Ī	T		-		Ì	1
PHEF HYZRO	MEGATIVE FACTOR	•	23:45				İ	-	
PREJ INVISIO	PEGATIVE FACTOR	37	109-150				İ	-	
PREJ HYZST	MEGATIVE FACTOR		101.101					İ	!
PARE CIVES	AECATIVE FACTOR	SIMILAN BONDMODEFICIENCY VIRIS (ISOLATE AGM / CLONE CA)	٥						:
PHILAH IABBA	MEDINAMORDASE		T				i		-
PRAM IACAD	AFURAMONDASI	PRESENTAL VINES (STRAIN ACTUAL		1					
PREAM MOR	MEURAADVIDASE	T		†	1		-		Ī
MALLE LACKO	MEURAADNIDASE	MIST VANIALITY		†	T		1	+	
Γ	NEURAMBMEDA SE	INFLUENZA A VIRUS (STRAIN ACHER ENPENNSY, VANIAAI 29)	148-101	1	1		+	1	
	MEURAMENDASE	NYLUERZA A YIRUS (STRAIN ADUCIKOERAKANYAN)	=	\dagger	\dagger			+	i
П	MEULUMMOASE	USWEYBAD	Γ	25.25	$ar{I}$		†	+	T
	MEURANGMIDASE	INFLUENCA A YIRUS (STRAIN ARQUINICONINA		117:61			†	+	1
	MELRAAMMDASE	MUCKYIIAI)		107-191				+	
PRAM IAKE	MEURAMMOASE	INTLUENZA A VIRUS (STRAIN AKIEVIŚYTY)	30.01		H		Н	H	
		•							İ

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					П	П	Ιī	1	Т	i
JACO N	ALLMOTIS	user (no hacteriophoge)	ABEAL	ARGAI	TABLA	1	4	1		-
200	PROTEIN	VIRUS	10.00				1	1	İ	<u> </u>
NE AN INCH	MEURALAMINDASE	MELL ALIYATA	2.00				1		İ	_
	NET BEALDINGS	DATLUENZA A VINUS (STRAM APREMINISTEM PROCESSES AND AND AND AND AND AND AND AND AND AND	10.00				+		İ	
1	VEH TO A VEH TO A SE		1					j		_
FRAME IARUS	LANGE AND AND			Ī						
PRICE INSUE	33 4 0000 7 010	Т								-
PRANI LATER	Machine Company	IALIAGRO?)								-
PALAH IATRA	MEDIAMINEDASE	PARTIENZA A VIRUS (STRAIN ACUSSAMOT?)	5			I		İ		
PHRAM IAUSS	NEURANDASE	DELIENTA A VRUS (STRAIN AMHALEAIAINE)	19:01							
PHILAM LAWING	DELILAMINIOASE	ACTION A PORTS (STRAIN BARLINGIA)		3				Ì		
FRAM PROF	MELIRAMIDADASE	INTERNAL BUILDING TO AND MAINTAIN BANDARD KONGALOTS	2.46	149-113			Ì	Ì		. !
MANA PASS	NEURANDEDASE	INCLUENCA E TIMOS (SI PARA ESTANO	146	344.383						
	MEI III AMBIEDASE	INTLUENZA 9 VIRUI (STRAIN BALLONY)	T	7117						:::
	San in Asserting A.C.	LIGHT STORY							_	-
PACK BOLK	TRUMPINION ST.	INGLUENZA B VIRUS (STRAIN BALARYLANDYS)								
PRAN PEND	MECHANISM SE	DELLENZA B VIBUS (STRADA DAEATHUS/MS)	7							
PRICE DONE	KEULAMONAS	MELLIENZA B VIRLIS IS FRAIN BIORE CONSMO)	Ž	300				İ		
PRIME BROK	NEURANAMON SE	SALISANIA SI WALLE PETRATOR BEDROAFORE/11/79)		3.5						
PRAM PRS	NEUBAANMEDA SE	TATELOCKET CONTROL OF THE PARTY CALIFORNIA	5.30	100-303						
PART DATE	NEURANGEMBASE	TOPLOCACE VINOS (STEWARD COSTS)	5	341-312						
200	ı	INTLUENZA B VIRUS (STRAMA POR LONING	100							:
2000	PROBABLE STRUCTURAL PROTEDY PRECURSOR	BOARTY DENSONUCLEOSO VIRUS	Γ	204.23						
200		INGATIENS MECADIIC SPOT MAUS (STIMINALIN)	I						Ī	
PASS INSVI	TOTAL SECTION AS ASSESSED.	FORLATO SPOTTED WILT VIRUS (BRAZILIAN ISOLATE CPONTION								
PASS TSWVB	NON-STRUCTURAL PROTEIN	TOMATO SPOTTED WILT VIRUS (STRAIN L.)	Ī							
PRIS TSWM.	MON-STRUCTURAL PROTEIN	AMERICA APPORTE ENTONOPOXYIAUS	٦	100						
PATE AMERY	MUCLEOSIDE THE HOSPIAN I AND I	CURRENT A DIENNIS ENTONOPOXYIRUS	132-169	113-440	36.33					i
PATE CIETY		CACALLA COMPANIA COMPANIA CACALLA CACA	26-90	34F30	309.500				Ī	
PATE VACCE	MUCLEDSIDE TURNOSPHATASR I	VACCINIA VIAUS (3130417 CV LT.)	26.00	111.339	\$49.590				Ì	
AVA INCA	MAICL EDSIDE TRUPHOSPHATASE!	VACCIMIA VIRUS (STRAIN WATE	_	19.30						1
7010	MAICL EGSIDE THIPHOSPHATASE!	VARIOLA VIRUS	Γ	611.73						
۱	MAINS ANTICING STRUCTURAL PROTEIN	HERPES SIMPLEX VIRUS (1 TFE 07 31 PAILS CONTINUED	131.110							-
1	HER WALLOL WIELASE CATALYTIC SUBUNIT	VACCINIA VIRUS (STILATIN COPEMIAULIA)	2							
	POR WALFOL WASTASE CAFALYTIC SURLANT	VACCINIA VIALIS (STANIWAR)	2	1				٦		:
ı	ANY WALKS THE LASE CATALYTIC SUBURIT	VARIOLA VIRUS	77							
١	ACCUMANTAL AND VACERASE AFOULATORY SUBUNGE	CAPILIPOXYIRUS (STRAIN KS-I)								
3		FOWLPOX VIRUS								
PPAPE FOWEN		VACCINIA VIRUS (STRAIN COPEMIAGEN)	101							
PAN VACOL		VACCENA VIRUS (STRAPI WR)								
PASS VACCV		VARIOLA VIRUS	20.20							
PPAPS VARV	POLITICAL PRINCIPLE OF THE CHOICE	ALTIOCRAPHA CALIFORNICA MUCLEAN POLYIEDROSIS VIRUS								
PPEI3 NPVAC	12.1 KD FROIEN WAS GEGOVE	ORGYLA PSEUDOTSUGATA ARR TICAPSID POLYTEDROSIS VIRES								
PPELL NOVOP		AUTOGRAPHA CALIFORNICA MUCLEAR POLYHEDROSIS VIAUS							İ	
TELL MOVAC	MAJOR DOUBLING CAME V PROTECT	ORGYNA PSEUDOTSUGATA MARTIC APSID POLYNEDROSIS VIRUS 199-149	T							
PPESS NOVO	MAJOR DEPLEATE IN THE BATTER OF NICE AFGION	AUTOCRAPHA CALIFORNICA NUCLEAR POL MIRDROSIS VIRUS	T							
PPER MPVAC	AL S RO TROI BLY IN TO 124 BATEROEPIC REGION	GREYIA PSEUDOTSUGATA AUD. TICAPSID POLYTIEDROSIS VIRUS 47-43	7							
PPAR NOVOP	O I KO MOJEN WATER	HUMAN ADENOVIRUS TYPE ?					İ			
PHYS ADEO!	MATURAL PROJECT	HUNLAW ADENOVIAUS TYPE 1	1.3							
PPIVE ADEAL	PACTER VI PRECIEDOR	MURIAN ADEMOVIRUS TYPE \$	12:21			1	771.0 341.	106.330	1142,360	
PPIVE ADEDS	PROTEIN VI PRECURSOR	MARIE SY VELLOW MOSAIC VIBUS (GERNIAM ISOCATE)	129-363	=	1	E)-(2)	7	Т	917.10	114.2407
PPOLI BATMO	GENOME POLYPROTEIN I	E. S. C. C. CON LINEAR VIRIS (IAPANESE STRAIN II-1)	179-363	431.705	741.377	4		Т		
POLI BATAU	GENOME POLYPROTEIN I	SOUTH TELESTRICE CHICAGE MOSAIC VINUS	130-161	165-216	36.3	12.	7	Т	170	
700 I	AWA! POLYPROTEIN	HUMUNAMAN CAN BAR VIBIR	130,211	410-919	636.677	<u>:</u>	20.12	278.1012	Z.	
PIOL OF	RUCK I POLYPROTED	CAN ENTRY OF PARTY WATER STATE AND AND STATE OF THE PARTY	213.270	479-977				1		1
POL! TINYS	NAME POLYPROTEIN	TORATO BLACK MAND VINCE AS INC.	#.E							
PAGE 1 TASM	RIVAI POLYPROTEIN -	TOWALL MANAGE THE VALUE (CREMIAN ISOLATE)	740.55	211.690	139-777	117:01		1		
PROL 3 BATARO	GENOME POLYTROTEIN 2	BALET TELLOT FIVERING TOWNS TO THE								
1										

MCGENE	IALLMONS	All Water (se harmelands and								
TILENAME	PROTEIN	YRU	ARGAI	ARCA 5	7877	AREA 4	AREA S	ARFAG	ARFA 9	17387
PPOLI BATHU	GENOME POLYPROTEIN 2	BARLEY YELLOW MOSAIC YRUS (JAPANESE STRAIN II-1)	Γ	139-773	717-123				Π	
ייסני מוני	INVAJ POLYTROTEJN	GRAFEVING FANLEAF VIRUS	ş	20725				-		
PPOLY TRAVS	ANAS POLYFROTEIN	TOMATO BLACK RING VIRUS (STRAIN S)	Ę							
PPOLY TREVA	RAKAJ POLYPROTERM	TOMATO RINGSPOT VINUS (ISOLATE RASPBERRY)	136-206	74.75						
PYOLO BOYEV	GENORGI POLYPROTEIN	BOVING ENTEROVIALIS (STILAIN VG-1-17)	111-111	701-1001	1313-1416	1459-1507	1534-1617			
POLO BYDYN	GENOME POLYPROTEIN	BOVINE VIILL DIALULA VIRUS (ISOLATE HADL)		160-900	(99-62)	1033-1674	1363-1344	1393-1443	1869-1910	2226-2260
	GENOME POLYMOTIEM	BOVING VIDAL DIALUIEA VIRUS (STRAIN \$D-1)		165-929	(97-629	1033-1034	1303-1344	1391-1443	1775-1120	2136-2170
•	GENOME POLYPROTEIN	BEAN YELLOW MOSAIC VIRUS	0(1-94							
1	GENOME POLYTROTEIN	COXSACKIEVIRUS A21 (STRADY COE)	(1-6	966-195	B69*144	1045-1100	1694-1546	1607-1641	1805-1839	1901-1946
_	GENOME POLYPROTEIN	COXSACKIEVIRUS AP (STRAIN GRUGOS)		1040-1044	0961-7681					
ı	GENOME POLYTROTEDY	COXSACKIEVIRUS BI		1901-1201	1261-9481					
١	CENOME FOLYPROTEIN	COXSACKIEVIAUS B1	18-09	1074-1070	1878-1504	4				
	GENOME POLYPROTEDM	COXSACKIEVIRUS B4	15.49	199-139	1937-1061	1177-1922				
	GENOME POLYPROTEIN	COXSACKIEVIAUS BS	3	1024-1070	1879-1974					
PPOLO CYVY	GENOME POLYPROTEIN	CLOVER YELLOW YERN VIRUS	38.50							-
PPOLO DENIS	GENOME POLYPROTEIN	DENGUE VIRUS TYPE I (STRAIN 836-1)	34-106							
PPOLO DENIA	GENOME POLYPROTEIN		36-106					-	•	
	GENOME FOL YPROTEIN		34:106							
ŀ	GENOME POLYMOTEM	DENGUE VIRUS TYPE I (STILAIN SINGAPORE 5275-90)	24-106	112-673	26.08	1142-1179	1314-1420	1614.1648	331.3354	2946-1016
L	GENOME FOLYPROTEIN	DENGUE VIRUS TYPE I (STRAIN WESTERN PACIFIC)	74.106	133.674	\$66-196	011:01				
	GENOME POLYPROTEIN		167-07							Ī
PPOLO DEN12	GENOME POLYPROTEIN	DENGUE VIRUS TYPE 2 (ISOLATE MALAYSIA N2)	567-83				Γ			
	GENORG FOLTPROTEIN		Γ	728-777	504-198	011-11	134-1250	1410.103	1613-1649	2517-2551
	CENONG FOLTPROTEIN	POKSI	74-198		<u> </u>	30170	124-1750	1416-1455	1615-1649	ZG:33
	GENOME POLYPROTEEN		118-177							
	GENOME POLYPROTEIN		497.546							
П	GENORGE POLYPROTEIN		Г	718-777	\$64-196	1144-1110	1246-1380	1416-145:	1615-1649	1517-1551
ł	GENOME POLYPROTEIN	(EAC)	113-243	394-03						
	CENOMB POLYPROTEIN		14-101	728.777	825-508	941-985	1144-1360	1344-1280	1410-1433	1017161
roto pout	GENOME POLYTROTED	974)		352-595	681-715	006-991	966-1000	661-1961		
- 1	GENOME FOLYTROTEIN	(STRAIN PUG-218)								
	GENOME POLYPROTEIN			959-993	1315-1419			1704-2730	2940-2938	2910-3014
ı	GENOME POLYMOTEIN			1380-1414	2514-2555	1701-2735	1241-2975	1977-3011		
700 5010	DENOME POLYMOTEIN			076-113						
i	Charles Oct (No. 1)	ENCENTIONAL DATACETTS VIRUS	611.76	1	221-124	1665-1706	178-162)	-		
•	CONTRACT VALUE OF THE CONTRACT	ENCENAL ONOTO A DITTIE VITTIE STAND ENC. D DIABETOCINI LE 130	T		1074-137B	1334-157	100			
PPOLG ENAGS	GENOMO POLYPROTEIN	MENGO ENCEPHAL DAPYOCAEDITIS VIBUS (STRAIN 174)	T		100	2/61-0761	871.18			
ı	GENOME POLYPROTEIN		=======================================	T						
PPOLO FLOVI	CENCHE POLYPROTEIN	NA10-61)	Ŀ	394-326	178-12	101133	1697-1528	2165.2200		
PPOLO PADYA	CENOMS POLYPROTEIN	Т	Ī.	Γ	111411	1100-1164	Т	216-213		T
PPOLO, PADVO	GENOME POLYPROTEIN	FOOT-AND-MOUTH DISEASE VIRUS (STRAINS OIK AND GIBES)	231-255	101-1131	1493-1528	2164-2189	Т			Ī
PPOLO FADYS	CENONG POLYPROTEIN	ANTA PAU IC.S		493-778						
PIOLG FADYT	GENOME POLYPROTEIN	AUS (STRAINCI)		203-317	111745					
POLO HCVI	GENOME POLYTROTEIN		364-398							T
PPOLO HCVA	GENOME POLYPROTEIN	HOG CHOLERA YTRUS (STRAIN ALFORT)			84-749	1033-1070	190-1335	130.1313	1779-1820	2136.2170
			2464-2500	1515-1559	2667-2708	3057.3088	Т	3606-3460	1	
POLO HOVE	GENOME POLYPROTEDY	HOG CHOLERA VIRUS (STRAIN BRESCIA)	440-493	626-660	622-549	1033-1070	1175-1235	177-1170	2136-2170	2381-2436
PPOLG HCVBK			۰	2515-2559	3647.1706	3057.3098	Т	Г	Т	
PPOLO HCVES			_	1311-2365				г		T
PPOLO HCVN	OCHORE POLYTROTERY	IRPATITIS C VIKUS (ISOCATE ECIO)	65.59					T		T
]

		All Victors (as hecertoshiess)			П	П	П	П	П	
יייייייייייייייייייייייייייייייייייייי	PENTANA PENTAN	VIRUS	AREAL	AREAL	1414	AREA	1	N N		ANTA I
1	CENTRAL DOL VALOTEDI	HEPATITIS C VIRUS (ISOLATE M)	364-368							
TOTAL MANAGEMENT	COURT OF COURT	MEDATTELS CYTELS (ISOLATE HCV-436)	364-398							
1	WANTE FOLLIANS	LICES THERE IS VALUE (ISON ATE MOTER)	134-270							
П	GENOME POLITICIES	LEGATORIC MAIN AND ATE HOTIS	14.311							
	Dendre Political Lay	LEST TITLE CHAIR CIGOLATE HCV.EST	197-398							
ł	CENTRE POLITICAL	LINES ATTITION WOLLD ATTEMORD	157.791							
ı	CENCHE POLYMOIELN	AREA TITLE COMING OCCU ATTENCIES	¥.35							
PPOLO HCVA	CENCINE PURITING BANK	MEDATTING CHAILS GOOD AT MC-161	- F	311-11	3042-2116					
100 KW	UENCHE FULTINOIEM	TAREA ATTENDED TO AND ATTENDED TO	34.38							
Proto HCVIS	GENOME FOLYTHOTHEN	MENALTING CYTHOS (1904-1917)	Τ	1714.1746	2087.3116	2448-7502	3538-2377			
PPOLO MCVIA	CODYCHES POLYPROTEDY	REPAILING VALUS (ISOLATE PC-48)	T							
PPOLO HCVIT	ODNOME POLYPROTEIN	HEPATITIS C VIRUS (ISOLATE JAPAMESE)	1	600						
PROLE HEYTY	GENOLG FOL YPLOTEIN	HEPATITIS C VIRUS (1SOLATE HC-JT)	7	331.235						
ł	GENORG POLYPROTERY	HEPATITIS C VIRUS (ISOLATE TAIWAN)	2	338-3365	2444-250)					
L	CONCLUSION FOR YPROTICIN	HEPATITIS A VIRUS (STRAIN 24A)		101-135	201-217	20.00	1021-1035	3:		
ł	CENTRAL PROTEDI	HEPATITIS A VIRUS (STRADI 40C)	1-1)	101-135	201-137	20.00	101-102	=======================================		
١	Appeared for venoticity	HEPATITIS A VIRUS (STRAIN 189)	143	101-135	101-101	138-904	1021-1055	13.13		
STATE OF THE PERSON AND THE PERSON A	Course for the Other	HEPATITIS A MAUS (STRAIM CRUSS)	2	101-138	181-801					
2000	Course for the Other	HEPATITIS A WAUS (STRAIN GA16)	11-01	113:216						
TANKS STATE	CONCRETE ON CONCRE	INFOATIFIE A VIRLIS (STEAM PAI-175)	Ş	101-135	165-695	10.904	\$501-1001	1103-4151		
TOTO POANE	CONCRET COLLEGE	LEPATITIE A VIEWS (STRAIN LA)		101-135	107-101	130-804	{\$01:1201	1807-1131		
MOTO NO VAN	DEMONS POLITICALIN	LEGA PATHE A VIBILE ACT BATH LANDS	Γ	101:101	20.237	130-504	1001-1033	1103-1150		
POLG POAYS	GENOME FOLTPROTER	TEPAINS A VINCE LANGE MANUAL AND A CALL ST.	Ī	67.0	207.24	140.00	1623-1039	1115-1155	1136-1193	
POLO POAT	GENOME FOLTPROTEDM	SUMMA PERMITTER A VINCE (STRAND POLICE)	Ī	101.135	783,237					
PPOLO HOVIA	CONOME FOR TPROTEIN	SUMAN ILANIELS A VINOS (SI PARA CITAL)	3	100.100	1170-1111	1417.1920				
PPOLO HEVIA	CENONE POLYPROTEIN	HUMAN BURNOVIRUS 14 (MRV-14)	Ţ	100						
PPOLO HEVIB	GENOME POLYPROTEIN	HUMAN INIMOVIRUS IA (MRV-IA)	T			ľ				
PPOLO, HRV2	CENONES POLYPROTEIN	HUMAN RUMOVIRUS IB (HRV-18)		W. 191	1011					
PTOLG HENTE	OENONG POLYTROTEIN	HUMAN MAINOVIKUS 2 (HAV-2)								
PPOLO INCEVI	GENOME FOLYTROTEIN	INDIRAM REINOVIKUS BY (PAK V-87)	Ţ		1000	177	1017			
PPOLO INDVO	GENOME FOLTTROTEIN	MUMAN ENTEROVIRUS 10 (STRAIN 167071)	Т		200		1			
PPOLO IARVI	STRUCTURAL POLYPROTEIN	AYAN BRECTIOUS BURSAL DISEASE YTRUS (STRAIN OH)	32.5	- F	23.5					
PECK O 1AEVS	GENOME POLYPROTEIN	IAPANESE ENCERHALITIS VIRUS (STRAIN SA-14)		311.336	25.65	#0-1014 #	22.459	1667-2019	2776-2777	2767-2823
			1122-1159	31.743						
PACE O TARVI	CENCHAR POLYPROTERY	JAPANESE ENCEMALITIS VIRUS (STRAIN SA(V))		111.136	578-576	1014	1409-1430	240.1407	115.17	33:33
			112.119	3303-3428						
2011	CENTRAL POLYPROTEIN	JAPANESE ENCEPHALITIS VIRUS (STRAIN JAOARS913)	74-128	211-296	378-576	900-1014	1409-1430	2463-2497	111.111	131.311
1			3338	3387-3424						
AUMIN D SOME	GENOME POLYPROTEIN	JAPANESE ENCEPHALITIS VIXUS (STRAIN MAKAYAMA)		131-113	44.50	ş	<u>=</u>			
	GENOMOS POL YPROTEIN	KUNUM VIRUS (STRAIN MRMAIC)	74-108	307-251	831-488	344-348	22.23	1740-1771	200	365.763
200	CENTACE BOL VEROTEDA	LANGAT VIRUS (STRAIN 1921)	84-102	431-465	943-996	101-102	1932-1966	1836-1991		1003-3017
			3107-3145							
VI C COM	DENOME FOR YPROTEIN	LANGAT VIRUS (STRAIN YELANTSEV)		\$ 1						
1 0 1044	CENOME POLYPROTEDI	LOUPING BL VIRUS (LI)	(4.12)	23:22	534-65					
ACM D MOSA	GENOME FOLYTROTEIN	LOUPING ILL VIRUS (STRAIN SB 536)	131-145							
200	CONCAST NO. VPILOTEIN	MOSQUITO CELL FUSING AGENT (CFA FLAVIVIRUS)	90-114	908-942	204-2067	2630-2669	2014-2095	240.34		
	CENONG POLYPROTEIN	MUTUAY VALLEY ENCEPHALITIS YINUS		209-253	123-477	3	100-			
	CENTRACE POLYPROTEDN	DIANTHOGALISM MOSAIC VIRUS	481-515	75576	1073-1106					
	CONTRACT VALOUEDA	PEPPER MOTTLE VIXUS (CALIFORNIA ISOLATE)	35-100	201.24	177411	704-72	877-962	17-467	103	1167-1701
			1488-1579	1717-1621	1941-1943	200.43% 200.43%	1136.D10	2005-2039	1003-1037	
21 00 000	CENTRAL POLYPROTEON	POLIOVIRUS TYPE I (STRAIN MAHONEY)	ī	1046-1101	14141	100-134	92.40	10: 1X		
2000	CONCAST POLYPROTED	POLJOVIRUS TYPE 1 (STRAIN SABBY)		66-633	1947-1162	1415-1449	1561-1549	160.00	106-1642	
	CENTRAL POLYPOTED	POLIOVIRUS TYPE 2 (STRAIN LANSING)		118-248	1045-1180	1412-1467	1902-1547	1604-1649	106-1940	1902-1947
POLO POLIT	GENORE PLATERING									

								-		
FILE NAME	Pactren	All Virtes (no bacteriophages)				I				
POC 00.33	GENOME POLYPROTEIN		AREA	AREA	48542	AREA (AREA 5	AREA	ARCA	AREAS
11 DO 0 104	OPNOWIR BAY VOS CHERA		Ī	167-431	1045-1100	1413-1447	1503-1543	1604-164	1804-180	100
WAS 0 1044	Carried for the press	(POLIOVILUS TYPE) (STIAM 20127)	9-43	016-348	1044-1098	1412-1446	1494	1607-1643	185	100
	VENNER PULTPAULIN	EONUT AND PACEON ITALIBY	3	26.25	1044-1099	1412-1446	1491.1144	1607.1641	180	
1	UENUME POLYMOTEIN	PLUM POX POTTVINUS (STRAIN D)	25.20	3.5	920.260	115.067	1			
THOUS PLANS	GENOME POLYPROTEIN	3	16-33	784-418	1166-1197					
TOTO LEVICA	GENOME FOLYPROTEIN		E 20		60.03	N. II		1		
MOCO PLEM	GENOME POLYPROTEIN	OWC)	164-204	401-04	40.50		77.7	1		
100 M	CENCHAS FOLYPROTEIN		201-10	434-464						
TOLO PIENY	GENOME FOR YPROTEIN	MUTANT HA S-1)	35.359							
Proto Pasiery	GENOME POLYPROTEIN	I	125-359							
HOLD PYTC	GENOME POLYPROTEIN	AIN DPD!)	201.314	161.10	36.00	1				
			100		1000		101-101	1	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	20 10 10 10 10 10 10 10 10 10 10 10 10 10
POLO PYTHU	OENONG FOLYPROTEIN	POTATO VIJUS Y (STIAIN C)	131.104	100		20,000				
PPOLO, PVTM	GENOME POLYMOTEIN	MOASTA M	R	66.133						
				26-75 20-75	9	\$ 8	101	143-1336	1726-1772	1777-1818
PPOLO PYYO	GENOME POLYMOTERN	POTATO VIRUS Y (STRAIN IN	20.00							
,			200			22	40:	2	- E	137.18
PPOLO PWYSE	CENOME FOLYPROTEIN	POTATO VIRUS Y (STRAIN O)	1	17.						
POLO PENTIS	CENOME POLYMOTERN	VIRTIGACE AND CONCERN				2				
PPOLO PYFVI	GENOME FOLYPROTEIN	5								
PPOLO STEWN	GENOME POLYPROTEIN	Ī								
POLO SYDYN	GENOMA POLYPROTEIN		T	7111	1374-141)	3	926	2703-27/7		
PIOLO SYDYU	GENOME FOLYPROTEIN			673-707	775.773	27.00 27.00	1404-1438			
POLO TREVS	GENOME FOLYPROTEDY	1		201		226				
POLO TIENW	CENTRAL POLYPROTEIN	T	L	Т	27 - 20					
			1	Į,		761	2	P064-424	3127.	2535-2500
PIOLG TEV	DENOMB POLYPROTEIN	TICK-BORNE ENCERNALITIS VIRUS (WESTERN SUBTYPE)	1	331.372	1177	1144.1180	2071			
			E	3053.30M	3162-3148		7441-162-	*	1807-9007	2867-300
POLO TIEN	THEREBYS MARINE ENCEPHALOMYELITIS VIXUS (S	ALOMMELITIS VIRUS (\$ TOBACCO ETCH VIRUS	Т	16533	Т	1				
		-	2	174741	Ţ,	2385,3414	1787.3191	26	001-01-0	1496-1515
Proce meyo	OENCIAE POLYPLOTEIN		Ť	4151	1601-1633					
OLO DIGINA	GENORAL FOLTER	THERE BY MURING ENCEMIALOM TELLTIS VIAUS (STAAIN DA)	F	Т	1378-16E			T		
TOTAL STORE	CENCHA PALTFROIDS	THERE EAS MURINE ENCEPHAL CANTELITIS VIRUS (STAAIN GOVII)1306-1340	1	100-151	1601-1633			T		
A MAN OF THE PARTY	VENCER PACTIFICIEN		216-259	314-362	Г	76-139	144-1473			
TOUR WHAT	CENCING FOLTPROTEIN	TOBACCO VEIN MOTTLING VIRUS			107-794	34.413	Т	\$ 101.3	101.103	141.143
VACA () VACA	Charles and Second	,	1616-1725 2	12 TO 15 TO 15	3701-3749	L	Γ		1	
- Wall Co.	CAMPLE TOLITACIONIN	SAJC VIRUS II	10-105	201-136						
127	UENCHE POLITING	WEST NELE VINUS	74-101	182-191	117-148	13.E	435-1447	261.243	3135,3176	3111.1111
200	TO SEE A SEE A SEE ASSESSMENT OF THE PARTY O		1320-1337	365 X36	Γ		1	7	_	200
	CENTRE POLITICIES			215-363	21-349	130 . ISA	227 122	7	3018.3004	1417.1441
TEN TEN	CONTROL TO THE CONTROL	R 170-304)		Г	Γ	Г	T-	X31.35	Т	1711 1895
	CENTRE POLITICIEM		75-116	М	125.543	Г	1	_	Т	
100	CENCEL POLITICIEM	POLIDYALUS TYPE I (STRAIN MAHONEY)		1017-103	1415-1449	-	1616161	100	1904.1940	
יותה יכית	MONSTRUCTURAL POLITIKATERY	VENEZUELAN EQUINE ENCEPHALITIS YTRUS (STRAIN TRANIDAD) 145-312	Γ	•	1	1	1-	-		
1	MUN-STRUCTURAL POLITICALEDA	/61 FTV)	310-344						T	
THURS DEVINO	MON-STRUCTURAL PUR TPROTEIN		57	97	984-1610	1007-1001				
FROLK PEYNO	MORESTRUCTURAL POLYPROTEIN			134-113	T			T	T	
OLY HEWAY	HON-STRUCTURAL FOLYPROTEIN		21:33					1	1	
POLY MENTA	NOW ITTUCTURAL POLYTROTEIN		35.33	300			Ī		1	
TOCH KIDOV	MON-STRUCTURAL POLYPROTEIN		137-336	25-136		T		†	1	
	CONCINCIAL BAT BOX CABOATER.						•			

PCCEME	ALMORD	AN VINTER OF DESCRIPTION OF THE PROPERTY OF TH	Γ	. 7.4.4	N VAUV	ABFAA	A REA S	AREA	2	
FILE NAME			4	Ţ,	151777			Г	Г	
POLY RUDY	JETURAL POLY		T	Т		1617.1916				
POLY RAY	NON-STRUCTURAL POLYPROTEDN	5	Τ	Ţ,						
POLY RAY	MONSTRUCTURAL POLYPROTEIN	3	22.6	Т						
POLY RUBY	NONSTRUCTURAL POLYPROTEDM		7		. 77. VIL.	7017.1741				
POLY STV	NONSTRUCTURAL FOLYMOTEIN	AUBELLA YAUS (STRAIN THEMEN)	1	200						
PPOLIN SENDO		SEACHTY FOREST VALUE	1000	16111071	1041.1994	2444.2478				
PFOLM SPIDV		COLON STRAIN COST IN CO.	T.	70.70	340.34%					
MOLL DAY	HONSTRUCTURAL POLYPROTEIN	30	т	131.061						
MOLS EEEV	INVA REPLICASE POLYPROTEIN		1							
POLL SELVI	STRUCTURAL POLYPROTEDM		277	100010						
POLI ELVI	ITTUCTURAL POLYPROTEIN	3	(1)	11.54.54						
PIOLS EEWT	STRUCTURAL POLYMOTER	VENEZUELAN EQUINE ENCEPHALITIS VIAUS (STRAIN TC-1)	062							
POLE BOVS	STRUCTURAL POLYPROTEIN	3	т		1					
PPOLS TROVA	STRUCTURAL FOR YPROTEIN	AVIAN DESCRIBUS BUNSAL DISEASE VINUS (STIAIN 52/70)	3	2017						
ı	STRUCTURAL POLYPROTEIN	3	3	982-162	22.22					
1	ISTRUCTURAL POLYPROTEIN	=	T	207-162	CICAL D				ŀ	
L	MONSTRUCTURAL PROTEIN VP4	П	T	20.00						L
1	STRUCTURAL POLYMOTEIN	AVIAN DEECTIOUS BURSAL DISEASE VIRUS (STIAM PRO-M)	T							
FOLS DAY	STRUCTURAL POLYPROTEIN	AVIAN OFFICTIOUS BURSAL DISEASE VIRUS (STIVAM STC)	Ţ							L
L	STRUCTURAL POLYPROTEIN	3	1	Circuit						ļ
PYOLS CRONNO	STRUCTURAL POLYPROTEIN	US (STRAIN NI)	716-780							
POLS DAYS	STRUCTURAL POLYMOTER	סאייטאסאייטאס ימונט (נתעמא מנונע)	1021							
PPOLS LLYN	STRUCTURAL POLYPROTEIN		Т							
PPOLS MAYT	STRUCTURAL POLYPROTEIN	72)	Т	29-61		1				
PYOLS RUBYH	STRUCTURAL POLYPROTEIN		2				-			l
PPOLS RUBYR	STRUCTURAL POLYPROTEIN	RUBELLA VIRUS (VACCINE STRAIN HIVYT)	999-100							l
POLS RUBYT	STRUCTURAL POLYPROTEIN	RUBELLA VIRUS (VACCINE STRAIN RAJIO)	11.103							
PICE STORE	STRUCTURAL POLYPROTEDI	AUBELLA VIXUS (STRAIN THEALEN)	71							
POLS SPOY	STRUCTURAL POLYPROTEIN	SINDBLS VIXUS (SUBTYPE OCKELBO) STRAIN EDSBYN (2.2)	M. C.							
אסמג בזטאו	STRUCTURAL POLYPROTER	_1	1							L
HOLS WERV	STRUCTURAL POLYPROTEIN	FROM STRAIN ACUS								
PPOL BAEVM	STRUCTURAL POLYPROTEIN	WESTERN EQUING ENCEPTION ILLS VIAUS	T	474.363	1	<u>8</u>				
POL BLVAU	POL POLYMOTED	BABOON ENDOCEMBED VICTOR (1) MAIN								L
PPOL BLVJ	POL POLYPROTED	BOYING LEAGUE A VINIT (IABANGS ISTA AT B) V.II	25.63						L	L
TOL CAEVC	POL POLYMOTERA	A SERVICE A STATE THE BACEPIAL THE VIETE (STRAD) CORE)	171-974				L			
TOL CAND		CASE OF CHASE MOSAIC VIRUS (STRAIN DAN)	177.211							
TO CONT	ERCTMATIC FOLTFROIDS	COLOGE DAY VELLOW ADTELL VINUS	12:21	100.00	447-498	20178	194-970	1310-1331		
POLETAY	POTATIVE POLITICAL	EOLITHE DATECTIOUS ANEWIA VIRUS (CLONG 1349)	313.346	1021-1056						
200	POR POR YPROTEIN	EQUINE INTECTIOUS ANEMIA VIRUS (CLONG CL22)	913-364	1033-1056						\perp
	POT POT VPROTEIN	EQUINE REFECTIOUS AMENDA VIRUS (ISOLATE WYOMENG)	\$12.565	1021-1055						\downarrow
100	NO POLYPROTEIN	FELDRE ENDOGENOUS VOUS ECE!	33,400	623-639	131-139					1
PPCI PIVED	FOL POLYPROTEIN	FELDIG DIGKUNGDEFICIENCY VIDUS (ISOLATE PETALUMA)	479-473	3						
CIVE COM	JACK POLYPROTEDY	FELINE DOGRADOEFICENCY YOUR (ISOLATE SAN DECO)	423-473	3						1
	POL POLYPROTEIN	FELDIE DAALINDGEFICIENCY VIRUS (ISOLATE TIVE)	2.7.T	3						1
ATVO.	ENZYMATIC POLYTROTEIN	FIGWORT MOSAIC VILUS (STRAIN DXS)	9							1
7170	POL POLYPROTEIN	HEDRAN SPIDARMETROVIDUS (FOAKY VIRUS)	2	2 × ×	200					1
AL MA	POL POLYPROTED ^N	GEBON APE LEUKENAL VIRUS	34.55	5,58						1
POL HTLIC	POL POLYPROTEDA	HUMAN T-CELL LEUKENDA VIRUS TYPE I (STRAD) ATK)	578-711							
PPOL HVIAS	POL POLYPROTEIN	HUMAN T-CELL LEUKENDA YIRUS TYPE I (CAKIBBEAN ISOLATE) 679-711	670.71				1			\downarrow
PPCI. ICVIB.	INDL POLYPROTEIN	HUMAN DOKUNODESICIENCY VIRUS TYPE I (ARVZSF2 ISOLATE, SOI-51)	<u> </u>	1						1
101/20	BOT BOX VAROTERY	HUMAN BAAMODEFICIENCY VIRUS TYPE I (BHIO ISOLATE)	513-549	5)1676					_	

PILEHAMIE	PACTER	And the second s				L				
HOL HVIBB	POL POLYPROTEDN	MANA PARENT	AREAL	AREA 2	ABEAJ	ARGA	AREAS			
POL HVIEL	POL POL YPROTY DA	HUMBER DANIES OF THE STATE I (THE ISOLATE)	513.549	200					O DE	
POL HVIID	POT BOX VOCATION	HUMAN BONCHODEFICIENCY VILUS TYPE I (BAU ISOLATE)	£.	9279			\downarrow			
WINE DA	MISTORIUS DE LOS	MUMAN INDRINCEDICT VIRUS TYPE I (ELI ISOLATE)	300	177	1	\downarrow	1			
100	re-recireotetin	MOMAN BARNODEFICIENCY VIEWS TITTE 1 (WAS 1501 ATE)	51.13	707		1		İ		
5	AL PALTMOTEIN	MANAN BORANDEFICENCY VIRUS TIVE I (IRCS) ISON ATEN	5			1				
a la la la la la la la la la la la la la	PUL PULTPROTEIN	HUMAN BOADNODERCEMENT VINIS TYPE I DAME I GOLD ATEL								
TOT HAINS	POL POLYPROTEIN	HUMAN BORDNOOFFICIENCY VIEW TYPE I DANIES THE		8						
NA WIND	POL POLYPROTEIN	HOMAN BARADODEST SELECT CONTRACT CONTRACTOR		609-467						
POL HVIOY	POL POLYTROTEIN	HUMAN BARANDERSCHALL VINING THE LINEW TORKS 150L		23.664			L			
OL HVIPV	POL POLYMOTERY	MALAN ARABONESION WAS TITE I (NOT ISOLATE)	ž	636-463		L	L		L	
POL HVIN	POL POLYMOTERS	CONTISOLATED	501-537	747.93		L	L			
PROL HOUSE	POI BOLVBOOTEN	HUMAN DOWNNOOFFICENCY VIRUS TYPE I (PV21 ISOLATE)	27.50	4			1			
MOL NAITH	TO TO SECURE	HUMAN INDIGINODEFICIENCY YIRUS TYPE I (NEMAT ISOLATE)	58.534	101.00						
	THE THE STATE OF T	MOMAN INDRINOGETICIENCY VIRUS TYPE I ISTILATIVITATION	, to , was						_	
TOL HYZE	POL POLYPROTEIN	MUMAN DOADNODESCIENCY VIEW TYPE CONTROL	9000	69-100						
or HAZCA	POL POLYPROTEIN	MANAN BARBERIES COMMISSION CONTRACTOR	300-336	620-663						
POL HYZDI	POL POLYPROTER	LANGE AND ASSESSMENT VINOS I TPE 2 (ISOCATE BEN)	49-13	414-512	653-447	100				
OL HY2D2	POL POLYPROTEIN	TOTAL STATE OF THE STATE OF THE STATE CAND	336-390	464-363	432-464	L				
MOL HYZGI	POL POL VPROTERA	NUMBER DESIGNATION OF THE 2 (1501 ATE DIM)	302-400	£ 1.0						
MOI MANUT	The second second	HUMAN DIGHUNDDEFICIENCY VIRUS TYPE 2 (150LATE 520), TI	•	414.134	130 100					
2000	W. N. I'MULE	HUMAN BOILDHODETICIENCY VIRUS TYPE 2 RISOLATE GHANA.								
The myang	POL POLITIKOTEIN	HUMAN DORUNGDEJCIENCY VILLIS TYPE 3 (1902) A FR WIN 31								
Of HY25B	POL POLYPROTEIN	HUMAN DORUNODESICIENCY VISIG TYPE 3 ARAI A PE S. C.		8	64-579	633-467				
A. HYZST	POL POLYPROTEIN	MALAN BARANDERICANO OBJECTOR		195.30	634-468					
K, 074.A	POL POLYPROTEIN	MAKAN BARBASETTE STORY OF A CONTRACT SELISM		473-563	633-463					
PPOL ISAV	PUTATIVE POL POLYPROTEIN	MANATER PATRICTOR ACTIONS 1 17 2 (150LATE 57)	\$ - 2 = 1 2 = 2 = 1	\$22.577	139-(59		L			
PPOL MEVAK	POL POLYPROTEIN	CHEED HE LONG TO THE PERSON NAVALINE	462-503							
C MCVAV	POL POLYTROTEIN	AND TO THE STATE OF THE STATE O	190-231							
PPCL HOLYES	POL. POLYPROTEIN		260-520							
CHANE	POL POLYPROTEBU		677.344							
PPOL NA VIP	POL POLYMOTEIN		617.749							
C MC.YMD	POL POLYPROTEIN		476-279	Γ						
POL M. VID	POL POL VPROTEIN	OLATE PVC.211)	602-749							
POL MAYNE	POL POLYPROTEIN		677.744		Ī					
POI MONEY	PART POLICE DE		13:34	Ī						
2000	WILLIAM IN THE PROPERTY OF THE	A VIRUS (STRAIN KAPLAM	62:120							
200 000	ACT PROTEIN		L	17.5	1					
ľ	TO THE PROPERTY		Τ							
	TO THE STATE OF	QUE C)	Τ					~		
T	CALTROIEM	Τ	T	3						
Ī	rocirrolein .	RUS (ISOLATE PHILIPPINES)	Ī	T	T	97.4	Ī	244		1405-1439
	TOUR TYRUIEIN	Τ		T.	T	2	32.363	433-474	1005-1039	1405-1439
T	TOL FOLKTING TEIN	Ī	I	T	66.					
1	POL POLYTROTEIN	ISOLATE)	T	T	1					
	POL. POL YPROTEIN		Ţ		מצעו	28-679				
	POL POLYPROTEDI	I	7	1						T
	POL POLYPROTEIN		7	7					T	T
	POL POLYPROTEIN	SINGAN PARAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAPAP	1		641-700 541-700	M3-91)	1020-1054			T
	POL POLYPROTEIN		٦	32.76						T
POL_STYNEE	POL POLYPROTEIN		3				Ī	1	T	Ī
PHOL STYNCK	POL POLYPROTEIN				629-673	21-12	912.946	†	1	T
PPOL SIVE	POL POLYPAGITED		48-519 6	819-559		Г		†	1	Ī
	POL POLYMOTER		П	634-488			ŀ		T	I
Ş	POL POLYPROTEIN		7	- F					T	
PPOL SAVI	ENZYMATIC POLYTROTEIN		-	£30-634				 	T	
			267-795	371416				t	t	Ī

THE RABIE FOLG. "ALL" FOLG. "A	rigiter Pol Polymotein Pol Polymotein		П	178-613					
**************************************	ol polytroted Ol polytroted	. 1510)	1			-		П	
**************************************	OL POLYTROTEON			-	-				
X 5 3 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5			٦	134-128	1	-		•	١
		MASA LEMINATUS (STRAIN 1914/CLONE LVI-1KS1)	419-534 67	626-918	_				
	TO THE STATE OF		489.524 174	426-161					
	TOLINA TRADICIA		116.150	113-23					۱
		9	131.200						
	PROTEIN PR.73		2.3						
	KOTEDS PR.73		Ī	143-201					
7777	MOTED PA77			176-21:1	-				
	PROTEIN PR.T		Г	10(7)		-			
	ROTEIN PRTS	MOUSE MUNICIPAL TURNOR VIRUS (STRAIN OR)	Т			-			
П	POLYHEDRIN PRECURSOR	_				-			l
Ī	POLYNEDILDY	IS VIKUS	7		$\frac{1}{1}$	-		Ī	
	POLYNEDRAM	AGROTIS SEGETURI NUCLEAR POLYREDROSIS VIRUS	3		1				
Г	POLYMEDRIN	BOMBYX MON NUCLEAR POLYNEDRÖSIS YIRUS	ž						
C NAM GIVE	XX YABDEDI	BUZURA SUPPRESSARIA MUCLEAR POLYHEDROSIS VIRUS	7						
Т	PAR MARINE	OSIS V	14-48						
T	POL YARDRIN	MAJESTILA BRASSICAE MUCLEAR POLYMEDROSIS VIRUS	10-48			$\frac{1}{1}$			
SON OF OWNER	NO. YNSTORIN	ORCYTA PSEUDOTSUCATA MALTICAPSID POLYNŒDNOSIS VIRUS 13-47	12.0		-				
Т	POLYNODADN	GROTTA PSEUDOTSUGATA SINGLE CAPSID NUCLEAR POLYTED	4 5	1					
T	POL VIGIDADA	PANOLIS PLANGEA MULTIPLE MUCLEOCAPSID POLYREDADSIS	3						
T	MATTER N	SPODOFTERA EXIGUA MUCLIAR POLYMEDAOSIS VIAUS (STAAIN) 14-48	14						
T	A VIEW DE	SPODOPTERA FRUGIPERDA MUCLEAR POLYMEDRÓSIS YIRUS	14.8						
T	Contractor Contractor	SPODOPTEJA LITTORALIS MUCLEAR POLYKEDROSIS VIRUS	18-31						
Ţ	Contraction of the Contraction of	KIRSTEN MURLINE SARCOMA VIRUS	941-291						
T		BOVINE BAMINODEFICIENCY VINUS (1501-ATE 127)	17.115			$\frac{1}{1}$			
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	SEC PROTEIN	EDUTINE DIFFECTIOUS ANENDA VIBUS (CLONE 1369)	11-00						
T	LEV PROTEIN	EQUINE BRECTIOUS ANEAGA VIRUS (CLONG CL27)	3-8						
Ī	ALEV PROTEIN	EQUINE DIFFICTIOUS AMEAUA YIRUS (ISOLATE WYOMING)	6:10						
	AEV PROTEIN	HUBALN BARUNODEFICIENCY VIRUS TYPE I (CLONE 12)	67.5	1					
Γ	AEV MOTERN	51		+					
Ī	AEV PROTEDI	HUMAN DAMINODEFICIENCY VIRUS TYPE I (BILLO ISOLATE)	23.49	1					
	AEV PROTEIN	HUMAN DANIMODEFICIENCY WAUS TYPE ! (BH\$ LSOLATE)	25.5	1	1				
	ALTY PROTEIN	HABALAN DIDAMMODEFICIENCY MAUS TYPE I (BILAIN ISOLATE)	10.17		1		1		
Γ	REV PROTEDY	HUMAN INDICANDEFICIENCY VIRUS TYPE I (BRU ISOLATE)	*	-	-				
Γ	AEV PROTEIN	MANAN DOALMODEFICIENCY VIRUS TYPE I (ELI ISOLATE)		-	+	-			
	ARV PAOTEIN	MAKAN BORANGDEFICIENCY VIRUS TYPE I (MXIII ISULATE)							
	ALV PROTEIN	HEMAN BORANDOEFICIENCY VIRUS TYPE I (3H) ISOLATE)							
	LEV.PROTEIN	HAMAN INDIANOGER CIENCT VIXOS ITTE I (IALSP ISOLATE)			+	-			
Γ	AZV PROTEDA	MOMAN INDIGING FIGURET VIRUS ITTE I INAL INCLUSIO		+	-		-		
	NEV PROTEIN	MUNICAN INFICINCEPTCIENCY VIEWS 177E 1 (NIN 190LA 18)		+	-	-			
AGIAN ATT	LEV PROTEIN	HOMEN BEACHOOFF (ENCT VINC) ITE (UTILISACATE)							
Γ	rev protein	HUMAN CARACHERICIEMON VINCOS ITTE (PV22 ISOLATE) AN				-			
	AEV PROTEIN	MUNICAN DESCRIPTION OF THE STATE STA		-		-			
	AEV PROTEIN	HORAN INDICATE LIERCY VINOS 1776 1 (34 1904) 1.		-	-				
PREV SIVAG	REY PROTEIN	SINGAN INCOMEDIATION TO THE CASH SOCIAL SOCI	152		-	-			
PILEV SIVAL	AEV PROTEDI	SAMILAN BANDOSE ICECACI TOUS (1801 ATT AGAILE) ONE CA	16.37	-					
	REV PROTEIN	SIPILAT DEPARTMENT LIEUCY VIRIA (TVC.) ISOLATE)	24-35	-	-				
	ALV PROTEIN	SURAN ENGLISHED STREET	1	-					
MEV VILV	AEV PROTEIN	CARACA ENGINEER AND AND AND AND	25.2	-	-				
	LEV PROTEIN		Γ	11-133 635-483	_				
	UDORUG EOSIDE DIPHOSPICATES ILLUNCIASE LA	DOPPEATE ALDUCIASE LOS PARTOS	9	(16.33)		-			

1000									
CALCALLY STATES	ZEDITE	AREAL	VEEL	AREAL	AREA 4	AREAS	ARTAG	AREA 3	ABFAT
	DOMESTICAL REDUCTASE LAN	632-461			Γ	Γ	Т	Γ	I
AN RAY	DOMOSPIATE REDUCTASE LAS	16.110						Ī	
PLAN VACC	DOMOSPILATE REDUCTASE LAN	124-165						Ī	
MUNI VACCY	DEPHOSPHATE REDUCTASE LAR	367-403						1	
PRIRI VARY	DIPHOSPHATE AEDUCTASE LAR	367.402							
אמא אמא	RIBONACLEOSIDE DIPHOSPHATE REDUCTASE LAR VARIOLA VIRUS	167.401							
ACO COL		113-257							
SAC POR	DOHOSPHATE REDUCTASE SALA	99-137						1	
PRINCE MENTE	RESONACE LOS ESCRIPIOSPILATE REDUCTAS É SINA BOYDA HERPES VIRUS TYPE I (STRAIN 34)	101-133						1	
PUTU MSVSA	MINORICAL EOSIDE-DIPHOSPHATE REDUCTASE SHIA EQUING HERPESVIAUS TYPE I (STRAIN ABIF)	106-140						1	
THE THE		125.159					1		j
PART VACCC	ALBONIACLEOSIDE: DOMOSPIKATE REDUCTASE SINA SHOPE PIBRONA VIRUS (STRAIN RACZA)								
PURI VACCE.	CHOSPHATE REDUCTASE ISLA								
PAIN VACCY	CHOSPHATE REDUCTASE SALA	133							
PRIRE VARV	PHOSPHATE REDUCTASE SALA								
PILL HSV2H	PHOSPIKATE REDUCTASE SALA	300							
PRIM VACEV	NEUROVINILENCE FACTOR INCRESS SINCE EX VIRUS (TYPE 2) STRAIN WILL)								
PRIMA VARV	ASSOCIATED TRANSCRIPTION S	Т	***					•	
J	RMA-POLYNEBASE-ASSOCIATED TILANSCRIPTION SVALIGILA VIRUS.	2	20.71	187-161	1				
	DHA-CHECTED RNA POLYMERASE 147 KG POLYTE VACCINIA VIRUS (STRAIN COPENIAGEN)	I		26-11					
PRPGI_YARY		1	Т	134-38	7	100-1037			
l	POLYNEMAS 147 KD POLYPS	1		736-78	٦	1034-1058			
١	POLTNESASE 113 FOR THE	_[Т	734-78	2.5	1004-1057			
ľ	POLYMERASE 1335D POLYME	T	Т	9		1			
ŀ	OL DEBASE 112 ED FOL TYE	2	Т	133-134					
	DIVA-DIRECTED RIVA POLYACIANTE 111 KD POLYPE I VALICKA VIALIS	T	Berge						
١.	CLTNESALE 11 KD POLYPEP	T	T						
PROG VARV	POLYNERASE 33 KD POLYPEP	41-114							
	DNA-DRECTED ANA POLYMERASE 11 KD POLYPEP VALIDIA YRUS	41.69				1	1	1	
П	DNA-DIRECTED RNA POLYNGEASEE SO KD POLYPER VACCINIA VIRUS (STRAIN COPENHAGEN					1			
	DNA DRECTED RNA POLYNGRASE 19 KD POLYPEP VACCINGA VIRUS (STRAIN WR.)	-					1	1	
PRIOS VACCY	POLYNGBASE 10 KD POLYPEP					1	-	1	
PRPOS VARV	POLYNGBASE 12 KD POLYPEP	97:2		1	1	1	1	1	
PROJ VACEV	POLYMERASE IN ED POLYPEP	5		Ī		İ		1	
PUO! VARV	POLYNGBASE 19 KD POLYYEP	69-63			T	T		1	
PRPOA LELY	POLYMERASE 19 KD POLYPEP	(3.6)			Ī		†	1	T
75 CV	POLYMERASE	1333-1367	1731-1756	1936-1992	2109.2133	-		1	T
TOTAL MANUAL	1	•	1137-1511	П		ľ	t	\dagger	T
222	COLUMN SUBURIT		219-313				 	T	Ī
	COLVERANS SUBURITY			150-391			-	l	
2004	CULTMENAS SUBURIT		278-313				-		T
TOTAL INCOME	PULTMEMASS SUBURITOR		279-313				-	l	Γ
PREDITIVE E		T	3.51						Π
2021	יייייייייייייייייייייייייייייייייייייי		278-313				-	\mid	
12 17 1 24 60	TOUT PERCASE CITE INC. 1:	1	275-313						
	COLUMN STATE OF THE PARTY OF TH	7	27-213				- 	-	
TAN ME	COLT MEANS SUBURIT FI		33.313				- 	\mid	Γ
TAN INTE	COLTINERAL SUBURITY		179-313				-		Ι
TOUR LANGE	ACACHILE ILM ACATACAM SUBURITY I INT. LEVA A VALIS (STIAN ALEXINADA) SUSTAIN	71.343	275-313	Ī	,				Ī
71001 10ME	CULT MERCASE SUBURITY PE	171.242	27.21.3				- 		
2 MY 1 04 8 00	BUA DEPOTED BUA DA VAREAR (IRINATE)	I	=					-	
river incre	TOP I MENOS SOBORIL FI	171-242				_			
									1

2003	ALLMOTIS	seri (no becterlophages)	AREAL	ABEAL	AREAJ	1474	AREAS	VIEV	ABEA!	4
Ę		VIBUS	П	278-313						
1450	CTED RMA POC		131.242	01:44						
7,22,7	BMA JOHN TED DICK POLYNGRASE SUBURIT PI	01/14/10/0	Γ	135.313						
1	ANA DIRECTED RVA POLYNGRASE SUBURIT PI		131.342	178.311						
١	ANA DIRECTED RIVA POLYNCRASE SUBUNIT PI		161.762	175.13						
1	NA DARKTED RNA POLYNCRASS SUBURIT PI		144.342	138-313						
1	ANA DESCRIPTION AND POLYMERASE SUBJECT PI	1	11.342	375.33						
1	ANA DRIEGTED BUA POLYAGRACE SUBLECT PI		131.30	27.313						
1	NA DESCRIPSION POLYMENASS SUBURIT PI	Ţ	3671	28.313						
ı	ANY PROPERTY DAY FOL WASTACK SURLINIT PI	111077								
ı	MA COURT I DO MAN TO COME A CO. C. M. MITT PI	П								
1	RNA-DILECTED ANA POLITIMENASE ANSWERS	WILD-TYPE)	200							L
_	ANA DESCREE MA POLTMENARE SCHOOL: 11		204-249	٦						
1	RAY DOLECTED RAY FOL TACEASE SUBURIT PI		130-10	940-076	101.131					
Ļ	ANA DOLECTED RNA POLYNGRASE SUBURET PI	A P INC BAK/80)	77.5	117.210						
ı	ANA DIRECTED ENA POLYMERASE SUBURIT PI		¥161	177-318						1
1	RNA-DIRECTED RNA POLYNERASE SUBURIT PS	INFLIENCA A VIRUS (STRAIN ADMINANTER AND MAINTENANTER	101	177-2116						
1	PHA DIRECTED RNA POLYNGRASE SUBUNIT PE		11014	133.216						
I.	BWA DORECTED BHA POLYMERASE SUBUNIT PA	T	1	117.211						
١	BWA DIES CTED LINA POLYNGRASS SUBURT 71	T		111.111						
ı	ANA THREFTED BUY POLYNODASE SUBURIT PT	33EE/2/10)		315.31						
	ANY CONSTITUTION AND PORTINGENALS SUBUNGE PT						_			
١	THE PARTY OF THE PARTY OF STREET PLANT PR									
- 1	HARACHEL BOOK AND THE WASTACE SUBIDITY FOR	_					-			
WWW.	MANAGEMENT BALL BOY VACE AND EAST OF TARBOUT PA	A730711)								
TIME TANK	MANUAL TO THE WASTAGE SUBLINED TO	INTLUENZA A VIRUS (STIVAÎM AMTRIONI)								
NKT WE	MACHINE THE PARK FOR VICEASE SUBURER PT	INFLUENZA A VIRUS (STRAIN APINTAB/ALBERTA/11979)								
MUT WATE	NAME OF THE PARTY	INTLUDIZA A VINUS (STRAIN APPURATO RICORDA)								
MAN IMED	THE PROPERTY NAMED AND PARTY SUPPORT PA	DOT. LENZA A VIRUS (STRAIN ARLIDDY TURNSTOREMEN FELS								
TOWN LANGE	ALLY THE POTTED BINA POLYNOBLASE SUBLINET PS	DATE LENZA A VIXUS (STILATM ASINGAPORE/1971)		177.211						
- N	ANA DIRECTED ANA POLYMERASE SURUNGT PT	DIFLIDICA A WAUS (STADIN ATUNCATION AND AND AND AND AND AND AND AND AND AN	4	177.11						1
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	SHA DISPECTED RNA POLYNERASE SUBUNIT PI		71.01	177.218						
MAKE IVANIE	NAME ASSESSED BY POLYMBASE SUBURIT PS	Γ	1	111.311						
MAN IADA	AND PRESCHED BINA POLYNGRASE SUBURIT PS	Г	1	117.711						
2021	BAY DONE TED BAY POLYMERASE SUBURIT PS	П	79.01	17.210						
- N	ANA DRIBETTED BNA POLTNESASE SUBURIT PS	П		33.211						4
	BAA DONG THE BAA POLYMENASE SUBUNIT PS	П		149.380						
TOTAL STREET	BWA DREETTED BWA POLYNGDASE SUBURIT PT			346.390						1
200	ANA DRIFTED BYA POLYMERASS SUBLANT PT		1	34.30						4
2002	HAY DONE THE BUY POLYNGAASS SUBURIT 72			163.400	25.5	701.733				4
	ANA DRECTED BYA POLYNCEASE SUBURIT PT			363-402	100	316.367	101.711			4
THE PARTY	ANA THRECTED BUCK POLYNGRASE SUBLINIT P.			197	200	32-732				
THE TACK	CATA PARCETTED BULK POLYMERASE SUBUNIT PS	BATLIENCA A VIRUS (STIAM ACHOLEMAS)		107.151	20.514	36.55 20.55	-	į		
אאו נשא	THE PARTY OF THE PARTY STATE SUBURITY PO	Г		1 1 1 1 1 1 1	13.61	100	-			
PREP INTR	THE PARTY OF YACHASE SUBURIT P.	Г		141.48	35.514	357.52				_
PRAPY IAGUS	AND THE CHAIR BUY POLYMERASE SUBURIT PS	П		100.00	1	731.157				_
ALL MAN	THE SALE STATE OF THE PARTY AND SALE SUBURITY PA	1				32.23		Ŀ		
PILLY IANGE		Ī	<u>:</u>			1				
PRRP) IMIRO	MANAGEMENT BUT INCHASE SUBURGE PS	Γ				25.33				
MUND WOR		1	•			18.00				
MAN INCE	NAME OF THE PART OF TAXON ASS SUBSTITUTE POR	Γ				1	-			
PULLY LAKOR	MUNDELLED DUS PORTOR AND UNITED BY	Г	3			1		L		_
PRES WEEL	MA ORIECTED MAN POLITICAL SERVINGE STRIBUTED	Т	3	707-401			1			L
	THE PARTY OF THE P	1	•	į						

PCGENE	ALLMOTIS	All Virant (ne betterlaphages)				L				
THERANT	PROTEIN	YARUS	AREAI	A R CA	AREAS					
PIUD UNIAN		INTLUENZA A VIRUS (STRAIN ALEMPICRADVI) 44195)	3	35.55 25.55		100				3
PREPT IAMES	RNA-DIRECTED RNA POLYMERASE SUBUNIT PJ	INTLUENZA A VIRUS ISTRADY AMALLARDAEW YORKATOOTI	19.69	10.00	1			1		
PRUP LANTA	RMA-DEAECTED RWA POLYNERASE SUBURIT PI	BOTHENZA A VIRING CETRANIA ARTECOMICAMIN			2					
PRUM LAPUE		BOLLENZA A VIETE CTS AND A APPLANCE.				61.18				
PILLED LARKED	NAA-DOLECTED INA POLYNGRASE SUBSINITY PA	BOLLENGA A WRITE COTE AND A MARRED OF STANDS	7		21.2	£			_	
PRUM LASES	RNA-DOLECTED INVA POLYNGBASE SUBUNIT 21	DOLUMENZA A VIRTIE (STRAIN ABILITON TI BANTONEAGU TREET A	7		ž.	S F				
PRATI LASON	RNA-DRECTED RIVA POLYMERASE SUBURIT PO	DRILLENZA A VIRUS (STRAIN AGEA) NASCOCO RETTOLISMAN	7	20-00	2	101 J				
PRED LATELY	RNA-DIRECTED RNA POLYMERASE SUBURIT PS	DOLUENZA A VIRIS (STRAM ARMOAMARILIS)				707-733				
LIAYI (AYNA	RMA-DIRECTED RMA POLYDGRASE SUBURGE 23	DELLENCA A VINIC (STAAM ACTIONS ACTIONS	7	0	200	301-755				
PRAJ LAWE	ANA-DIRECTED RNA POLYNGRASE STRINGE PS	ORI IEMPA A MARIE (FOR AND ADDRESS) ALL	7	200	473-514	£				
PRILP, LAZII	RVA-DIRECTED RVA POLYAGRASE SURINGT PS	BOTH HENDA A VINEY COTO AND AND FOR PASSED	7	163-63	35.5	ğ.				
PLUS LAZTE	TAMA-DIRECTED BINA PCH VACERACE CI MICHET 91	MATERIAL A VINE OF THE PARTY OF	~	16)-402	Š	3.73			L	
PIUM BRIAC	ANA-DORECTED RNA POLYNGRASS STRENGT PT	DESTRUCTA A VIOLET AND A DESCRIPTION OF THE PROPERTY OF THE PERSON OF TH	3	363-402	3.5	701.75\$				
TAUT BREAD	RVA-DIZECTED RNA POLYNGRASS STRUNGT P1	DOT HEAT A BY VIOLE AT A VALUE AND A VALUE	7	163-402	27-514	701.155				
PER DICE	BMA DESCRIPTIONA BOX WATERACT OF THE STATE OF	MATERIA COLONO C								
Ped Pri Purit	California de la companya del companya de la companya de la companya del companya de la companya	1/66 [WILD-TYPE])	35.5							
ADDIT TOTAL	WANDER IN MA FOL TREASE SUBURITY	DVIAS)		175-309			Ŀ	L		
THOU THOU	MANDUECTED HAN POLYNCHASE SUBUNT P	LUS (STILAIN CLIMO)	215.26	375-316						
THEY CARE	WANDINGCTED KWA POLYMERASE SUBUNIT P)		107-01					1		
THE CAMER	MAK-DEEL TED INA POLTAGAASE	HIMAN CORONAVIRUS (STRAIN 129E)	354-392	165-589	72:178	197:16	364.1774	7017.100		
7 TAKE BEV	WASHIEL IED KAN POLTHERASE	MAVIRUS MIN (STRAIN JIBA)	159-619	34136	1769-2803	3584-3420	101.185	5	200	
CYMAN CAMPA	MANDELIED RAY POLYNERASS		1702	157.19	943-1009					
TAVE CVIOR	KING-DULECTED INA POLYNERASE		8	1301-1337	- CS-	1692-1726	3639.2670			
TACE DVB	NYA-DIKECTED RYA POL TAGRASE	MURLINE CORONAVIRUS MAIV (STRAIN JIPA)	22:132:1	1303-1337	143.18K	1690-1724	3673.3644			
TAULT UNIX	MA -DIRECTED RIVA FOL PAGRASE	(TIE)	35.56	650693	M41-099-1	1895.1548	2744-1767			
TANK SIVIO	KWA-DULECTED NAA POLYAGIASE		115.156							
and posts	AMA-UDITECTED RMA FOLTMEDIASE	IEROTYPE 10 / ISOLATE USA)	304-342	705.748	135.003	1021-1036	10017111			
	MA TOLI MENASE		1-36	11-01	306-363	21712	1306.12	1602.1861	188.1931	
1	NAM POLITICALIS BELA SUBURI	IN ONDERSTEPOORT)	15-01							
TOUR HOOM	MA MATMERASE	HANTAAN VIRUS (STIAAIN 16-118)	94-139	174-208	172-01	187-591	89759	131-763	905.000	1774.11.0
70000			2	1342-1776	1991-1927					
MAN 1948	BUT AND COURT BUT SON OF THE	IRUS (STRAIN AS		137-161	1131-1179	1185-1220	1665-1517			l
TOTAL MANAGE	NAMED BY THE TABLES	(g)			1490-1552	104-1038	2029-2063	3194-3264		
MAY PEASE	KNA-URECTED INA PULTMEJASE			Ī.,	1490-1552					
MONOTO TO SE	MAN POLITICANS BETA SUBURIL		112-261	190-824	169-903	1064-1109	1213-1317	311-1115		
MACL ROVE	KWA KULTMEKASE BETA SUBURIT	MUNIPS VIRUS (STRAIN MIYALIARA VACCINE)			267-304	576-429	733.807	131-136	1447-1481	1417-1531
ווווער אוווער	INA POLYNERASE BETA SUBUNET	NEWCASTI E DISEASE VIBILE (STRAIN BEAUTIE CALL	J	2191-2223	П					
PRRM. MINA	RNA POLYMERASE DETA STREBAT	T	Т	Т	_	2043-2077	2106-2142			
			┱	Ž	736-785	1236-1294	1314-1317	1413-1479	1564-1630	1617-1711
PERP. PURGI	RUM POLYNGRASH BETA SUBUNIT	HOMAN PARAPPELUENZA 3 VIRUS (STRAIN NIH 42115)	(MI-19)	171.60						
PRUL, KABYP	RNA-DIRECTED RNA POLYMERASS	Ī	T.	Τ	T	T		Ţ	2014	1924-2016
1			į	Τ,		321-38	26.5	9:10	22.22	3
l	RMA POLYNGRASE BETA SUBUNIT	RABIES VIRUS (STRAIN PV)	Ť	T	2007	Т	_			
	ANA POLYNGRASE BETA SUBUNIT	9 819)	T	T	Т		Т	7	≘: ::::	
	MA-DOLECTED RIVA POLYMERASE		T	T	T	7	Т	122.530	36-33	
1	RWA-DOLECTED RWA POLYMENASE	VINUS (STIADY 2H-548 MIS)	Ī,	T	T	Т	Т			
l	RWA POLYNODASE BETA SUBUNIT		T	Τ	1	_	т	7	7	
l			Ţ,	Т		761-781	\$ \$	200	1696 1534	2000-2034
PLUL SDIDZ	INA POLYNORASE BETA SUBLIBET	COMAT VALLE (CTD ATM ENDERS)			7	Т				
			7	2	25.5	- P	184-739	1059-110)	1319-1356	1120-1154
		7	1966-7036							

47444			A 25 F A 1			4		1	t	
CGENT			T	Ī	1	I		1219-1260	144-1536	2000-2034
TELEVANIE	The I May	J VIRUS (STRAIN Z)	т	B	2		Т		Т	
MUN. SEOUR	RNA POLYMERASE BETA SUBURI		2146-2216						Т	1
		9 01 01 70 version in the second	961199	174.704	187-581	633-474	71.765	41:17	Т	707.164
PRICE SYSWR	MANDGECTED MA FOLTACTASE		10.01	343.781	1221-1280	1319-1353	1893-1626	1674-1715	104-101 201-101	1
PREPL STAY	ANA POLYMERASE BETA SUBUNIT		Γ	Г	101.014	1039-1137	1676-3033	3059-3107		
PARK, TSWVB	ANA POLYMERASE BETA SUBUMT	SONORUS YELLOW NET VITUS	Τ	Τ	134-573	ğ	1119-1133	90015611	1311-1379	1534-1572
PRIN UNK	INA-DOLECTED INA POLYMERASE	TOWATO SPOTTED WILT VINUS (BILAZILIAN ISOLATE CPRINTED FOR	1	Τ,	101.111	214,238	130-131	3315-2344	2371-3419	1809-1141
			T	Т		100	141.1313	2017-104	100 - 10M	
Section County	BWA POLYNGBASE	UNKUMEM VIKUS	T	Т		3				
	RINA POR YNGRASE BETA SUBUNIT	VESICULAR STORATITIS VIRUS (SEROTYPE NEW JEARRY / STRA 1114.138	Т	Т	100					
2		VESCULAR STOMATITIS VIRUS (SEROTYPE NEW JEASEY / STRA (118-359	٦	Т	200	4				
MUN. VEVS	MA TAL IPLANCE BOIN SUBMIT	VESICIE AR STOMATITIS VIRUS (STRAIN SAN JUAN)		136.767	1015-1674	E I	1012-02			
PRING ACLSV	KNA POLYNEJOUSE BEIN SUBURI		226-362	357-596	916-938	20-CE				١
PIUDO BWYY	NA DOLECTED INA POLTMOLANS	KATE FL-I)	304.341							
HUND BYDY!	PUTATIVE RNA-DRECTED INVA POLYMENANE	ŝ	24.305							
MOUS BYDYP	PUTATIVE INA-DIRECTED RNA POLTMENASE		24.265							
PREFO BYDYR	PUTATIVE EDIA-OFFICITED RNA POLYNERASE		334.215							
PREPO CARMY	PUTATIVE BUA-DIRECTED RNA POLYAESASE	AUS (ISOUNIE FRANK)						_		
PREPO COMOS	PROBABLE ANA-DIRECTED BNA POLYAGRASIE	CANNATION MOTTLE VIRUS		117.476	444.410	716.767	145-1479			
	MITATIVE BNA. DIRECTED RNA POLYNCIASE		-							
200	MITATIVE BIALDINECTED BYA POLYNERASE	AVIAN INFECTIOUS BURSAL DISEASE VIRUS (STRAIN 53/70)				1				
VACO 0004	TOTAL THE BUY DISCOUNT BOX POLYNG BASE	AVIAN PGECTIOUS BURSAL DISEASE VIRUS (STRAIN AUSTRALITIES	100	166.307	101.10					
PULS DINY	FUINITE MANAGEMENT OF THE PARTY	INTECTIOUS PANCREATIC NECROSIS VIRUS (SENOTIVE JASPEN) 147-181	167-181	25.407	2 2 2	E .				
PLUTO DHMS	MIATIVE MA-DIRECTED MACKETINE	INTECTION & PANCE SATIC NECROSIS VIRUS (SEROTYPE SP)	147-101	764-407	501-335	22.60				
PRUPO LYCVA	PUTATIVE RIA-DIRECTED FOR FOLTPERATE	ş	991-100	983-508	976-960	1509-1343	2002			
PREND LYCYW	RNA POLTNEMASE	SAMOCYTIC CHORSOLGENTIS VIRUS (STRAIN WE)	\$91.345	X						
VOH OWN	INA POLTABUASE		181-315	167.769						
PRUPO PEANAY	PROBABLE RNA-DOZECTED KNA POLITHERASIE		321-158							
PRUPO PLAY!	NALDRECTED RVA POLYMENASE	1000	336-373	SPES						
PILLO PLAVE	MITATIVE RNA-DELECTED RNA POLYNERASE	Ammento	114.13	57.5		L				
PLATO PROVS	PUTATIVE BYA-DOECTED BYA POLYMBLASE	NEW)	97-16	20.66	197.60	2				
2000	PUTATIVE RNA-DIRECTED BNA POLINESIASE	LAU						L		
PER PEONE	PUTATIVE DIA-DIRECTED RHA POLYMERASE	ALD CLOVER NECROTIC MOSAIC VIRUS	3/40							
PACIFIC BEOW	ENA-DIRECTED RIVA POLYNORASE	REOVENUS (TYPE 3 / STILAIN DEALING)					L	L		
200	ENA DESCRIPTION NA POLYNCHASE	REGYDUS (TYTE 2 / STRADY DS/TONES)						L		L
	BALDINECTED RIA POLYMORASE	REGYRUS (TYPE I / STRAIN LANG)	100			1	1985	439.434	56.33	91:00
2	ANA DIRECTED BNA POLYMODASS SUBURIT VPI	BOVINE ROTAVIRUS (STRAIN RF)	3				5	79.50	480.734	11.60
2	NA CONSCIENT BAY POLYMORASE SUBUNIT VP1	BOVER ROTAVIRUS (STRAIN UK)	ş					1		
NOO NOIL	MANAGEMENT AND AND AND AND COMPANY OF THE COMPANY O	PORCENE ROTAVENUS (GROUP C./ STIVAEN COWDER)	3	12.5E	1	2			1	
PARAO ROTTO	MANUEL IEST MAN TO THE SAME AND THE TOTAL	PORCINE ROTAVIRUS (STIVAIN GOTTFRIED)	*:	5	1	2				
PRINO ROTS	MA-DOLECTED BAY FOLTMENAS SUSCISI	PERSON IL BOTA VIRUS (STRAIN SALE)	*	133-167	33.56 35.56	Ž	9	124		1
PARTO SBACY	ANA-DIRECTED BYA POLTMEAASE SUBURIT VI	CONTRACTOR MOTAL VIRUE	623-463		Ш					
MUND SCYLA	PROBABLE RNA-DIRECTED BYA POLTMEKASU	SOCIETY CONTRACTOR CONTRACTOR IN	<u> </u>	143-191	L					
PILLO TACY	RIVA-DIRECTED RIVA POLYNERASS	SACCIONACOMITCES CENEVISING VINUS ETA	100	220.77	97.6	16.31	861-928	1030-1081	1205-1319	191.2013
VADAT OFFI	INA POLYMERASE	TACANDE VRUS			197%	L	L	L		
Of Case	PUTATIVE RNA-DIRECTED RNA POLYNERASE	TOBACCO MELD GREEN MOSAIC VEIUS (TMY STRAIN UL)	1		3	1	L	_	_	Ŀ
	IN TA TIVE BYA DIRECTED BUA POLYNEBASE	TOBACCO MOSAIC VIRUS (MULGARE)	2							L
MINO INVEST	AND THE BUY AND CITED BUY BOLYMERASE	TOBACCO MOSAIC VIRUS (STIADN KOREAM)	3	2	2	1	1	-		1
	LOTATIVE MANAGEMENT OF THE PARTY OF THE PART		:		3	-	-			

	ATLANTIN	All Wanted And Land Assessed			-				l
DILLHAND	PROTECT	VIRUS	ABFAI	4054 1 4854 1		* 05.7	Í	П	
PRAFF BRSVA	INA-DRECTED MA POLYAGRASE	TOBACCO NECROSIS VIRUS (STRAIN D)	10.10	Т	1	V	1	67.0	V-SEC
MEN GIVO	INA POLINGRASE ALPRA SUBUNIT	BOVING BESPIRATORY SYNCYTIAL VIBUS 1578 AND A COME.		140.314	\downarrow				
PARTY IGEN	ENA POLYMERACE AL PHA SIMIBUT	T		1					
PLUP HOSY!		Ī		215 424	\downarrow			1	
PRAPE HISTYA	BNA POLYMERASE ALPHA CIRIBAT	TABLE BEST OF CONTRACT AND CONTRACT OF CON			-			†	
PRUP HESYL	BHA POLYMERASE ALPHA SIMIBAT	MELLAN BEERINATON CONTROL MAN CONTROL CONTROL		917-01	1	\prod		1	
10 VEV 00 100	DUA DOS SOCIOS AS AS AS AS AS AS	STATE OF THE STATE		180-216					
10000		MUMAN RESPIRATORY SYNCYTIAL VIRUS (SUBGROUP A / STRAI 99-158	2	160-316					١
		MEASULES VIRUS (STRAIN EDMONSTON)	15.1%	\$40.05	4			_	
PAUP NEASY	RMA POLYMENASE ALPHA SUBURIT		315-374	543-091					
PAUP MAGN		PGASLES VIRUS (STRAIN YAMAGATA-1)	MC-51C	\$6.00°	L				
PRUP MAGE	RNA POLYMENASE ALPHA SUBUNIT		Γ	213-275	L				
PRIVE MARKE	RNA POLYMETASE ALPHA SUBUNIT	8	Γ		-	\prod		İ	
PREP, NOVA	RNA POLYNGRASE ALPHA SUBUNIT	A VACEDGO	214.2%		-	I		\dagger	
PLUT NOVE	RHA POLYNGBASE ALPHA SUBURIT	LIA-VICTORIA/321	180 X		-			\dagger	1
PRUP, PING	RNA POLYMERASE ALPHA SUBURIT	NEWCASTLE DISEASE VIXUS (STRAIN BEAUDETTE CAS)	100-136					T	
PRILE MINE	ANA POLYMENASE ALPHA SUBUNT	Γ	Γ	115.34 175.437	-			\dagger	
PRINT THE	RHA POLYNERASE ALPHA SUBURIT		Γ	T				1	
PRATE TINES	RNA POLYNGRASE ALPHA SUBUNIT	ê	Γ	Т				\dagger	
PULT PULT	RNA POLYNERACE ALPHA SUBUNIT	HUBANN PARAMELUENZA I VINUS (STRADI CI. 14810)	Γ	Τ	::5	I		Ì	İ
PRIME PERIT	NAM POLYNGRASE ALPHA SUBUNIT		Τ	Τ				1	
ממע בעמיו	IDVA POLYMERASS ALPHA SUBINIT	CETTE A PAY TO CAUTE A 1			-			\dagger	1
PRATP PIXE	RHA POLYMERASE ALPHA SUBUNIT	T	Т		1				Ì
PRRPP PIGA	BAA POR VASTRACE AT PILA STRUMET	Actor Control	T		-				
MAP NOB	ENA POR YAFRACE AL PIZA SI BI PAT		T		1			1	
Water Season	THE BOX WATER AT BUT OF BUT OF BUT OFFI		T	marin)	-			1	
17.00	I NO sone water or was to some	WINE LUCKEN AB VIKUS (STRAIN M-SIJ)	£						
VARY TANK	ANA POLTMERASE ALPIA EUFUNIT		13.134						
THUY MAY	INA MENASE ALMA SUBURAT		93-127					-	
TABAT	ANA POLYMERASE ALPHA SUBUNIT		13-127					-	
TALLY MANY	INA POLITARASE AL PIA SUBURGI	I), AND (STRADY PM)	97-127						
TRAFF INDIVIS	ANA POLITICASSE ALPHA SUBURIT		93-127						
2002	ANA POLITICANS ALTRA SUBURIL	INDIES VICUS (STRUM SAD BT9							
PERSONAL SERVICE	ANA PAR TAGENAS ALTTA SUBURII		I	375-47			Ī		
MIN SHOW	BHA PCF VAERACE ALPHA CIRCINIT	, was	10.42						
PALVP SENEZ	RNA POLYMERASE ALPHA SUBUNIT		T	177.56				1	
PRUP SVS	RNA POLYMERASE ALPHA SUBUNIT		Т	135,469			1	1	
PAUP STAV	NAA POLYMERASE ALPHA SUBUMT	#	Т				1	+	
PRUP VSVIO	RNA POLYMBRASE ALPHA SUBUNT	SONCHUS YELLOW NET VIRUS	E	23:311				1	
PICUP VSVDA	INVA POLYKESLASE ALPHA SUBUNIT	VESICULAR STONATITIS VIRUS (SEKOTYPE INDIANA / STRAIN Q3-4)					1	+	
PRATE VSVA	RWA POLYMERASE ALPHA SUBUNIT	VESICULAR STORATITIS VIRUS (SPADITIFI INDIANA / STRAIN M)-4)	7				T	l	
FRRP VSVJO	RNA FOLYMERASE ALPHA SUBURIT	VESICULAR STOMATITIS VIRUS (SEROTYPE NEW JERSEY / STRA 3-3)	2	-	L		1	T	
PRUM VSVSJ		SEY/STICA	133				† 		
PSPICE ANCEDY	ANA POLYNŒRASE ALPHA SUBURTT	N SAN JUAN)	143						
PSPE VACCY	SHEKODON	XVRUS	233-264	361-395					-
PSP13 VARV	SESTING PROTEINASE INHIBITION	(STRAIN WR)						-	
PSH3 VACCC	SERING PROTEINASS INVIENTOR 2							1	
ISPU VACEV	SEADIG PROTEDIALE DOMESTOR 3	EMILACEN	П	125-256			F	t	
PSPU VARV	SEUDIE PROTEINASE INVIDITOR 3	WACCINIA VIDUS (STRAIN WR)	111.167	994:577				-	ĺ

976	1	All Virgies (no bectertophoges)	I	\$ 7487	7.7.6.4	V V V	AREA S	AREAJ	7	
יייייייייייייייייייייייייייייייייייייי				T	Ι	Г				
THE WAY	ACTEDIASE PRUBITOR 3		Ţ							
SAM AND	MENTOR 3 MOMON OG FIRST		<u> </u>							
אואס מאוו		tus i	7							
A TWA TWALA	STATE ACTIVATOR PROTEIN AL	AND VAUGLA VI		102-61						
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		1	2							
PIAGE VALLE		(STRAIN WA) (STRAIN COPENHAGEN)	2							
140	TENCK		Т							
1747		EDGLING DISEASE VIRUS	٦	K Y Y						
PIALA PONIO			33.33	495.574						
אאסי אואסי		35		507421						
PTALA POVIC			153-113	٦						
אשר אשר	LAKGE T AMTGEN	LYDAIAVIRUS	=	206-758	13.43					
PIALA POWU	LAIGE T AMFIGER		109-144							
PTALA POWE	LARGE T APTIGEN		507.M2							
PTALA POYAC	LARCE T AMTICEN	AWFORD SNALL-PLACUE)	504-539							
	LARGE T ANTICEM	_	339-378							
١.	MEDOLE T ANTIGEN	TRAIN 33	211-245	117-133						
PTANG POWA	MEDICAL T ANTICEM		921-261	X69.403						
PTAJO POVAC	MIDGLE T ANTIGEN	AWFORD SMALL-PLAGUE)	193-236	(07-49)						
PTASM POVBO	MODELE T ANTICEN		\$1-17							
PTASH POWLY	SHALL T ANTICEN	CONTRACTOR DO VOLA VIIIIS	7							
PTATE HPVAC		A POLYNEDROSIS VIRUS	401-443	037-90	419-523					١
PTATE NOVEM	THANK ACTIVATING TRANSCULTIONAL MEDICAL	AUTOMOTIVA PAR POLYMODEOSIS VIIUS	413.447	451-483	125-340					
PTATE MOVOR	THANK ACTIVATING THANSCRIPTIONAL REGULATION		3	25.12						
PTAT SIVAI	TRANS-ACTIVATING TRANSCRIPTIONAL REGULAT	CALLIN A A A SACRETICAL VILLE (AGAILS) ISOLATE)	2.19							
PTAT BIVAL	TAT PROTEIN	SIMON IMMONOPER CENTRY VIRUS (ISOLATE ADM / CLONE ON	137-185							
FTAT VILV		SOULAN EMPLOYED FOR A 1814)								
PTAT VILVI	TRANSACTIVATING TRANSCUETIONAL ACCULAN	VIOLA I ENTINELIS (STRAIN 1514 / CLONE L'VI-1K31)	16-00							
MAT WEN			10.74							
VICE PLV	TAME ACTIVATING TRANSCLATINGS OF	PP! TAR I RESERVED VILLS	279-311							
PTECP HSVII	TOTAL RECEPTOR BETA CHAIN MELWISON	LABORER COLOR BY VILLS (TYPE 1/STRADE IT)	27-61							
TECP HSYEA	TECHACINI PHOSPHOPROTEIN UST	And at our case								
PTECP_HSVEB	NONSDIE									
PTECP HSVEK	HONSENSE									
PTECP HSVS	MOMSENSE									
PTECU EBY	NONIDOR	CASCHERA BARR VIETS (STRAIN BOLE)	168-402	831-055	938-773	101-1	130E-130	1	1	
PTEOU HOWA	LARGE TEGIMENT PROTEIN		1870-1916	1930-1934	104-248					
		HUNAAN CYTOME CALOVINUS (STIAIN AD 169)	14.91	215-34	5.0	ğ 2.	\$ -		100-103	
PTECU KINI	PROBABLE LANGE TROUMENT TROUTER		1337-1296	1300.133		┪		_		14/0.1440
		HEXDES SINDLEX VIAUS (TYPE I / STRAIN 17)	231-763	D) 10	622-1039	40.00	137	200		
PTEGU HSWO	LANCE I ECOMENI PROTEIN			174	201	7	911.1000	1003.1381	112-1233	1337.1400
	I ARCH TECHDAENT PROTEIN	HEAPES SINDLEX VIRUS (TYPE 4/STRAIN GS)	o o			200	1	3	100	£ :
3	A A B CO THE CARBOTT PROTIEN	EQUINE HELPESYMUS TYPE I (STRAIN ABAP)	100			701	1			L
TEG ISNA			100	<u> </u>					1	111,111
	March of the Control	HERPESYANS SABARU (STRAIN II)	20.00	<u> </u>	3		22.6	E		
PTCU VZVD	PROGRAME LANGE I EVOTES I I I I I		1434-1502							123.1470
		VARICEL LA COSTER VINUS (STRAIN DUNAAS)	657-496	113-743	¥ 40	2				
PTENN ADERS	LANCE TECHNORY PROTEIN		1633-1705	1719-1756	2	32.22				
		HIGHAN ADEROVICUS TIPE 2	490-572							
PTEAM ADEOS	DRA TEDIGRAL PROTEIN	MINAMAN ADENOVIRUS TYPE S	440-591			4				
PTELM ADEM	DAYA TERJAMAL PROTEIN	Carried Andrews (1989)	181.181							
	PALL TERMINAL PROTECT	HUMAN AUTHORING I II -	-							

								:		
1000	ALMOTIS	All Vicuses (no bacteriophages)								
10 C C C C C C C C C C C C C C C C C C C	CANADA TANADA TANADA		14.8	777	7737	ABEAS	AREAS	AREAS	AREA?	43541
PTATE ANDREA	THE STATE OF THE S	HUMANY ADEMOVIRUS TYPE 12	1977	107-201						
A PORT	HAMS COUNTY PROTEIN JUN									
Y AND L	THANGS ORLAING PROTEIN MAS	JACOMA VIRUS AS42		04(168						
200	DPA TOPOSOMETASE	SHOPE FIBROMA YIRUS (STRAIN KASZA)		269-310						
107 4570	DAY TOPOSONETASE D	AFRICAN SWINE FEVER VIRUS (STRAIN BATIV)		\$15-10>	27 + 13	26.53	1038-1093	137-1162		
VINS WALAY	DRA TOPOSOMERASE II	AFRICAN SWING FEVER YIRUS (ISOLATE MALAW) LIL 10/1)	146-110	115-062	119-009	M6-206	1446	1031-1091	1911-2211	
2077	POGF-ABLATED TRANSFORMEN PROTEEN PALSIS	SDGAM SARCOMA VIRUS	16-7							
DAY TEST	THYMODYLATE SYMTHASS	VANCELLA-ZOSTEA YIRUS (STRAIN DUNIAS)	115-160							
Mai KOWA	UBIQUITING IN PROTEIN	ORGITIA PSELEDOTSUGATA MALTICAPSED POL THEDROSIS VIRUS	97		Ŀ					
PCESS HSVII	MINOTHETICAL PROTEIN UL!	HUMAN CYTOMEGALOVIAUS (STRADY AD189)	169-303		-					
PUCAS HSV2H	PROTEIN UE.3	HERPES SIMPLEX VIAUS (TYPE I / STRAIN IT)	£.5							
PULO) HSVED	PROTEIN U.J.	HERPES SINGLEX VIRUS (TYPE 2 / STRAIN HGS2)	92-126					-		I
PUCA HSVII	OEME 60 PROTEIN	EQUINE HERPESYIRUS TYPE I (STRAIN ABAP)	20.00							T
PULOS EBV	PROTEIN U.A.	HERPES SINGLEX VIAUS (TYPE I / STRAIN IT)	102-116							
PULDE HChrya	WINDH PROTEIN BBILTI	EPSTEIN-BARR VIRUS (STRAIN 893-1).	2.5	13.347	977					
PULOS HSVII	MYPOTHETICAL PROTEIN ULA	HUMAN CYTONEGALOVIRUS (STRAIN AD169)	216.350							
PULOS HSVEB	VINON PROTEIN ULA	HERPES SINDLEX VIRUS (TYPE I / STRAIN IT)	3.5	103.141	344.130	111.11	414.474			
PULDE HSVSA	WILLON CENT SA PROTEIN	EOUTHE HERPESVIRUS TYPE : (STRAIN ADAP)				T				
PULDE VZ VD	VINION CENE 43 PROTEIN	HERPESVIAUS LANGRI (STRAIN 11)	T	10.10	10,114	1				
PULBE HCMYA	VIUON CENE 14 PROTEIN	VANCELLA. ZOSTER VIRISCAPRAN DIALACI		40, 40	304.330	(0)				
PULOS MSVEB	HYPOTIGETICAL PROFESSION US.A.			170-00	10.00					
200	Marchae Death In which appears as present		200							
	Concern of the second second second	EQUINE MENTES VIXOS 177E I (STROUN ABAP)	74.70							
		WALLELLA-COSTER VIRUS (STRAIN DUNIAS)	9							
4	MUNDENDE.									
ACT HOUSE	MYPOTHE INCAL PROTEIN ULTS			115-227						
POLIS PSVEB	MYPOTHETICAL PROTEIN ULIA	HUMAN CYTOMEGALOVIRUS (STRAIN AD184)	105-243							
PUT IN PRIVID	IMPODIETICAL GENE 48 PROTEIN	(AB4P)	13.96	(17-7) 2						
P.0.14 V2VD	ULH PROTEIN HOMOLOG		\$4-0							
PULIS HSVEB			101-19							T
PULIT HSWG	EN		364-100				Ī			T
PULIT HSVED	PROTEIN IOR	ANDA-1102	239-280						†	T
PULD HONA			Ē	\$4-100 100-100			Ī		T	Ī
MEM HONA	TEMULIN		_		Ī	l	Ī		T	T
MASA RIVE	EN ULM	HUDAAN CYTCHEGALOVIRUS (STRAIN ADIAS)	5			Ī	Ī			Ī
PULT HOWA	100	RAIN THORNE VIL	161-191		Ī	Ī	Ī	1		Ī
म्बस् भ्रह्मा	EM ULJS		155-341	351-398					 	Ť
			370-411				T		İ	T
		AIM AB4P)	364.413							
- 1	2	HERPESVIRUS SADARN (STRAIN 11)	Г	12:31	267-68		I		l	T
702.35 VZVD	AL I KD VINON PROTEIN	INTECTIOUS LARYNGOTIACHEITIS VIRUS (STRAIN THORNE VIEISIA	П	163-206					l	Ī
i	2017	IN BARN CYCOMECAL OWNERS OFTH ANY ADVISOR	111.77							
W. 11 VZV									1	
MA 12 HSVER								1		
70.13 7270	CLYCOPLOTER 106	JETT A CALL A BUT						1		
KUI KOWA	VELOPE CLYCOPROTEDY 26	T	Ţ		1	1		1		
27.00	O PROTEDI COUPLED RECEPTOR HOWOR OG ULTS		Ţ			1	1			1
PUEJ4 EBV			T				1	1		
NE 14 HOLOVA			10.45					1		
10000 71 100	77 22 75 25 75 75 25 75 75 75 75 75 75 75 75 75 75 75 75 75		200	1			-			
	ייייייייייייייייייייייייייייייייייייייי									
700	11 21 72	THE TANK TO SECURE A PRODUCT OF THE PROPERTY O	77.7			1				
1000	- Constant		31:32							

PCENE	ALLHOTIS	All Virgins (no bacteriophiges)	ARTAI	AREAL	AREA?	ARIAA	AREAS	AREAS	AREA?	ABEAI
TILEMAME				Г		ŀ				
HISNII	PROTEIN BOLF!									
MAN NO WORLD		HERPES SURCLEX VIRUS (TYPE I / STRAIN 17)	653-801	٦						-
	2		12-137	311.345	\$14-64\$	115.250	781-833			-
ALV RIVIA			Ī	683-741					-	ļ
מעבע גרווע		200000	316.351	786-423						
TULIS HOWA			١							
אמרו אבאם	3	HUBAAN CYTCHE GALLOVIAUS (STILLIN AD187)								١.
PLEAS HEVIL	KOTEN		370-706							
HILCH MSVED			3.5	192-122						
AVAILA MATERIA	KOTEN		131-172							
			72.109			-				
13 to	A LONG OF		11-48							
NCV CVD			112.36)			ŀ				
PUTAS HSVIK	GENE IS MENGRANG PROTEIN		100			Ŀ				
PULAS JASVIN	PROTEIN ULAS			1		ŀ				
PULAT HOWA	PROTEIN UL45			207 377	244.154	ŀ				
PUTAT HSVII	PROTEIN U.C.			Т						
MEAT HSVIP	VINON FROTEIN ULA?	7)	677.318							
THAT MEVAP	VINCON PROTEIN ULA?		473-511							
PLE 47 HSVE4	IN 1 KD ALPHA TRANS-INDUCING PROTEIN		201-612	7						
DER AV DEVER	17 KIL ALI PHA TRANS-INDUCINO PROTEDI	EQUING HEAPESVIRUS TYPE 4 (STRAIN 1942)	113-246	312-670	\$ 2					
2.01	LICTING PROTEIN		119-253		117.666					
2000	PROTEIN		14-135	156-209 66	101-101					
יייייייייייייייייייייייייייייייייייייי			135-189							-
POCSI POSTI	and the state of t		116-169							
MOI ROVE	TAULEIN DESI	ECHANT MERPESYIKUS TYPE 4 (STRAD) 1942)	131-162							
POLSI PLYE	OEAL FAULEIN		130-161							
מאא וקדוו	CENE STROIGH	VARICELLA-20STER VIRUS (STRATH DUNIAS)	122-163							
אונים אונים	PROBABILE ON A REPUTATION PROTEIN BSLF1		118-255							
ME CO MOVED		AIN 17)	≘			1				
١	DNA REPLICATION PROTEDY ULSS	ADV ABAP)	3	030.070						
ı	PROBABLE DRA REPLICATION GENE 34 PROTEIN		7							
L	PROBABLE DRIA REPLICATION GENELS PROTEIN		2		۱					
ı	JONOTTON LE SI		17.5							
L	PROTEIN LB 19	2)	131-183							
10 CO CO CO	INPOPULATION PROTEIN ULA	HUMAN CYTONEGALOVINUS (STRAIN AD169)	33-33							
10 W	PROBABLE THA REPLICATION PROTECN ULTO	HUNGEN CYTOMEDALOVIRUS (STILAIN ADIST)	£							
10 to 100/411	INTERPORT PROTEDIULIA		5				·			
ME 01 DEVIA	WYNOTHETICAL PROTEINS	HERPES SOULEX VIIUS (TYPE 4/ STRAIN UGANDA-1102)	24.72							
120	WASTERNAL OFFE 14 PROTEIN		366-400	562-616						
2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	AVAINTMENT OF PROTECT URAL	HERAN CYTOMEGALOWRUS (STRAIN AD169)	187-391							
200	WASHINGTON CENT TO PROTEIN	HERLIES VIRUS SAINITU (STRAIN II)	5.5							
W.C.	INTERPORTED PROTEDI BOLPA	EPSTEIN-BALL VIRUS (STIAIN 195-1)	107.144	110-213						
אוניים אוניים אוניים	SAMOTHET PROTENTAL	HEMAN CYTCHEGALOVIRUS (STRAIN AD187)	¥							
1 20 20 20 20 20 20 20 20 20 20 20 20 20	AVPORTETICAL PROTEIN PA	HEAPES SOULEX VIRUS (TYPE 4/STRAIN UGANDA-1102)	<u>5</u>	174-216						
200	INNOTICE COST 11 PROTEIN	HEAPESYTRUS SAIMON (STRAM II)	11.13							
,	44.00 (M. 1976)	HUMAAN CYTOMEGALOVIRUS (STRAIN AD169)	13-57	299-314						
7000	LOSOCIATES AL PROTEIN LA 95	HUNGAM CYTONEGALOVIRUS (STRAIN AD16")	14.31	159.293						
200	INVESTIGATION PROTEIN IN	HERPES SHIPLEX VIRUS (TYPE 6 / STRAIN (KGAN)A-1102)	=	23.23						
TOTAL MANAGE	INVESTIGATION PROTEIN (J.96	INMAN CYTOMEGALOVIRUS (STRAIN ADIES)	55							
DE LA LISTA	LIVEOTIETICAL PROTICINITAL	HERPES SIMPLEX VIRUS (TYPE 6/51 RAIN UGANDA-1102)	3							
A Hand	hivroriserical GENE 19 PROTEIN		45-130 021-4							
	INVESTIGATE PROTEIN IA.102		9	75e.772						

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JAJ JUG	1411 1100								
FILENANT	TOTAL PARTY OF THE	Ad Viruses (no batteriaphages)							
MAC HEVIT	MANUAL PROPERTY AND	YIKOS	SEAL SEAL	ABEAJ	ARTA (AREAI	1 9 AZA 6	AREAT	27.7
HING HIVE	- 12	HUMLAN CYTONEGALOVIRUS (STRAIN ADIES)				Г	Γ		
200	UNITED A GET TO THATE	HEAVES SINGLEX VIRUS (TYPE I / STRAIN 17)	127-366		-			Ī	Ţ
MAN MAN MAN	UMCELONA GETCOSTLASE	HERPES SINDLEX VIRUS (TYPE 2 / STRAIN 111)	111.339	L	-			T	Ţ.
ACT COLON	UNACILIONA CLYCOSTILASE	HEAPES SHULEX VIRUS (TYPE 2 / STRATA 14GS)	141.189					1	F
TAKE SAIL	URACIL-DNA GLYCOSYLASE	HELPESVINUS SAIMEN (STRAIN II)	33:13					1	-
PUSO MSVE	URACIL-DNA GLYCOSYLASE	SHOPE FIBROMA WRUS (STLAIN KASZA)	S11:18	-				1	
TOSOL ROVER	CEPE W PROTEIN	EQUINE HEAVESYIRUS TYPE I (STEADY ABA?)	75.130	-				T	1
VUSUT HONNA	USI PROTEIN	EQUINE HELVESVIRUS TYPE I (STRAIN KENTUCKY A)	16-130					1	
PUSI HOPA	INTOTACTICAL PROTED/HOLES		2.36	-				T	
PUSI4 HOLVA	HYPOTHETICAL PROTEIN HOLF!	HUMAN CYTOMEGALOVIERS RETRAIN AD1401			 				
PUSIS HCHAYA	HYPOTHETICAL PROTEIN HYLJ1	HUNCAM CYTOMEGALOVIRUS (STRAB) AD 1601	100	+					
PUSTS HOWA	MENDRANE PROTEDY HARLES	HE BLAN CYTOMEGAL OVER IN ATTACK ATTACK		+					
PUSIA HONYA	HYPOTHETICAL PROTEIN IGALF?	KIRKAN CYTOMEGAI OVREK ATRANA ADILAN	Т	-					
PUSSE HONYA	HYPOTHETICAL PROTEIN ING. FG	HUBIAN CYTOMEGALOVIER (STRANDA DIAM)	235-378						
PUSIT HONYA	HYYOTHETICAL PROTEIN HALFS	HUMAN CYTONEGALOVIRUS (STRAIN AD169)	777.661		-				
PUSIO HCAYA	HOLIGLOG US17	HUNGAN CYTOMEDALOVIRUS (STRAIN AD 149)	97.9				1	j	
PVI15 AMLE	Г	HUMAN CYTOMEGALOVIRUS (STRAIN AD168)	110.140	-					
PVIO NEVAC	Г	ALFALFA MOSAIC VIRUS (STRAIN 425, 150) ATE 1 FINEN	T				1		
PVI6K TRVPS	METICASE	AUTOGRAPHA CALIFORNICA MICI PAR POLYHEDEGGIS VIRTIS	١	100					
PVIGK TRYSY	HE KID PROTEIN	TOBACCO BATTLE VIBUS (STRAIN PEC)	1	Т					
PVIA BRAZV	16 KD PROTEIN	TOTACCO BATTI E VIBILE CETEAN CALD							
PVIA BMV		BEOAD BEAL AOTH B VIETE			Į	٦			
PVIA COM		BROKE MOSAL VIBIL		492-536	710-751	3.5	990-924		
PVIA CANTA		CONDEA CIR DEDITION LINE CARLIE							
PVIACHO		CUCIAMER MOSAIC VIRIS (STRAB) SNV)	243.7%	346.319	417.526				
PVIA CHVQ		UCLA COER MOSAIC VIRIES (STRAIN O)	Ī	314-619	166-916				
PVIA PSVI		CUCLINGBER MOSALC VIRUS (STEATH O)	10-101	410-24	916-1919				
PVIA TAV	IA PROTEIN		T	+					
HLASH XIEA	IAPROTEIN		11.50	100 000	-	1	1		
PV24K BDV		TURKEY HELPESYRUS (STRADN HZ)				1	1	†	
PV35K MPVAC		_	63-121 130-171		ŀ	T		†	I
PV26K PLRVI		A POLYMEDROSIS VIAUS		-		1	1	t	T
MIN MINN		1	116.150				1	†	T
LV2NO ASPLO		GEN	116.130			T		†	
VVIN PEBV		AUS (STRAIN LISS?)	136-183	-		T	T	1	T
PVINE IRVSY	2		115.192			T	\dagger	1	
WINE INVIC		AND (STILATIN PSQ)	167-203	_			\dagger	\dagger	T
100	NI	S	45.79			İ	+	t	T
PV2A CAVPN			768-to6			l	\dagger	t	T
24	to be created	IN PAY)	214.73					l	Ī
		נאוא	117-717			T		1	Ī
PUTCO ASERT	March March	TOWATO ASPENAT VIRUS	22.756					t	Ī
			_						
TOTAL ASSESS								İ	Ī
١	The state of the s		54-102 161-212	190-124		r	-		Γ
		VIRUS (STRAIN BA71V)	153-199			l			
NAME OF THE PERSON NAME OF THE P			145			T	\mid	t	T
100 VCA		٦	215-255				-	1	T
T	A POTOTO A		215-25				\mid		Ī
Ī,		COCOMBER MOSAIC VIRUS (STRADA O)	215-255				-		
1			215.255					l	T
									1

Ш	NOTES ALMOTES		Ш	Ш	Ě	E	1 [1]	AREAL	1 1 1 1
\$ 5	SA I KD PROTEIN			3	Ц	104-05	104-051	0461	00-431
VYSK PLAYI	SI KD PROTEIN		47.41	DIA.		Charles			
	SA STA PROTEIN	POTATO LEAFACIL VALUS (STRAIN WAGENDIGEN)		102.2		13	3	75	3
L	N CO TOOLER	BARLEY STRIPE HOSAIC VIRUS		122-371	٦			71	7
ANTA NOLA	6.2 KD PROTEIN	BEST WESTERN YELLOWS VINUS (ISOLATE FL-I)	10-144	27.5%	1	*	+	*	*
	49.7 KD PROTEIN	POTATO LEAFROLL VINUS (STRADI WAGEMINGEN)		100		3 314-348			
Ĺ	ST PROTEIN	DLATE LEIDEN)	_						
ANDW AVCCA	MOTER A4	VACCIDEA VIRUS (STRAIN COPENNAGEN)						3	
1	PROTERI A I	VACCIMIA VIRUS (STRAIN WR)			4	\$	\$	\$	
1	NOTEN A4	AYBOTA' AIVIA							
AJOYA WYA&	PROTEIN AS	VACCINIA VIRUS (STRAIN COPENSIAGEN)		512	MCCI	N. S.	NC.	X	240
AWA BOVA	PROTEDI AA	VACCINIA VIRUS (STRAIN WR)		=1:	250	-58	\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\	}){0	239
PVAOD VACCC	PROTEIN A	VARIOLA VIRUS	176-236						
AWA BOYA	PROTERY AS	AVCCUIN ANGLES CONTRACTOR	176.236	_					
PYAD VACC	PROTEIN AS	VACCIMIA VIKUS (STRAIN COPENNAGEN)	1	-		44	400	317	217
PVAD9 VARV	PROTEINAS	SURIA VIORYA	4.93	-					
PYAII VALVE	PROTENAII	VACCIDIA VITUS (STRAIN COPENITAGEN)	9.5		141-175	191-177	\perp	\perp	\perp
PVAL LIVA	PROTEINAII	AVIOLY AND	10.14						
YALY ELAY	PROTEIN ALL	AVOCIMIY ADMOS (STEWNIN COLEMBINACE)	111-152						
PVAIS VACCE	PROTECT ATT PACTED	VACCINIA VIRUS (STRAIN COPENHAGEN	433-467						
TANK TALES	M IT ABOUTINE TATE PROTEIN	VACCIMIA VIXUS (STRAIN WA)	307-341		102467	403-467	0346)		Was a series of the series of
PVAY PLAY	36 KD ABORTIVE LATE PROTEIN	AVIOLY AND THE TANK CONTRACTOR	5						
AYYA GYYA	PROTEIN A20	AVECUAL A AUTOS (STROM COLEMBOSCE)	-67						
DOON TIVA	PROTEIN AJO	VACCIMIA VIRUS (STRAIN COPENHAGEN)	4						
ANYA ETYAS	PROTEIN ALL	VARIOLA VIRUS	3		1	11 11 11	L	100.78	100.78
YAAY LLAY	PROTEIN ALL	VACCINIA VIRUS (STRAIN COPENHAGEN)	3.5		73.20	1	235-209	235-209	235-209
ANA INA	PROTEIN ALL	AVOICE ALVOS	¥.						
ANDVA ECVA	PROTEIN ASI	VACCIDITA VIRUS (STRAIN WA), AND (STRAIN COPENHAGEN							
AYYA ETYAA	PROTEIN ALL	SUKIN V TORVA	217-251						
TANK TOWN	PROTEDY ALL	YARIOLA VIRUS	5 5						
VALV BLAV	PROTEDI AJS PRECURSOR	VACCINIA VIRUS (STRAIN WAL AND (STAAIN COTEMINAGES)	į						
DOON (CVA	PROTEDY A36 PRECURSOR	VACCINIA VIRUS (STRAIN COPENHAGEN)	24-65						
ASSWA LIVAA	TROISIN AL	VACCIMA VIRUS (STRAIN WR)	ž4š						
ANCHE AVERE	PROTERIAL	VACCINGA VIRUS (STRAIN COPENRAGEN)	1						
PVAN VALLY	PROTEIN AS	VACCINIA VIAUS (STIANI WA)	1		1				
SOLV BOAR	PROTED A31	AYBIAY ATION							
AJOYA 6FYA4	PROTEDI AJI	AVCCINA AMOR (STEVEN COLEMANOCA)	3.13						
DODAY BYAG	PROTEIN A39	VACCIBIA VIGUE (STRAIN COPENNAGEN)	1.13						
PYAM VACCY	PROTEIN A4	VACCING VINUS (STRAIN WR)	81-126	_					
ANYA MYA4	PAOTEN A46	VARIOLA VIRUS	11-126	-					
PYAN VACCE	PROJECT AND	VACCINIA VIRUS (STINAIN COPENNAGEN)	62-38	ŧΞ	Ç	Ī)- [A	7-104
PYACEY TO A	THOUSAN AND	VACCIONA VIRUS (STIVAN WR)	62.96	Ξ	J-184	143-146	-114		7-104

JA40.76	IAS I MOTH	A. C. Care by gradenheem!								
FILE NAME	PROTTIN	VRUS	ABEA	AREAS	7877	1054		ABEA 4		
PVAM VACCC	PROTEDI A47	VARIOLA VIRUS	Г	10 TE		Γ			1	
PVAM VACCV	PROTECN A49	VACCINIA VIRUS (STRAIN COPENIAGEN)	Γ	136.160						
PVA49 VARV	PROTEIN AAP	VACCEDIA VILUS (STRAIN WR)	\$	36-160					-	
PVASS VACCC	PROTECN A49	VALIDLA VIRUS	3-40	136-160						
PVASS VACEV	PROTEIN ASS	VACCINIA VIRUS (STRAIN COPENHAGEN)	26-13							
PVAST VACCE		VACCINIA VIRUS (STRAIN WIL)	81-132							
PVASS VACCV	GUANYLATE KDIASE HOMOLOG	VACCINIA VIRUS (STRAIN COPENHAGEN)	134-168							
PVALI MSVK	GUANYLATE KINASE HOMOLOG	AACCINGA VIRUS (STRAIN WIL)	134-161							-
PVALI MINN	ALI PROTEIN	MAIZE STREAK VIRUS (KENYAN ISOLATE)	230-269							
PVALI MSVS	AL! PROTEIN	MALLE STREAK VIRUS (NIGERIAN ISOLATE)	126-262							
PVALI SLCV	ALI PROTEIN	MAIZE STREAK VIRUS (SOUTH-AFRICAN ISOLATE)	278-262				ŀ			
PVALL TYDYA	ALI PROTEIN	SOUASII LEAF CURL VIRUS	113-631							
PVILJ ABAIVW	ALI PROTEIN	TOBACCO YELLOW DWALF VIRUS (STILLIN AUSTRALIA)	191-225							
איאנון ממאוא	AL) PROTEIN	ABUTILON MOSAIC VIRUS (ISOLATE WEST INDIA)	Γ	20:00						
PVAL) PYMVV	AL) PROYER	BEAN COLDEN MOSAIC VIRUS	14.78							
אסוז נואא	ALJ PROTERM	POTATO YELLOW MOSAIC VIRUS (ISOLATE VENEZUELA)	20.00	100						
PYALD TGNIV	ALJ PROTEIN	SQUASH LEAF CURL VIRUS		21:12						
PVAT CANING	ALJ PROTEIN	TOMATO COLDEN MOSALC VIRUS								
PYAT CALIND	APHID TRANSMISSION PROTEDN	CALEBLOWER MOSAIC VIRUS (STRAIN CH.1141)	2:2	£ 50						
PVAT_CAMVE		CALE-BLOWER MOSAIC VIRUS (STRAIN DM)	22.70							
PVAT CANIVA	APHIO TRANSMISSION PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN BBC)	23.70	93-127						
PVAT CANIVE	APHIO TRANSAISSION PROTEIN	CAULIFLOWER MOSAIC VIRUS (STRAIN HYSIS)	22.30	9.137						
IVAT CASIVE		CAULIPLOWER MOSAIC VIRUS (STRAIN PVIST)	2:2	1000						
PVAT CANTW	APHID TRANSMISSION PROTEIN	CAULITIOWER MOSAIC VIRUS (STRAIN STAASBOURG)	22.70	9:130						
PVAT CERV		CAULULOWER MOSAIC VIRUS (STRAIN W160)	24.70							
PVB03 VACCY	APHID TRANSMISSION PROTEIN	CALMATION ETCHED KING VIRUS	961-66							
PVB04 VACCC		VACCINIA VIRUS (STRAIN WR)	104-142							Γ
PVBOA VACCV		VACCINTA VIRUS (STRAIN COPENHACEN)	18-133	111.111	696-530					
PVB04 VARV		VACCINIA VIRUS (STIXAIN WR.)		24.186						
PVB05 VACCO		VARIOLA VIRUS	19-134	124-372	492-530					
PVB05 VACCC	RANGE PROTEIN PRECURSOR	VACCINIA VIRUS (STRAIN LC16440)	154-398					•		
PVROS VACCL	MANGE PROTEIN PRECURSOR	IAGEN)	184-391							
PVIIOS VACEV	PLANCE PROTEIN PRECURSOR	VACCIMA VILUS (STRAIN LISTER)	254-398							
PVB01 VACEV	KANCE PROTEIN PASCURSOR	VACETIMA VIRUS (STRATIN W.K.)	24-20							
PVDG VACEC	NO.	AIN COPENIAGEN)	27-12							
PVBOR VACEV	TRUISIN BETRECANOR	VACCINIA VIRUS (STANIN COPENHACEN)	3							
אלינילי	5	CANAGES								
PVB11 VARV			Ţ	- T		T			1	
PVBIS VACCE			Т	6 1.53	Ī	T	Ī	1	T	
PVR19 VACCO		CEN	Г						T	Ī
PVBIS VACCV	PRECURSOR		====							Ī
PVB79 VACCC	8 PAECURSOR	VACCINIA VIRUS (STRAIN WR)	11:119							I
PVB21 VACCV	PROTEDY 578	VACEINIA VIRUS (STRAIN COPENIAGEN)	48-85							
WELL BOAR	,		\$6'19							
PUBLI SLCV	BL! PROTEIN	US	188-193							
PVBLI TCAIV	BL: PAOTEIN		158-193						F	
PVBRI BGLIV	SCI PROTED	US	159-193							
PVBRI_SLCV	BAI PROTEIN	US	901-241							
TVRAI TOMV	BRI PROTED		19-00							
PVC01 VACCC	7			. 1						
PVC03 VACCV	PROTEINCE	VACCEMA VIRUS (STLADA COPEMHAGEN)	37.62	362-302	391-442					

A 70 A 10 2 A 4	DODAY (0344	ANYA ROBAL	PYEOJ VACCY	DODYA 103A4	PADEL CYMAS	TYTHEP CANIVA	PADDS CYMAE	DAMYD 400MA	AND CANA	NO VALV		500	WOLD FOWP	AYVA GOGA	A3DVA 60GA4	DODAY WOOV	AND SOUNA	AUDOS AVECA	SOON FOOM	LAMOS COMA	SYALM (DOLVE	76.00		200	VSASH CY.3.Ve	BYSH & PAR	DOATH SYNA	LIASH AVOID	VAICH PYDIA	PNCAP EBY	SOOVA 61314	AXVE BISA	MCII AVCCC	DOOYA (1314	232YA 11314	ACO SENKA	VX.15 21.114	AVYA OLUM	100 VACCA	SACIO AVCCC	AJOYA 400.N	DOWN MON	AXAS 603AE	MCDI SFYXA	PYCOS YARY	PYCDS VACCY	DOOYA FIDA	VXAS SOAN	PYCON VARY	PYCON VACCY	SOOW MORE	PACON STAKE	SHVNE	SCORE	
PROTEIN BJ	PROTEIN ED	PROTEIN ES	PROTEIN SE	DNA-BINDONG FACTORS	DNA-BINDING FROM	DNA-BINDING FACE BATT	DNA INDUSTRIBUTE	DNA-BINDING PROTEIN	TAGEST PROTECT	PACIFIC DIS	PAGIN ON DIO	PROTEIN DIO	PROTEIN DI	PROTEIN D9	PROTEIN DY	PROTEIN OS	PROTEIN DS	PROTEIN DI	42 6 KO PROTEIN	DAM-BUILDING LYON	AND PROTEIN	NATION CAPSID PROTEIN	NAME CAPSID PROTEIN	NUOR CAPED PROTEIN	NAJOR CAPSID PROTEIN	MUCA CAPSID PROTEIN	MAJOR CAPSID PROTEIN	MAJOR CAPSID PROTEIN	MAJOR CAPSID PROTEIN	PROTEIN CIMBES	PROTEDY CIP	PROTEIN CIEWAS	PROTEIN CITALL	PROTEIN CIONAL	PROTEINCID	HYPOTHETICAL PROTETY CIZ	PROTEIN CIO	PROTEIN CIO	MOTEIN CIO	MOTERICO	PROTEIN CO	HYPOTHETICAL PROTEIN CO	HYPOTHETICAL PROTEIN CO	PROTEIN CS	PROTEIN CS	PROTEIN CS	PALLOLOGICAT MOLETA CO	PROTEIN CA	PROTEIN CA	PROTEIN CO	PROTEDY CO	PROTEIN CO	INDICE:	VITACINA	
VACCIMIA VIRUS (STIAMI WIL)	VACCIMA VIAUS (STRAIN COPENNAGEN)	AVNOTA ADIAN	VACCIMA VIXUS (STAAN WX)	VACCINIA VIBUS (STIMAN COPENHAGEN)	CAULIFLOWER MOSAIC YIAUS (STINAIN STRASBOURG)	CAULITLOWER MOSAIC YIRUS (STRAIN NYSI)	CAULUI LOWER MOSAIC VIRUS (STIVAIN BBC)	CAULIFLOWER MOSAIC VIRUS (STRAIN DH)	CAULIFLOWER MOSAIC VIRUS (STRAIN CAPTURE)	VARIOLA VIRUS	SHOPE PIBRUPA VINCE (STAND POSCO)	POWLICK SINCE (SINCE IN TAXABLE)	TARIOUS TIMES (CTRAIN PR.)	VANCE A WALLS	VACCIMIA VIRUS (STRAIN WR)	CACCIDIA VISUS (STRAIN COPENNAGEN)	VARIOLA VIRUS	VACCINIA VINUS (STRAIN WIN)	VACCINIA VIRUS (STRAIN COPEINIAGEN)	FOWLPOX YIRUS (STRAIN FP-1)	AUTOGIAPHA CALIFORNICA NUCLEAR POLYNERROSIS VINCE	AVECEITY-TOXIEN AINOS (2) MANA PARAMANA	ASCHOOLING CONTACT AND ASSESSMENT OF THE PROPERTY OF THE PROPE	A VACUATION OF THE PROPERTY OF	EQUING TEXT SECTION (STEAM STEAM)	TOTAL MEDICATION TYPE (/STRAIN ADAP)	PERSEL SINDLEX VIRUS	HEADER STROLLY VIRUS (TYPE I / STRAIN 17)	HUNGH CYTOMEGALOVIRUS (STRAIN AD169)	EPSTEIN-BARR VIRUS (STRAIN 895-8)	VACCIDIA VIRUS (STILAIN COPENNAGEN)	SHOPE FEBROAIA YIRUS (STRAIN KASZA)	VACCINIA VIRUS (STIVATA COPENTIAGEN)	VACCINIA VIRUS (STRAIN COPEMNACEN)	AVCCINIV AINTR (RINVIN CONEMINCEN)	SHOPE FIDRONIA VIRUS (STRAIN KASZA)	SUMPE FINE DATA VIRUS (STRAIN RASZA)	ACCION ADDITION OF THE PROPERTY OF THE PROPERT	TACCOME TROUBLE CONTRACTOR	TACCOLA VIOLE (STRAIN COSENHAGEN)	VACCINIA VIBER (STRAIN WA)	STOCKE STRANK COMMANDEN	THOSE PROPERTY (STRAM KASZA)	PARTY SIDE ON A VIEW OF LACK KASZA)	VARINA VIAUS	VACCOMA VINUTE (STRAM WIL)	VACCIMIA VIRUS (STRAIN COPENHAGEN)	SHOPE FEBRUARY VIBUS (STRAIN KASZA)	VARDIA VIRUS	VACCIMA VIBUS (STRAIN WA)	VACCINIA VILUS (STRADI COPENNAGEN)	SHOPE PERCONA VIRUE (STRAIN KASZA)	VACCINIA VIJUS (STRAIN WA)	S. S. S. S. S. S. S. S. S. S. S. S. S. S	IAH Wanas (an Institutionhopes)
17-41	17-01	212-336	287-385			1	1 2	١			Ş.	÷	65-99	126-100	126-160	124-160	123-157	123-157	123-157	_	-	_	20.191	3.28	479-530	130-184	116-174	116-175	136-174	156-184	211-252	36.97	ŝ	100-135	142-176	1.44	3.36	136-130	136-176	136-130	12-116	12-116	63-106	45-86	12-70	31- 46	¥.	13.125	Ē	į	ž	175-222	J7-42	ARIAL	
ŀ							t	t		1			111-222	-			1						3113	292-326	673-714	304-352	230-294	108-336	191.22	676-709				375-339		137-102					160-226	₹61-226			79-121							276-400	L		
t			1	t		†	1	1						ŀ	T			T							755-799		310.312		200-274							199240					219-323	209-325					Ī						271.77	ANGLA	
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	PROTECTION	ALL VIEWS (AN EXCHANGE OFF)			T		T	T		
PVE05 VACCC	PROTEINED	VARIOR A VIRUS	J	Τ		Τ			Т	4
PVE05 VACCO	MOTERIE	VACCEMA VIRUS (STRAIN COPENHAGEN)	1				T			
PVEOS VACEV	PROTEINES	VACCOMA VIRUS (STILAIN DAIREN !)	15.103							T
PVEGS VARV	PROTEIN ES	VACCINIA VIRUS (STRAIN WR.)	5.5							
PVEOF VACCC	PROTEINES	VANOLA VIRUS	36-163							Γ
PVEG VACEV	PROTEIN EA	VACCINIA YINUS (STRAIN COPEMIACEN)	105-139	132.266						
PVEOS VARV	PROTEIN E4	VACCINIA VIRUS (STRAIN WR)	103-139	995-868						
PVEIR NPVAC	PROTEIN 64	VALUOLA VIRUS	661-501	367-401						
WEI HIVIA	EALLY IS KD PROTEIN	AUTOCRAPHA CALIFORMICA NUCLEAR POLYTEDROSIS VIRUS	113-163							
PVEI HPVH	EI PROTEIN	HUMAN PAPELOMAYTRUS TYPE IA	171-171							
PVEI HPV33	Et PROTEIN	HEMIAN PAPILLOMAVIRUS TYPE 31	96-95							
PVEI HPV35	EI PROTEIN	HEBIAN PAPELOMAVIRUS TYPE 33	19-((133-167						
BVEI HOVE	EI PROTEIN	HURIAN PAPELLOMAVIRUS TYPE 35	8.3							
PVEI HBV4I	EI PAOTEIN	HUNGAR PAPILLOMA VIRUS TYPE 39	26-5K							
PVEL HOVES	EI PROTEIN	MUNION PAPILLOMAVINUS TYPE 41	60-55	312-346						
PVEI NOVS	EI PROTEIN	HUNDAN PAPULICALA VIRUS TYPE 43	13-52							
PVEL YOVER	EI PROTEIN	HUMAN PAPELOMAVIRUS TYPE SE	19-66	115.174						
BAAYA TBAA	EI PROTEIN		365-299							
PVEN NPVAC	EI PROTEIN	EUROPEAN ELK PAPILLOMAVIRUS.	176-310							
PYE2_CUPYK	EALY 25.9 KD PROTEIN	AUTOGRAPHA CALIFORNICA NUCLEAR POLYNEDROSIS VIRUS	2113							
PYE2 HPV05	PROBABLE E2 PROTECT	ILLOMA VIRUS (STILADA KANS	176							Γ
PVE2 HEVOS	PROBABLE EZ PRÓTEIN	HORAN PAPELLOMAVIRUS TYPE S		376-310	342-313	12-13				
PVEZ KPV16	PROBABLE ES PROTEIN		\$.13	146-102						Ī
PVEZ MPVIS	EZ PROTEDI			696-516						
PVE1 WPV1A	E2 PROTEDI	HUBLAN PAPIL LOMANIRUS TYPB 18	65.130							
PVE2 KPV2A	E2 PROTEIN		П	159-197						
PVEL	E2 PROTEIN .			139-193						
PVE2 KPV73	E2 MOTEIN									
PVE2 10V35	E2 PROTEIN		1	10.79						
PVE2 HPV39	E2 PROTEIN		1	129-192						
PVEZ HOVAI	E2 PROTEIN			25.57						
rve level	EJ PROTEUW	REMAN PALLOMA VIRUS TYPE 41								
PYEZ HOVSI	EJ FRO I E IN		1	146-112						
FVEZ HOVST	ES FROTEIN					1	1			
THE PERSON	The state of the s	MUNICAL PART CALL CORT STORE ST	J			1		1		
PVET PAPVO	DECEMBER 9 PROFESSION		2 3			1	1	1		
PVEL PAPVE	PROBABLE EX PROTEDA		101.10	1	T	1	1		1	
PVE3 PCPVI	PROGNALS IN PROTEIN.	MAVIAUS	21.50			T	T	1	T	T
PVEL MOVI	E2 PROTEDA	PYCMY CHILPAUSE PAPILLOMAVIRUS TYPE I	316.36			T	T	T	T	T
PVEJ9 NOVAC	E2 PROTEIN	HESUS PAPELONAVIRUS TYPE I	8-3	307.341				İ	T	Γ
PVEJ9 NPVOP	EARLY 19 KD PROTEIN	AUTOGRAPHA ČALIFORNICA NUCLEAR POLYHEDROSIS VIRUS	15.05							
11ADE 13Ad	EARLY 39 KD PROTEIN	A SID POLYNEDROSIS VIRUS	19-156						İ	
PVE4 HDV41	PROBABLE EA PROTEIN		170							
FVES_HDVSB	PROBABLE EN PROTEIN		10-01							
PVEF GVTN	Probable Es Protedi			96-130						
PVENY BEV	VIDAL EPHANCING FACTOR (YEJ) (104 KD GLYCOP	LANGLOSES VIRUS (THGV)	611-719							
PVEHV DHYY)		,	195.229							
1	ENVELORE GLYCORIOTEM PRECLASOR		278.211							
	MAJOR ENVELOPE PROTEDI (4) KD PROTEDI) (PUK		253-246							
. 1	MAJOR ENVELOPE PROTECT (6) NO PROTECT (FOR	MULLIDICATO CONTAGONOM VULUS SUBTITE 3 (MCVII)	232-226	1		1	1	1	1	
TVENY WALLE	EN VELOTE UN TUNKNI EIN FREUNAUM (SUNTALE			1		1			1	7
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PYGIL MADY	INSH CIDA	PACH MANA	PIASS CIONA	PYGIO HSVII	AYYA 600.14	ACC.		DOWN MOON	ATTA COOA	MAN AVORT		INM COUNT	11/24 900A4	PYON YARY	PYOO! VACCC	ANA CODA		NEVEN 1907/6	11/24 (P3/4	ANYA 180A4	ACCA LACCA	TYCON VALLE	2000	ILANH IUZIN	AJOVA SALVA	NTUS VACCC	NIPL FOWPI	MAN LOWER	W. P. 1041.		Vemos law	WAY PIEN	ASDYA NASCA	JANA NIEL	NT IJ VARV	1315 AYECA	AND VACEE	1111		1		VARY MEN	7103 VAV	130 VACCY	ATM VACCE	DODAY BOLY	AJOYA 101A	PATOL VACCE	VIOI AVCCA	PATOL AVCCC	MALIS NAAVE	PALKY AND	INV YALL	IN MARK		TE CARE	CLAR	314.5.5.	
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ERPES SINCLEX VIRUS (TYPE I / STRAIN IGEN!) 447-481
MAIAN CYTONIEGALOVINUS (STRAIN TOWNE) 101-136 692-749
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0.070		STAN BEARY AILLD YELLOW EDGE-ASSOCIATED VIRUS (SAIVE	\$PE'101 3.	931.965						
34.74		WHILE CLONER ANDSAIC VIRUS (STRAIM AL) (WCMV)	240-1210			-	-			
	-	WILLE CLOVER MOSAIC VIRUS (STRAIN DI (WCALV)	÷							
		AUTOGRAPIIA CALIFORNICA MUCLEAR POLYHEBROSSE VIRTIE								
á		ORCYLA PERIPOSERICATA LES TICABETS DE L'ESPACE								
Kio.	PROTECT S10	BICE OF ACT AND ALLESS THE PROPERTY OF THE PRO								
W.IV.	NONSTRUCTURAL PROTEIN PASSO	BLE CALL STREAM OWALD VIRUS (RESOV)	119-162	195.429	506-354					
NO.		THE OWLL DWAY VIRUS (RCDV)	186-273							
71.7		WOUND TUSION VIRUS (W.TV)	176.234			-				
	STATE OF THE PROPERTY OF THE P	ACE DWALF VIAUS (ADV)	1					,		
	MONSTRUCTURAL PROTEIN PUSI	WOUND FLATOR VIRILE AWAYS	B. C.	216-21.2						
2	SONSTRUCTURAL PROTEIN PLI	BICE DAYAR STATES	16-74			L				
N.C.A	NONSTRUCTURAL PROTESS PARTY	THE DEATH AND (MIN)	100.101					I		
HELTH		WOUND TURIOR VIRUS (WTV)	68.108							
	POSTRICT TORAL PROTEIN PASIS	WOUND TURIOR VIRUS (STRAIN MILLOTO)						_		
TENEZ TENEZ	CAPSID ASSENDED AND DNA MATCRITION PROTE		5							
HSSE	PROBABLE CANSID PROTEIN (PS)		18-23			L		I		
100.	PRINTER CAPCID PROTERLY ST.	TOTAL CALL CALLES (STRAIN AD 169)	11-12	081-941						
	CAN CHICAGO TO THE COLUMN TO T	7	1							
İ	PENNING ASSOCIATED STRUCTURAL PROTEIN	₹								
	CAPSID PROTEIN VPM	FOUNT MESSECO. IN SAME	B							-
¥0.14×	CAPSIO PROTEIN UP 26	LEBERT STATE OF THE TOTAL ABILITY (C. IV. I)						Ţ		
51.5	7121044	MENTER MAN SAISHIN (STRAIN II)								
	NI TOUR AND A TOUR AND	ORGYIA PSCUDOTSUGATA NAM, TICAPSID POLYHEDBOCKS VIBTOR	-							
	CAPSO PROTEIN 1716	VARICELL A. 2001 FEB UPBLICATE AND PARTY.					_	-		
	OUTER CAPSID PROTEIN VP)	אלאולגיין וויים אוויים (אוויים וויים אלאולגאו	2.5					Ī		
Ī	The state of the s	WHICH HORSE SICKNESS VIAUS (SEROT VPE 41 STRAIN VACCI	2	20.00	177 017					
Ī	Section and the section of the secti	PLUE TONGUE VIAUS (SEROTITE 197 ISOLATE HEAT	Ì		2	7	27. 170	34.1014		
	OUTER CAPSID PROJEIN VT2	BLIE TONGER VINITE SEPRENCE 11 1500	Ī						T	Ī
	OUTER CAPSID PROTEDS VP	TOTAL THE STATE OF THE USA		550-510				İ		
EXOX.		PENCHANCE VINUS (SENDITTE 17/150LATE USA)	77.	20,10					j	
Ī		PLUE TONGUE VIRUS (SEROTYPE I / ISOLATE SOLTIN AFRICA)		ī						
١	COLEA CACADO PAGIEN VP?	EPIZODIIC MENORALIAGIC DISEASE VIRING (CRACTIVAE IL/FEITH	Ţ	٦	201-101					Ī
ı	RAA-BINDING PROTEIN VP3	BOVINE ROTAVIBLY (CTRANSC)		٦	(0)-431	Ş	629-629	Ĺ	ŀ	
	CMA-EMOTING PROTEDY V72	BOWING BOX USE IN THE PARTY OF		407-516	23-55	111.100	25.5		İ	
101	OKA-EINDING PROTECT (9)				24.51	77.7.75				
Porce				Ť						
I	CAN-BINDING PROJECT VP3	2	T	7	313-347	617-638	615.764			Ī
Ī	RMA-EINDING PROTEIN VP3	1			194-238	\$19.331	199-441	100	t	
_	PHOSPHOPROTEINPO	-	36.94	415-517	919-909	580-755			t	
Ī		MALCH SWINE PEVER VIRUS (STRAIN E-15) (AST V)	29.69	Ī						
Ī			137-161	Ì	I					
		AL PENER VINUS (STRAIN BATIVITASIVI		Ì	1					Ī
Ī	X PROTEIN (P)5	~		İ						
Ī		CALIFORNICA MICE EAS AND COMPANY	A .							
	EALT 11 KD PROTEIN	-:								
	CATIONS PROPERTY.	VIAUS (BND/P17)		31.311		Ī		+	1	
Ī	1 000 000 000	HAGEM	100	İ	Ī			1		
Ī	CONC. MOI CONT.			İ						
Ī	ELUTE PROJEIN PJS	S (STRAIN WR)		İ				- 2 -	L	Ī
İ	TEMTLOPE PROTEIN P11							-	\mid	Ī
		CLYNE CO Wests 451 200 200	╗					-		Ī
	VP) CORE PROTEIN		٠	140.314	\$67. Pos	Ī				
BTVIA			Г	Γ	İ	Ī	İ	-	1	Ī
Value of the			1			Ī		-		
Ī		VIX.	Ī		Ì					
		1	1	ī				 	-	Ī
	HOICIM		٦	_	111-tm			 		Ī
				75.770	W. E.	100	İ	Ī	<u> </u>	
PVPJ ROTPC	MAJOR 114 KD STRUCTURAL PROTEIN			İ	Γ	Ī	Ì	+	1	
ROTSI			205-337 01	117-611		T	1	+	$\frac{1}{ }$	
		CONCINC RULAYIRUS (GROUP C / STRAIN COMDEN)	25.57	Γ	100	I	+	1		
			1	1	7		10 A C	-	_	Ī
										7

-					98.226	2	DECAMBLAYEN VIRTY (ORT)	DOLDY CASH AND STATE AND ADDRESS OF THE PARTY OF THE PART	0.6
	H				113-329	13	AFRICAN HOUSE SECRNESS VINUS (NEROTYPE 4/STRAIN VACCE	NONSTRUCTURAL PROTEIN PRO	PASITY 1414
H				Ì	٤	Ē	שמאה זוונים עומני ואיועו	DE OUTER CAPSED PROTEIN VES	AIM PANA
		331.44	414-510	MI-SPI	3	٤	SINIAN IN BOTAVIBUS ISTRAIN SAIL SEND	OUTER CANSO PROTEIN AND	SSION PAA
				224-AM	Ē	٥	SINGAN DE BOTAVIRUS ISTRAIN SATT-FCAT	OOTEN CATSIO PROTEIN TO	PYPA ROISE
-	5)144	484-322	138-379	1)1.JM	112-144	=	DIG SUS BOTAVIRUS	COURT CASE AND LESS AS	PATO ROTAN
-	İ	121-629	404-318	237-274	113-144	.33	POLCINE ROTAVIRUS (STRAIN THI)	CARRIED BOYEN YOU	TATE ROLL
-	767-67	Š	2	110-170	28.32	Ē	PORCINE ROTAVIRUS (STRAIN DOTTFRIED)	OLUCE CAPEID PROTEIN VP4	
+		30-614	30.22	241-277	133-163	į	PORCINE ROTAVIRUS (GROUP C/STRAIN COMOEN)	OLDER CARRO PROTEIN VIV	
+	T					13.74	POICINE BOTA VIBUS (SEROTYPE S/STRAIN OSU)	OUTER CAPSID PROTEDY VP4	210
\dagger	1	1				١	MURINI ROTAVIRUS (SEROTYPE 1/STRAIN WA)	OUTER CAPSID PROTEIN YP4	1100 141
\dagger	†						HUNAM ROTAVIRUS (SEROTSTE OF STRAIN PAIN	OWIER CAPSID PROTEIN YP4	MAION 1414
+							MUNION ROTA VIRUS (SERIOT FIRE 47 STRAIN ST. INCHINA J.)	OUTER CAPSID PROTEIN 174	VII 101 14.14
-		Ē	M3.40		111.		MONTH WIND CONTROL OF THE PROPERTY OF THE PROP	OUTER CAPSID PROTEIN YPA	PATON NEWS
	1			2	2			OUTER CAPID PROTEIN VP4	PAPA ROTION
		517-452	413-517	110.00	214-223	٤		SOUTH CASIN LANGING ALA	PAPA XOTIO
		531-445	414.310	131.37	217-210	Ξ	Ē	COLEX CASIS TACIONS	MAN KONTA
-	l		Ž	10.517	117-320	-	HUNIAN ROTAVIRUS (SEROTYPE I / STRAIM HIJ)	CAPTER CAPTER PROTECTION VAN	701100
	T	20-12	3	137-374	1	١	HUNIAM ROJAVIRUS (STRAIN LIS)	OUTER CASSID PROTEIN YPA	201101
†	T			9000	2012/12	٤	HUDIAN ROTAVIRUS (STRADI RU)	OUTER CAPSID PROTEIN VP4	BOILD.
+	t							DUTER CAPSID PROTEIN 474	PVP4 ROTION
1	1	177.321	112	1			To see the see of	OUTER CAPSID PROTERY YP4	DITON PENT
	1			27.32			TOUR TOTAL STREET STREET STREET	OUTER CAPSID PROTEIN YTY	PAPA KOTIED
	331-444	434-511	MERIC	237-234	12:16		CAN KIND SALIGORS STREET	OUTER CAPITO PROTEIN ALL	PVP4 ROTIM
\vdash		327-432	411.513	337-330	116-271	<u>:</u>	INDIAN BOTAVIBUS (SEROI YPE) / STRAIN RV-3)	COURSE CASE AND LESS AND LAND L	MIN' YANG
+	T	Ž	1	117.310	114-373	-35	INDIAN ROTAVIRUS (SEROTYPE I / STRAIN 10%)	CALLED PROTECT VA	
+	T				176-319	3.131		CANADA MOLEN VA	
\dagger	Ž	404-518	Š	227-270	112-146	١		CAN MINISTER CASE OF C	
l		220-025	=	336-377	12.14	₹		CHIER CAPAD PROJETY YPA	
1	T			77-77	1	Ě	BOVING ROTAVIAUS (STRAPI C184)	CHIER CAPSED PROTEIN YPA	10101
\dagger	T				3	١	STRAIN BAI)	OUTER CAPSID PROTEIN YPS	75 PG.V6
1	t				144.478	16.08		MONSTRUCTURAL PROTEIN PRISE	PO104 74.NA
+	†	1					MEBRASKA CALI DIARRIEA VIRUS (STRAIN NOUV-LINCOLIT)	DUTER CAPSIO PROTEIN YPS	VOA PANA
1	Ť	1				1	<u> </u>	VP4 CORE PROTEIN	7.2. XOV
1	†		Ī					VP4 CORE PROTEIN	ALA IO PANA
1	1		1	Ì				VP4 COAL PROIEIN	UNIU PANA
1	1						STOR LONGOE AND STREET AND STORY OF A STORY	VT4 CORE PROTEIN	11/16 14/1
1	1	1						MAJOR CORE PROTEIN PAR PRECURSOR	01A18 P414
1	1	1	1	3			VACCOSIA VIRUS (STRAIN WA)	MAJOR CORE PROTEIN PAR PRECURSOR	PANY UPAN
+	1			30.20			CHIAGEN	MINOR COME PROTEIN PAR PRECURSOR	PAPER VACCE
_	1			3.2				MANUA COME PROTEIN PAR PRECURSUR	DODAN BEAN
					-			MAJOR COME PROTEIN PIA PRECURSOR	PAPAD BONTY
			3	E	2		1317014 477	MAJOR CORE PROTEIN PAA PRECURSOR	PLPIA VARY
		157-451	Ž	3	2	2	C. House	MAJOR CORE PROTEIN PAA PRECURSOR	AJOVA VIENA
			3	¥.				OUTER CAPSID PROTEIN VP4	PUPIA VACCC
	1	j		<u> </u>	115.5		-	OUTER CAPSID PROTERS VP4	PYPE NOTSI
				521-53	=	٤		STAUCTURAL CLYCOPROTEIN C.F.	PAPIL ROISI
						- -	I SUALLY SHOULD BE THE STATE OF	CAPSID PROTER PA	219 1 29 1A
-	Ī				496-523	2	_1	CAPSID PROTEIN PAR	5/14 P4/14
-						57.49		CAPSID PROTEIN PAR	PAPE SCHIC
+		Ī			109-337	.35	511 3000	CATSIO TROUBLE TO	ALT BANK
+	T	Ī				PG-745	(IV.NI)	200	ľ
+	Ť	İ				12	_		١
1	T		Ī			2	INCH AN INCHES ! MUS 4)	CAPCID PROTEIN PAR	1
1	T		1	Carter	244-378	1	N II ROTAVIRUS (STRATY SAII)	WILL COLL PROPERTY (7)	List, all
-				1		Ì		20114	

27200	111 110 110	All Married for hardwales and				_				
(II.E MANE	PROTEIN	VIRUS	ARGA	AREAI	AREAD	AREA	AREAS	AREAS	AREA?	AREAJ
PVPIOIVII	OUTER CAPSID PROTEIN VPS	BLUETONCUE VIRUS (SEROTYPE 10/150LATE USA)	14.56	93-150	154.222	16-10				
CIAIR SANA	OUITR CAPID PROTEIN VPS	BLUETONGUE VIRUS (SEROTYPE 11/150LATE USA)	15.51	91.130	154-222	677700				
PVPS BIVIA	OUTER CAPSID PROTEIN VPS	BLUETONGUE VIRUS (SEROTYPE 13 / ISOLATE USA)	85-91	14-133	101-CH					
741 BIVE	OUTER CAPSID PROTEIN VPS	BLUETONGUE VIRUS (SEROTYPE I / ISOLATE AUSTRALIA)	14.11	97-143	146-223	1(770				
PVP5 DIV2A	OUTER CAPSID PROTEIN YPS	BLUETOWGUE VIRUS (SEROTYPE I / ISOLATE SOUTH AFRICA)	=	33.50	≅ ₹	-				
PVP5 EI OVI	OUTER CAPIED PROTEIN VPS	BLUETONGLE VIRUS (SEROTYPE 1715OLATE USA)	=	<u></u>	3					
ALES MIN	OUTER CASSIDMOTED VPS	EPIZOOTIC HEMONAJIAGIC DISEASE VIXUS (SEROTYPE I) (EHDV	=	92-136	2	391-335	3			
PVP5 WTV	OUIER COAT PROTEIN PS	RUCE DWARF YIRUS (ADV)	31-16	95.136	\$50.584					
PVP41 BTV10	OUTER COAT PROTEIN PS		106-919	347.381	181.786					
PVP61 MIRDY		BLUETOWOUS VIRUS (SERGIVYE 10/150LATE USA)	113.313							
PVP61 NPVAC	PROBABLE NOWSTRUCTURAL 41 8 KD PROTEIN	MARIE ROUGH DWARS VIRUS (NIRUY)	- F. KG							
PVP42 BTV10	41 KD PROTEIN	AUTOCRAPHA CALIFORNICA MUCLEAR POLYTICDROSIS VIRUS (2.5	31.18						
PVP64 KPVOP	VPS PROTEIN	BLUETONGUE VIRUS (SEROTYPE 10/150LATE USA)	97.6	159.707						
PVP6) NPVAC	MAJOR ENVELOPE GLYCOPROTEIN PRECURSOR	ORGYTA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS	- X - X	27.5		L				
PVP67 NPVCM	MANOR ENVELOPE OL YCOPROFEIN PRECURSOR	AUTOCAAMIA CALIFORNICA MUCLEAR POLYIII: DROSIS VIRUS (1.1	13.55	10.43	L				
PVP6 GIVII	MINJOR ENVELOPE GLYCOPROTEIN	VIRUS ICVE	107-701							
CIALD 94.16	VP6 PROTEIN	BLUETONGUE VIRUS (SEROTYPE 11/150LATE USA)	13.21							
P. P. DIVI3	VPS PACTEIN	BLUETONGUE VIRUS (SEROTYPE 11/150LATE USA)	118-81							
P. P. BIVIS	THE PROTEIN	BLUETONGLE VIRUS (SEROTYPE 17/150LATE USA)	£.50	Ē						
PLPS OTVIA	V PROTEIN	BEUETONOUE VIRUS (SEAOTYPE I / ISOLATE SUCTH AI RICA)	=	1 1 2						
PLP6 RDV		BLUETCHOUE VIRUS (SEROTVPE 27/150). ATE USA!	===	135.183						
71.M 84.4	STRUCTURAL PROFIEM PO	AICE DWAL VIRUS (RDV)	196.191	3.5	160-601					
PLPS WEWN	STRUCTURAL PROTEIN PA	WOUND FUNIOR VIRUS (WTV)	144-178	38-334	7.78		Ĺ			
PLP70 NPVAC	110647	WOUND TUNIOR VIRUS (STRAFF KI) (WTV)	144-178	116-314						
PLP 26 KPVCF	PLOTEN	•	100							
PVP19 HSVSA		_	115.0							
PLPM KPVAC	PRICE ARTICLE NEVIBRANT ANTICEN 19	HERPESTAUS SARGIU (STRAIK II)	I è	16.311	11.10					
PVP1 BTV10	THE DRIVERS		44.70	363.163	106-430					
P. P. BIVII	INT CORE PROTEIN	(SEROTVPE	16.278							
P. P. BIVI)	VP CORE PROTEIN		318-106							
MP7 BIVIA	VPT CORE PROTEIN		111-131			100				
PLP1 BTV1S	INTICOLL PROTEIN		114-335							
PLP! BIVIA	VP? CORE PROTEIN	HAFRICAL	14-130							
PLF! EHDVI	VP! CORE PROTEIN		184-836		12					
P. P. 100V	VPI CORE PLOTEIN	EPIZOOTIC IEMOKULAGIC DISEASE VIRUS (SEROTVPE 1) (CHUM	16.30	134-178						
7.34 MLV	NONSTRUCTURAL PROTEIN PHS?		63.95	123-235						
7 NO 100 VAC	NOVSTRUCTURAL PROTECT PKS?		=	193-343	10-30					۰
P. PS. KPVOP	CAPSID MOTEIN PIG	AUTOGRAPHA CALII ORMCA PUCLEAR PIR VIRLUROSIS VIRUS (<u></u>	19.14	₩.72	721-796				
N.M. BTV10		KOSIS YIRUS	2	Ī						
14.6	MONSTRUCTURAL PROTEIN PI		100							
11/41	-		3	2.5						
			2	2						
PYPE BEVIA	NOWSTRUCTURAL PROTECTION PO	BLUETOWGUE VIRUS (SERDI VPE 17/150LATE USA)	Z. 10							
PAPE BYVIS			14.102	25.5						
PYPE BTVIA	MONSTRUCTURAL PROTEIN PS	H ASRICA)	프	£ 5						
PIPE FOWPY	MONSTRUCTURAL PROTEIN PR	RUS (SEROTYPE 2/150LATE USA)	ž	=						
VO. 47.4			253							
PUP WIV	HOMSTRUCTIFIAL PROTEIN PMS9		3	106.3%						
PLPS WITH	STRUCTURAL PROTEIN PO		- C - C - C - C - C - C - C - C - C - C							
PINC BYDVI	STRUCTURAL PROTEIN PO	Т	140-313							
PIPIE MPVAC	PUTATIVE GENOME. LINKED PROTEIN PRECURSOR	BALLEY TELLOW DWAL VILLOS (BOLATE MAV-751) (BYDY)	2							
PVPIIE NAVO	THE KD FOLVIG DICAL ENVELOPE PROTEIN	AUTOCIAMIA CALIFORNICA MUCLEAR POLYTEDROSIS WAUS (144-22)								

									700000000000000000000000000000000000000	OLYCOPROTER YPI	PARON WOLL
DELINA CALLADOR						+	1		PURCH SCIA VINCE (SELECTIVE 1/ STEAM (MILIS)	GLYCOPROTEDI YP?	POLION 605A4
DEPTINE						1			SUPPLY AND A SECOND STATE OF S	OL YCOPROTEDI VYI	01101 1014¢
DATE DATE						1			NUMBER ROLL STREET CAST AND DATE OF THE PARTY OF THE PART	OLYCOPROTEDI VP1	DITOR POLYS
International content Inte							1	Š	HUNGA COLORIS (SECTION) (STEAM HUS)	CLYCOPROTEDI YPI	WILON 405.N
ACCOUNTS AND ACCO							-	į	MOTOR SOLD SECTION (SECTION AND OLIVERS)	OLYCOPROTEDI YPT	THION COLVE
INCLUDING	T	T					21.120	Ξ	MOLAVIAGE CONTROL OF STRAIN REAL	OLYCOPROTEDI VYI PRECURSOR	PITON POPIS
		l						÷	POTAMBLE MINUS PARENT DISC	CLYCOPHOTEM YTT PALCURSON	1910# 605Ad
	T	Ì						11.33	TOTA WHITE MEDICAL STRAIN ADAY! (AUULT DIAMUILA ROT	CT ACONSULEM ASI	V0104 401.14
								102-330	EXIDE BOYAVIBUS (STRAIN LUM)	CT ACOUNT CAN AND	THON 405.14
								10-316	CHARLEM BOTAVISUS A (SEROTAVE 1 / STRAIN CIT)	CT ACOMOLEDA ALI	50'SON NOTC!
					l		101.130	÷	POWER SOLVESTIC ISLETINGS	CLYCOPROTEIN ATT	PUSOR ROTOU
DESIGNATION CONTRIBUTION CONTR		Ì	İ				363-330	10.0	CAN ALVANIST I MALIORATION TO THE TANK	CH ACCENCITION ALL	TOTON MOENT
		•			l		161-110	1.M.	MOVE BOTA VIBUTI (STRADY NCOV)	CT ACOMPOLITING AAA	MBION BOSNA
	Ī	Ì	Ì	T			363-328	2.54	NOVER BOTAVIAUS (STRAIN XX.)	CLACOMICITION ALL	MOTON FORVA
DESTRIAL PROTECTS LIGHT PROTECTS L	T	Ì					11:130 11:130	2.54	POYNE BOTAVILUS ISEROTYPE 10/ STRAIN BILL)	CLACOMICITION AND	\$1.500 BOTOS
		T	T		Ī		261-329	2.54	BOYING BOTAVIRUS (STRADV A14)	CLYCOPROTLIN VY	AGION MOSA
MALEY PROTEST TOTAL PARTIES MALEY PROTEST	T	1	Ì	İ	Ì		313-320	134	POLY BOLY ABOLI OLD BOLLOU BOL	CL TEOTAGISTIS VIT	P.100 FOLK
AREAL AREA			T	T	İ		213-320	ž	BOYDE ROTAVILUS (STRAIN AS)	CLTCOTAGIENT TT	5410V 66514
100 PA PRICES 100 PA PRICE		†		T	I	İ	212-130	Ĕ	(IMB NIVELS / PALADESS) SOUTH PAIN (IMBADE)	CONTROL ON THE CONTRO	PATON ROLLA
ASSAL ASSA	T	T	T	T	İ	117.13	1	=	(I I AS MINERS) SUBTANTOR II MADAGE	MONITOR TOOL THOUSEN	PV 508 NO 151
1201344 1201210 1201		1	Ì	T	Ì	100-220	Ě	Ē	BOYDE ROTAVIAUS (\$18AIM UK)	TOTAL POST OF THE PROPERTY OF	Nation 105.N
100 100		1		1	Ì		17/2	E	SHUAM (I ROTAVIRUS (STRAIN SAII)	CANAL PROPERTY OF THE PROPERTY OF THE PARTY	10101
INTERPRETARY INTE			İ	T	Ī		2	Ē	PORCOUS ROTAVIAUS (SEROTYPE S / STRAIN OSU)	TOTAL PROTEDUCED	7 30 1017
PROTEIN			Ì	T	İ		1	15	BOYNG ROTAVIRUS (STRAIN UK)	CONTRACTOR DE PROTECULAÇÃO	120
ALLANDERS ALLA			1	1	Ì	Ī	į	٤	BOYDE ROTAVIRUS (STRAIN RN-1)	C. ACOSTOLICA (A)	74307 80183
ALLIANDERS		1				Ì			PORCONE ROTAVIRUS (GROUT C / STRAIN COWDEN)	VA 00018 D	
100 101 100 101					T			1	HUDAN ROTAVIAUS (GROUP C / STRAIN BRISTOL)	VIA PROTEIN	7 300 7017
AREA AREA						1	1		ROTAVINUS (GROUP B / STRAIN IDIR)	VPA PROTECT	
INDITIAN TOTALINA STANDAL ENVELOPE PROTEIN TOTALINA BARANCOSETICENCY VIRUS TYPE I (SIGLATE) (S								19.14	ROTAVIBUS (GROUP B / STRARY ADRY) (ADULT DIAGRES NOT	A PROPERTY	2010
ILD PIX PROTEIN SALEY FROM SALEY SAL				1	1	T	T	1	BOYING KOTAVIRUS (GROUP C / STRAIN SHINTOKU)		20103
INDICATE INDICATE			1	1	1			141.20	SDAWN IS NOTAVIRUS (STRAIN SAIT)	CONSTRUCTIONAL PROTECTION MCVP2	
ALLAUSES			1	1	Ī	Ī	1000	1	BACLEY STUDE MOSAIC VIRUS (BSMV)	AL PILLA PROTEDI	A CAN BONT
INDUING PROTEIN INDUIN				1				Ē		CAN 2001 D	77
ALLAIGITH ALLAIGITH ALLAIGITH ALLAIGH AND ALLAIGA AND TECHNOSIS VERNING VER				1	1					Valuation of the control of the cont	777
ALLAIGH ALL			İ		Ì	T		1	2	NO SECURITION	200
INDICEM IND				1				٤		MINISTER	
ALLANGER AREAL ANGAL AN			1	1	T			į		AND PROPERTY.	
ALLAIGITH ALLAIGITH ALLAIGITH ALLAIGITH ALLAIGITH ALLAIGAL AND ALLAIGH AN			Ť	1		Ī		å	ITUMAN IN BAUNCOENCENCY VIRUS TYPE I (PYZZ ISOLATE) (IB	Walland In	
ALLAIGH ALL				Ì				8		THE PROPERTY OF THE PARTY OF TH	200
I ROPLEM I ROPL								š	INDIAN DENNOOFICIENCY VIRUS TYPE I (MAL ISOLATE) BIL	2000	770 1717
ALLYGITS AREAL AR								ş	ITURIAN INGRUNOCEFICIENCY VIRUS TYPE I (IRCSF ISOLATE)(II	NPO TROITED	2 2 2
INDIVISION INDIVI								. yo		VT/U PAOTEIN	
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P1 500 AOTHO	GLYCOPROTEIN VP)	HIMAM ROTAVIRUS (SEROTYPE) / STRAIN MIT)	2	917:13						
PVSOI ROTHP	GL YCOPHOTE IN VP3	HUMAN ROTANBUS (SEROTYPE I / STRAIN MO AND STRAIN D)	2	202-330						
F1'500 ROTHA	GLYCOPROTERY VP?	IRDAAN BOTAVIAUS (SEROTYPE) / STRAIN P)	387-330							
PVSON ROTHS	GLYCOPROTEIN (*)	HUBIAN KOTAVIRUS (SEROTYPE) / STRAIN RAV)	313-330							
P. 306 RO1117	CLYCOPIOTER VP?	HIGH ADTAVRUS (SEROTYPE 2 / STRAIN S2)	11.170	П			1			
	CLYCOPEDIEIN VP)	INDALAN ROTAWAUS (SEROTYPE 4 / STRAIN ST THOMAS 3)			182-376					
PISIN ROLINA	GLYCOPROTEIN (P)	HABIAN BOTAVBUS (SEROTYPE 4 / STRATN VATO) :	•	146-343	143.370					
	CLYCOPROTEIN VP!			517-710				3		
١	GLYCOPROTEIN UPT		211.170							
	CLYCUPROTEIN VP1	11	911-112							
P1'509 ROTPS	GLYCOPROTEIN V71	PORCHE ROTAVIRUS (SEROTYPE 47 STRAIN OSU).	3.16	104-343	111.330					
P1 SON BOTTS	CL YCOPROTEIN VP)		M3:130			. [
PY SON BOTPS	CL YCOPROTEIN VPT	PORCINE ROTAVIRUS (SEROTYPE 5 / STRAIN TFR-41)	913-330							
P. 50 RO1PK	GLYCOPADIEIN VP)	PORCINE BOTAVIAUS (SEROTYPE 47 STRAIN BEN: 144)	2	2. 00 100	311.330					
	GLYCOPROTEIN UP!	PORCINE ROTAVIRUS (STRAIN R)	×=	113.30						
	GL YCOPADTEIN VP)	PORCINE MOTAVIAUS (SEROTYPE 4/STRAIN BAIL-1)	=	20.24	113.330					
PI SOF ROTRII	GLYCOPADTEIN VP1	PORCINE ROLAVIRUS (STRAIN YAL)	=	317.330		ŀ				
	GLYCOPROTEIN UP)	PHESUS ROTAVIRUS	201.130							
PV SIO ROTBH	GLYCOPROTEIN VP1	SINITAN II ROTAVIRUS (STRAIN SATI)	20:32							
PYSIO ROTES	MONSTRUCTURAL GLYCOPROTEIN NCVPS		1917							
PVS10 ROTBU	AINOR OUTER CAPSID PROTEIN	BOYDAE ROTAVIRUS (GROUP CASTRAIN SHINTOKU)	<u>=</u>							
PVSIG ROTH?	YCOPAGIELY NCVPS	BOWINE ROTAMBUS (STRAIN UK)	100			-				
PVSIG ROTH!	NONSTRUCTURAL GLYCOPROTEIN NCVP1	HUBICAM ROTAWAUS (STRAIN ATE)	201.6							
PVSIO ROTIE	VCOPROTEIN MCVPS		1).10							
PVS10 BOTHC			21.40							
PVS10 ROTHW		HUBLAN ROTAVIRUS (CROUP C/STRAIN BRISTOL)	131-138							
PVS10 ROTS1		LAIN WA)	¥1:4							
PVSII ROTGA	YCOPAGTERI NCVPS					10				
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PVSII MILBAPE	SAVALE HYDROPHOSIC PROTEIN		2					T	T	
PVSII MICHIE	IIC PROTEIN	MAMPS VIRUS (STRAIN BELFAST)	25.72					Ī		
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PYTHOS FOWPAI	HYPOTHETICAL BANDH DAFFFROIFIN	POX VIRUS (1501 A 12 10-4) HARDNETT		П					
PLDOS FORTM		FOWLPOX WINUS (ISOLATE IP-ATHAINSKIII)	1.37 41.05						
P. ROT FOWPLE	HYPOTIETICAL BANGH ORJAPHOTEIN	FOWLPOX VIRUS (ISOLATE IP-1) IJNILNICII)	115-149						
PIBIO FOWEN	HYPOTHETICAL BANKH CRESTRICIEN	FOWLPOR VIRUS (ISOLATE 19-ATHAUNICH)	144.378						
PUBLIC FOWPAI	HYPOTHETICAL DAVON-ORFIO PROTEIN	FOWLPOX VIXUS (ISOLATE 19-4) (NUSICII))	163-231	j					
PIBIT FOWEN		FOWLOR VIALS (ISOLATE IP-4) (AILAICH)	13:43	2			1	1	
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Print, TVI	HYPOTHETICAL 11 + KD PROTEIN	Ī	F51 P8-130						
P. URL 11VI	HYPOHIETICAL IS SKO PROTEIN	1	78-122						
171	HYPOTHETICAL 16 BKD PROTEIN		<u> </u>						
PVCMT TIVI	HYPOTHETICAL 71 KD PROTEIN		1						
PYCIAW TY:	HYPOTHETICAL IN THO PROTEIN		4.36	_					
P. P. B. B. P.	HYPOTHE HCAL 13 I KD PROTEIM	KRAUJ(TIVI)	13						
P.P. R. B.V.	HYPOTHETICAL PIZ PROTEIN		=======================================						
PYP24 RTDV		E PIEL (PPINES) (R.TC	13-73						
PIPIS ATOVP	HYPOTHETICAL PROPEIN	RICE TUNCHO BACILLIFORM VIRUS (RTBV)							
P1P46 BTBV		TE PITT IFFINES) (AT	٦						
PYP-4 ATOVP	HYPOTIETICAL PAPROTEIN			_					
PIPES HPVAC	MOTER		(6-11)	_					
PYPIA THVA	TEN IN PO 5 SECTION	HEDROSIS VIRUS	13.13						
PYPOH NPVAC	PROTEIN	TOBACCO MECROSIS VIAUS (STILAIN A) (TNV)	2	1		1	1		-
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PYSRI EBV	HYPOTHETICAL BRAFT PROTEIN	epstern-barr virus (staain bo)-i) (radian ierpesvirus 4) [1	96-136						
PYTRI EBV	HYPOTHETICAL BSRF! PROTEIN	epstern-barr vikus (stram bos-1) nribarah herpesyirus ay 🎮	141.19						
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PTVAC VACCE	SIYPOPIETICAL 24 BED PROTEIN IN UBIQUITIN THE	FOL YITEDROSIS VIRUS	S-49 170-304	_					
PYVAG VACCC	HYPOTHETICAL 14 4 KD PROTEDI		3						
PYVAH VACCC	HYPOTHETICAL 93 KD PROTEIN		2						
PYVAN VACCC	HYPOTHETICAL 163 KD PROTEIN	VACCIPIA VIAUS (STIAIN COPERIALEM)	2113]		1	1	7

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	9-51	16-91			6.B	74.28		3-39	133-517	44		
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TABLE VI

107 X 178 X 4 SEARCH MOTIF RESULTS SUMMARY

FOR ALL VIRAL (NON-BACTERIOPHAGE) PROTEINS

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KONTRACTOR	COATPROTED	GENOWE HOLLYPROTEIN	COAT PROTEIN	COATPROTEIN	PROBABLE COAT PROTEIN VPI	COAT PROTEIN	COAT PROJECT	COAT PROJECT	ANGENERAL CONTRACTOR	DECEMBER OF THE PROPERTY	COAT PROTEIN	CONT PROTEIN	COAT PROTEDY	CONTINUED	COAT PROTEIN	CONTRACTOR	COAT BOTTOM	MAKOR CAPAD PROTEIN	COAT PROTEIN	COAT PROTEIN	COAT PROTEIN	COAT PROTEIN	202 200 200	CONTROL OF THE PARTY OF THE PAR	PANT SECRETA	COAT PROTEIN	COAT PAGILIN VP	COVI MURION LVO	PROBABLE COAT PROTEIN 3	COAT PROTEDY Y73	COAT PROTEIN Y72	COAT PROTEIN V72	COAT PROTEIN YV	COA I PACIENT YES	CON CHOCKET TO	COLT BRANCH	CONTRACTOR NO	CYCLN HOWALDO	CELL FUSION PROTEIN PRICURSON	CELL SUMPACE-BORDOND PROPER	CELL SUN ACT BOOKED PROTEIN	CELL SUBJACE-BROWN PROTEIN	MULICIAN WOLVALLEY THYRL ! (TTE	MINDE BACLUSCH PROPERTY BALLIN	ALPHA TIMUSDO PROTEIN	ALPHA THANS-BED FACTOR II KD PRO	ALPHA TRANS-DID FACTOR TI KD PHO	ALPHA TRANS-DID FACTOR 73 RD FRO	III ED A-TYPE BYCLUSION PAG	M IO A. TYN BELLENON THE	ANTE PARTIES AND THE PARTIES A	THE WALL THE								POT IN ICO PAO	PROTEIN	107217834
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FERT LICITION	ENV FOLYPROTEIN	PRINKIN BARDHOOF ICHSHCY VIRUS TYPE 1 (22/CDC-2)4 (56), A16)	200	25.50	1		Ì	T	Ť	1	
- 1	ENV POL TROPEN	HOMAN MANCHOCKENCY VINUS TYPE I (ZAINE) (SOCATE)	E				Ī	İ	1	İ	i
THE PARTY	ENVIOLEN	HUBAAN BARANDES KIRMCY VINUS TYPE I (ZAINE & ISIN, A FE.)	1	195.55	1.150	12.2	i	İ	İ	1	1
1	EN PORTROITE	HUMAN BURNOOK KITENCY VIIIUS TYPE I 12:43 ISDLATES	10.4	2	100	33.65	Ì	T	+	-	i
1	ENVIOLEN	HUMAN INDADAGOETICIENCY VIRUS TYPE I (ZAIRE) (2) 11 ISUI ATE)	1	941.20		İ	Ī	Ī	İ	i	i
	EAV POLITICISED	HANAN BORNOOF ICHNOY WALS INSOLATE DISS	=	100	1	664.00		T	1	İ	ĺ
NAME OF THE PERSON OF THE PERS	EXY FOLITION IN	HUMAN INGROPOLITIENCY VIRUS TYPE 3 (150), ATE CASIS	214.58	29.72			İ	i	<u> </u>	†	:
- 1	EAV POLTPROTTON	HUMAN BENUNCOLF KENCY VIRUS 1776 3 (1501.A) E	=======================================	33.536	33.38	10773	T		\dagger	\dagger	İ
	ENV POLYMOILIN	HUNIAN BORDHOOF KEENCY VIRUS TYPE 2 (150), ATE CITANA 1)	3	15.55	26.53	ï	137	1			i
	EXV POLITICISM	HEMAN BORINODED ICIENCY VINUS TYPE 2 (1501 ATE KIH. 2)		12.51	1	ï		İ	i	-	i
· ł	EN POLYMOTEIN	HEALAN BEALMODES CIENCY VIRUS 177E 3 (150), ATE 100)				÷			İ	<u> </u> 	i
	ENV POLTPROTEIN	MEMAN BOARMOOK KENCY VIRUS TYPE 2 1150LATE \$1/24 KF 21	40.00	1			Ì	+	i	1	;
- 1		MANAM BOALMODE ICIENCY VIRUS TYPE 2 (ISULATE SM.TSV)	537.384	1		-	İ	-	-	:	:
•		HANAN BORROOFFICENCY VIRUS TYPE 2 (150LATE \$1)	20.00	121.17	100	- 100 m	İ	+	i	Ť	-
		MRG CELL FOCUS FORMING ARULINE LEUK EATIA VIRUS	211:00				İ	T	t	<u> </u>	Ī
		MINK CELL FOCUS FORMING AFURING LEUKSMIN VIRUS (150LATE CL.)	<u>6</u>			İ	İ	Ť	İ	<u> </u>	ì
A TOTAL		AKY MURDE LEUKEMIA VIRUS	3		Ī	Ť	1	1	İ	!	Ī
	SAN FULLYROTEIN	CAS-BR-E MRINE LEUKENIA VIRUS	100	Ī		T	t	1	1	1	
	ENV POLYPROTEIN	FALLING MUNINE LEUKEMAN VIAUS (1504.ATE 31)	31.33			T	İ	t		1	1
	FINE FOLVE SEE	FRIEND MURDIE LEUKEMIA VIRUS (1501.ATE FB19)	100				1	1	1	\dagger	Ī
	LAV PALTYNOISIN	FALSAD MANUEL LEUKEMIA VIRUS (ISOLATE PVC.) II)		Ī		T	1	1	+	1	1
	ENV FOLVERSEN	HOMOLY MONDAE LEUKEMIA VIRUS	26.58			T	1	\dagger	+	+	Ì
	SAN TALIFICA	KINSTEM MONDAE LEUKEAUA VIAUS	3	Ī		İ	1	t			Ī
PEN VEVID	NIZIONAL POLICE	MCLUPEY MUDGE LEUKEMIA VIRUS	50.ES					+	+	\dagger	1
	Many sea year	ACCAMINATION MAKEN LEUKEANIA VIIIUS	493.538				l	l	l	\dagger	Ī
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		MOUTE MANAGEMENT TRANSPORTINGS (STRAIN SAG)		\$41.500		l	l	I	ł	╀	Ī
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	ENV FOL YPROTILIN	NAUSCHER KAME CELL FOCUS-INDUCTING VIRUS	1				1	1			
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O TO	MICHAEL SOLD LANGER	CANIME LISTEMPER VIRUS (STRAIN ONOTINS)	<u>-</u>								
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		-		178-317	ECHINAL WALK TYPE 4	A DOCUMENT OF THE PARTY OF THE	114 OF 1770
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l		TOBACCO BATTLE VIRUS (STRAIN TCM)	7								
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PYZA CANTH	2A PROTEIN	CUCURGER MOSAIC VIRUS (STRAIN FHY)	92.419							F	1
PV1A PSVI		PEANUT STUNT VALUE (STICAIN !)	125-352	117.731							Ţ.
PVIA TAV		TOWATO ASPENAY VIEUS	313.340	33:75						Ī	Ī
PYJOK HOLYVE	ILY PROTEIN	HUMAN CYTOMEGALOWRYS (STRAIN EISENFIARI)T)	184-221								•
PYSK TRVIC		TOBACCO LATTLE VIRUS (STRAIN TCNI)	30.180					l			
PV31P ADE41	PROTEIN	HUMAN ADENDYRUS TYPE 41			!	_		:		•	:
Mic All		AFRICAN SWINE FEVER YAUS (STRAIN BATIV)	35-102								
PV763 ASP187	2	AFILCAN SWINE FEVER VIRUS (STAAIN BASIK)	5.00	13.140							
PV3A BACV		BROWE MOSAIC VILUS	=							Ī	
PYN CAMP		CUCUMBER MOSAIC VIRUS (STRAIN FINY)	232.55								Ī
TYSA CARM	14 PROTEIN	CUCLAMBER MOSARC VIRUS (STRAIN NI)	217.752							Ī	Ī
PYSA CANO		CUCUMBER MOSAIC VALUE (STRAIN O)	33.36	1					1	i	-
MY O W	NA PROTIEN	CUCIMBER MOSAIC VIRUS (STRAIN VI	1				1			Ì	
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1111		MALLET FELLOW DWALD VIRUS (1804A18 PAY)	9								!
South Brown		PERT WESTERN TOLLOWS VINOS (NO. 175 F.)	-1	(0.07)							
	SI NO TROI EIL	DEST WESTERN TELEVISION FOR USE (TILL)	-1	6.65							
		POINT LEAVING VAUS (STRAIN I)	ı	7							
	A LO TROITER	TOTALO LEAVABLE VIRUS (STRAIN WALENINGEN)		477							
		BALLET SIMPLE MOSAIC VIRUS	26-135								
		TOTALO LECURACIO VINCIO (STRAIN)	2								-
		TOTALO LEAVADLE VIALD (STRAIN WALCENINGEN)	10-140								
200		ALCALLA MANACE VIRUS (STRAIN 42) / ISOLATE LEIDEN)									
2000		VACCINIA VIGOS (SI INAIN COPENIACEN)	7	200	016-682	14.15					
VALVA VALVA	Pacition AA	VARIATION AND THE CONTRACT OF		017-07	107-747						
WALE VACE		VACCINIA VIBILISTERATA COPENNACEN	1	į.	2						
DAMA DANO		CABINE & CABINE									1
VAMP VARV		VARIOLA VILLA	3			1					
WATE VACES		VACCENTA VIETE STRAIN COPENIACEN	116.911								1
VALI VALV		VARIOUA VIRIU									Ī
PVAIL VARV	VE PROTEIN	VANIOLA VIIIIS									1
PVANS VACE		VACCINIA VILUS (STEAT) COPENHACEN	3	130.169						1	
PVASS VARV		VANOLA VBIUS	Τ	130.137						Ī	T
PVAH VACCE		VACCIDITA VIRUS (STRAIN COPENHAGEN)								T	T
PVAZE VARV	PROFEM A22	VANOLA VRUS	3					-			
PVALD VACCE		VACCINIA VIRUS (STRAIN COPENHAGEN)	95-144				î. '?				
PVAD VARV		ሃላህዕደ ሓ የ መ ሀሄ	₩1.56								
PVAN VACCV		VACCIDILA VIRLUS (STEALIN WR.)	22-49								Ī
PVAIS VARV		VAUGLA VIRUS	23-49								
PVAN VACT		VACCINIA VITUS (STRAIN WR.)	553					1			
PAN VACC	MOTERA ALI	VACCINA VIRUS (STILAIM COPENHAGEN)									
144		VACULA VIRUS	2								
TANK WALL		VACUADA VILLIS (STRAIN COPERMACEN)									
PVAN VALLY	PROJECT AND	VACUUMA VIIIUS (STIKUM W.R.)					-				
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WAM VARV		VALIGEA VIRES	17	Ī							I
PVAN VACE		VACCINIA VIRUS (STRAIN COPENHAGEM)	Τ	185.113						1	I
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AN HOW		ANNA INC	WI CW	AND CAX	ANDE ITEM	A YOU'V IPEAL	100		A MANA	A30VA 6/ EA4	COOVA 618A6	PVS (FEAT	77.		A DYA III WA	SOOVA BIRMA	ADDYA LIBAL	SOVA LIEAN	PASIS COME	AND INCH	AND THEAT		APIA PA	SOVA BOLAN	A-DVA LBGA4	PYDON VACCY	The same		VALUE OF THE PARTY	BOOV AND	AYYA MEAL	ATOWA MORAL	TOWN MORAL	ATTVA COGA.	170	TO THE PERSON NAMED IN		PWAT CHANN	WAT CLAYS	PVAT CAMPY	PVAT CUMVN	BANCO 1VA	PYAT CAMPO	YYAT CAMP	AND THE				W. T.	NA TAN	ATTA INA	DOWN INM	AYYA MYA4	AZOVA MYA4	SATURA LIVE	AYYA LIYAA	ANYA LIVAL	PVANT VALLE	77.00		Various Various	1	4	THE REAL PROPERTY.	NCC NC
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VACCINIA VIIIUS (STRAUN WX)	AYOCHAY ARIAS (\$117YIN CONEWAYORX)	POTATO YELLOW MOSAIC YEARS (ISOLATE VENEZUELA)	CASSAVA LATENT VIKUS (STRAIN NICEROAN)		DESCRIPTION OF THE PROPERTY OF	DEAN ON WALKE VIEW	VACCIBILA VILLUS (STRADI WK)	I VACEDRIA VILLUS (STRADA COPENHAGEA)	VARIOUA VIIIUS	VACCORIA VILLE (STRAIN WIL)	ANCTION ARMODISTICAL MINERAL OF	CANCELL AND MAINTAIN DAMES IN	AVGARAY AMITIN CALIND COARMACEN	AYBONY ARAS	VACCINGA VIRUS (STRAIN WR)	AVOITABLE CONTRACTOR CONTRACTOR	TOTAL CONTRACTOR OF THE PROPERTY OF THE PROPER	VACANTA VIDIR (CITALINI WIL)	VACABLE CHILARI CONTINUAGEN	COMPANY VIOLE	VACCEDIA VILUS (STRAIN WA)	VACCEMIA YELLE (STRAIN COPEMNAGEN)	VACCINIA VIAUS (STRAIN WX)	VACCORIA VOLUS (STRADN COPEMIAGEN)	AVCCIMY ATYRE (21 KYIN AT)	TORNER CONTROL OF THE PARTY OF	VACCIONA VII US CETTAIN WILL	IVACCIDALA VIDUS (STILADI LISTER)	VACCIDIA VIXUS (STIVADI COPENHAGEN)	(VACCINIA VILUS (STRAIN LCIMIO)	AND VACOVA	AVECTOR ABOUT A LANGE AND A LA	AND MAIN COUNTY OF THE PARTY OF	WARRING VIBLIN (STRAIN) COMMINICATION	VACCEDIA VIEUS (STEADS WA)	PIOWORT MOSAAC PULLS (STIAN DXS)	CANATION STORED LING VIKUS	CAULITLOWER MOSAIC VIRUS (STRAIN W260)		CAULIFLOWER MOSAIC MINUS (STRAIN PY 197)	CAULD COMER SOUSAR VIDIOS (STRAM PIXOLOS)	CVITTATOMEN HOUSES AND PRINCE OF LAND AND PRINCES	CARREST AND VIRUS	CARRAYA LATENT YIBUS (STRAIN MOGRIAN)	CASSAVA LATENT VIBUS (STILAIN WEST KENYAN M4)	BEET CURLY TOP VB.US	AVCCINY ABITS (SURVEY MAT)	VACCINIA VIRUS (STRAIN COPENHAGEN)	AMIA YASIYA	AVCCERTV AIYOR (STAVIN AR)	ANCTHE ATTENDED OF COLMONY	AND CHILD AND THE PRINCIPLE AND COMMENTAL COMM	TANCENTA VINCE (STANKE TO)	CANADA VALIDA (STRANA WA)	VACTRIA VIII IN TOPENNAGENI	AYRALY ARTIR	VACCINA VIRUS (STRAIN WA)	VACCIBIA VIRUS (STRAIN COPENIAGEN)	VACCORA VIRUS (STRADI WR)	VIRUS	Total list and an arrangement and arrangement and				
11:31	403-432	120-147			1111	12014	6.19	41-12	018-011	180-210	100	180-210	1182-213	117-171	13/13/3		117.331	251-2115	250-265	113-140	8 C-2	21-54	20-53	18-97		SILA)	254.214	254-284	234-214	1074.62		1	92.123	93-133	101-135	12-12	102-138	7	22-70	12-10	1 1 1 1	3 2	33.36	22.70	R:12	29.138 29.138	101-121	79-106	79-106	22.49	35-12	¥	91-71			6.0	N.	1	<u>.</u>	146-173	143.172	145-172	75-197	10,550	
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YAME ON THE	PROTEIN C4	SHOPE FIBEOMA VIRUS (STRAIN RASZA)	97.68	4 5	क्रम	1	7	N. P.	7	AREA LAREAS	3
1	MOTIPICA	VACCINIA PIRUS (STRAIN COPENHAGEN)	13.46						1	1	1
AVO AVO	MOTEBICA	VACCINGA VISIUS (STRAIN WR.)	9					1		1	Ī
WOR WAN	PROTEDICA	VALIDIA VIDUS	17.				I	1		1	
200	MYOTHERICAL PROTEGNICS	SHOPE PERIORA VIBUR (STRAIN KASZA)	100	112.170			Ī	T	1	1	7
1000	MOTERICS	VACCORIA VIDUS (STILAIN COPENHACEIN)	ž					T	1	1	4
ON CONTROL	MOTERIC	VACCINIA VIRUS (STILLIS VIR.)	1					Ī	1	1	I
AND HAND	MOTEON	VANOLA VIXUS	3						†	1	4
Part Charles	MOTERICA	VACCINIA VIRUS (STRAIN WR)	=			Ţ	ŀ	i	İ	1	:
ALL OF THE	MOTERIC)	VAUOLA VIRUS	1					T	1	1	Ī
	AND LEAN CO	VACCINEA VIRUE (STRAIN CONEXMAGEN)	\$	1	10,10	252.770	286.134	107.5	1	1	T
WC10 UV	PROTEIN CA	VACCINIA VIRUS (STRADA WR)	3	9	76-70	Т	Т		T	1	
PVEIS VARY	OF CHARLES		091-761			Т	Т		T	1	T
Day Orac	PENCHANCE OF THE PENCHA	STRAIN WE	34-163				Ī	Ì	İ	i	1
PAPEL SELECT	PROJECT CITY	VAUOLA VIRUS	36.15	:	:	•	!	•	;		
2000	PACKER ALAST	SHOPE FIBROMA VIRUS (STRAIN KASZA)	š	39.60	13.162	206-340	T		1	1	T
TOTAL ATTACK	MOUTEN CINES	VACCORA VIRUS (STRAIN COPENHAGEN)	131-131				T	1	1	İ	Ī
PWCIO GOVE	MOTEN CIVILIA	VACCIMA VILLS (STRAIN COPENHAGEN)	ž			Ī	T	Ì	Ì	1	
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AND STATE	- 15	STRAIN COPENHACION)	8.2				İ		İ	1	i
			206,176			T	İ		Ì	1	1
	MANCH CAPAID PROTEIN		147.874			Ī	1	1	1	1	
PUCAP LACTOR	LANCE CLUB TREET	STRAIN UGANDA-1102)	21-36	355.102		Ī	T	T	1	1	
Ł	MAKEN CAPAIL PROTEIN		369-790				Ī	1	1		
	CONTRACTOR FILE	MUCLEAR POLYHEDROSIS VIRUS	133-163	196.748		Ī	T		1	1	1
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1	PROTEIN DS		fy.	164.211	321.348		T	T	l	\dagger	Ī
•		VACCINIA VIALIBILITATIVI COPENHACEN)	240-267	113-360			T		t	\dagger	T
l.	PROTEIN DS		140-267					T			T
PVD09 VACCC			240.283						t	\mathbf{I}	Ī
		VACTORIA VIDIO (STRAIN)	2					ŀ	l	\mathbf{I}	Ι
Н			27-120							\mid	Γ
- 1					1						
1	DNA-BINDING PROTEIN	CARNATION STOKED RING VIRUS			1		1				П
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ı		HUBAN PAPALOMAVOUS TYPE II	Î	1-		T	T	T	1	\dagger	1
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ı		MARCA PAPELONAVIUS TYPE 3A	136.193	ŀ	T	T	T	\dagger	\dagger	+	7
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MOD VACY	AYYA 190Ad	AZDYA 100A4	PACOL AVON			NAME OF THE PARTY	MAD STAN	ALMOI WAN	ANTA 91 AA	SALE AVE		WAY A	AWA ELEAS	CONA BLANC	SOVA RIAM	7.W.A. 11.A.A.					AUTA BAN	WA AWA	AXXVA IDAM	DAYA DAYA	ADDIL ANGAL	71017	TYPEN VINE					1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		100 PA	PVE AVO	ICAM PANA	SIADI 93A	IACH FIAG	ESACH SBA4	STADY STAN	PARTY MAAGC	STADI VIBAS	TAME VERA	AND MAN	100	To the same	TAPE TAPE	SIAM PANA	SIAM PAA	1100 7104	PACH MAC	ACM TANK	SACVE TEAL	PSACK TEM	MAGI ERA	PVED 10VS1	ISABI FLA	DARN TRAL	PVEJ JOVIH	SCA.PH COA4	THAN TIL	PCCDH
IIIATE TEC DES PROTEIN	PROTEIN OI	LY LOT CO.	A CONTRACTOR OF THE PARTY OF TH	Section (I)	KILLON MOSTON	14 KUS PUSION PROTEIN	16 KD PUSION PROTEIN	PROTEDNETM	THE PROPERTY OF	The state of the s	MOTERA FILE	PROTEDITOR	PROTECH F13	PROTEDITIE	PROTEIN FILE	7 Published 1		MOTEO FIL	PACTED FILE	PROTEIN F	MY HANDE MENDERAND MECUNSO VACCIONA VIDER 1815 MAIN TO	THE WORLD BETTER TOWN OF THE	14 NETION 17	Ļ	L	L.	THE PART OF PLOTED	THE PARTY OF THE PROPERTY OF THE PARTY OF TH	ABY DAMAGRADIVE ON	SALLY M KIS PROTEDY	NOTION LE	MENTON WE	NOTES	EA PROTEIN	MINIOTE #3	אנטובוא	EA PROTEIN	MILITAL CE TYBYBOIL	PRODUCE IN PROPER	PROBABLE IN TRACE	PRODABLE ESA PROFILIA	THURNING BAN THAT CAN	TRUBANTA BATT TRUBE	THE CALL OF THE PARTY OF THE PA	MATON NO PLANTE	PRODUCE OF PROPERTY	MONABLE DA PROTEDI	PROBABLE BA PROTEIN	PROBABLE DA PROTEIN	PROBABLE BA PROTEIN	PROBABLE SA PROTEIN	Matori (3	PROBABLE ES PROTEIN	PROBABLE EX PROTEIN	ES PROTEIN	EX PROTEIN	EJ PROTEDI	EZ PROTUN	CI PROTEIN	EL PROTEIN		
VARIOUS VISUS	VACCIONAL VISITATION WILL	WALIOLA VISUS	VACCINA VIXUS (STIVAN WIX)	VACCORIA VOLUS (STILLIN COPENNAGEN)	VACCINIA VIXUS (STIVAN MA)	LAUCTIAN A PROPERTY COLONIA CO	CAN TOWN (STORY) AND COMPANY COM	CONTRACTOR AND AND AND AND AND AND AND AND AND AND	FOW YOU YOU	ANDIA VIOLA	AVCCIMIY ABITS (21 MAIN 1-144)	AVCCIMO ABIOR (STEAMED COLEMANIA)	ANDREA AND AND AND AND AND AND AND AND AND AN	WIND A VIEW	VACCINEA VISIUS (STRAIN L-147)	VACCINIA VILLE (STRAIN COPENIAGEN)	S/MON ANDINA	YACCONA VOLUS (STRAIN L-IVY)	VACCINIA VILLIS (STRAIN COPENNAVEN)	VARIOLA VIDUS	O VACCIDIA VIDER (STANKE WAY)	CITAL TORS (STORY)	AND					AUTOGRAPHA CALFORNICA NUCLEAR PULT HEUROSIA TIRVO	KIDAN PAPELOWAYING TYPE PIETO	MUDALAN PAPEL CALAVIRUS TYPE 31	KONAN PAPELLOWAVIRUS I TTE +>	MANANTA CHANCING TITE "	HUMAN PAPILLUMA VIAUS TYPE AT	TURNA TATALANA TAGA TAGA TA	TOWARD FOR COUNTY THE TANK I	TANAM DANI CHAVISTIS TYPE IS	AND THE PARTY OF T	BE 3241 CHAVINUS TYPE SB	INDIAN BARNI OMAYIRUS TYPE IS			HUMAN PARALLUS TYPE II	HUMAN PAPILLOMAVIAUS TYPE IS	HUMAN PAPELLOMAVIRUS TYPE (HYWAY SANTTOMY ADMIN 1 ALE 21	HOWAN PARTICIPANT CALL OF THE PROPERTY OF THE	HUMAN LYMPTON ALVO 1112 14	HUMAN PARILLEMAN TRACE	HUMAN PARTICULAR AND TAKES	FIGHT CHANNES IN THE COMPANY	CONCRETE SANTI DIMAVIRUS TYPE	THE PARTY OF A PARTY O	IN THE PART OF A VIEW AND A VIEW	HURAN BARNI I OMANARIM TARES	INTRAMEDIA OMA VIRUS TYPE S?	IN THE TAXABLE STYTE SI	MINION PART DAVANCE LANGE	CANATA AND LUTTANI IN LABOR 10	TANKS I MANAGER TYPE 13	AN VICTOR DE DECEMBER DE		
96-123	96-123	22-22	197	1	2700	4,6	37-44	ž	146-173	200		14.61	35-62	10-37	10-37	į		1	1	274.33	Ž	33-86	33-60	71.110	12.5			1			200		8	200	100	11.102	\$.2	75.102	35-62	11.4	27.54	9.60	E	ě	204.74			ž	ž	ŧ		627-754 10-754	767-196	120-150	13-31	2-36	184	139-184	17.31	7.34	134-192	LVIRV
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FILE HAMI	PROTEIN	Visit			7	7	Ŧ	7	Т	1	
PVOD HSVEB	GENE 3 PROTEIN	EOUNE HEXPESVILUS TYPE I (STRAM ARAP)		3	1	3	क्षापुर विक	0854. 4B	<u>त</u> स्		AKEA
PVOD) HEVEK	CENE 3 PROTEIN	BOUNE HEAPESVIRIS TYPE I KTHAIN KINGING VAI		!	-	!	-	:	:		:
PVOM VACCE	PADTEIN 33	VACCINA VIRUS ISTRANI COPENIACEN	2				1	1	1	1	1
PVOO! VALV	PROTEDUCE	VARIA A WILK				20.00		1	1	1	
PVCOJ HSVII	KYYOTH GENEE 9 LIELUS PRO	L'ALTANDE PERMENE		2	33.28			1			1
PVOM VACCE		VACCING MEIR (418 AN COREMINGEN	5				1				1
PYGOS VACCV	PROTECUEL	VAPORIA VIGIN CATA LA LES			į	:		:			!
PVOD9 VARV	PROTEINF	VARKEL VIRIE	10.								
PVOIL SPVIR	E	SPREAMA VIRUS SPVI-LIAZ B					1	+	1	1	
MARIA 1944	HYPOTHETICAL DEVE IS PROTEIN	ICTALUND JEDVESVINE 1	13				1	1	1	1	
PYGII MINI	HYPOTHETICAL GENEE 18 PROTEIN	ICTALINIS IETPERVIEW					1	1	1		
ı	CANSID PROTEIN	SPROPLADMA VIRLIS SPVI.RIAZ B					1	1	1		
WG BY	CAPSID PROTEIN	SPIROPLASIMA VIRUS 4						-		<u>.</u>	
PVCLU NSWII	HYPOTHETICAL GENE 11 PROTEIN	ACTALITATIS LEGISLECTION 1	1	2	┱			1			
PVG24 MSVII	HYPOTHETICAL CENE 14 PROTEIN	ETALIED SERPECHETE	3	200	ê	766-124					
L	HYPOTHETICAL GENE 28 PROTEIN	ACTAL Unity Membres Visite	-				1		1		
Z	HYPOTHETICAL GAR PROTECT	AMIACTA MOMBIE INFORMACIONIE	22.62	2							
ı	GENE S PROTEIN	CHRIST ACIA VIRILE CRV1 BEAT B	3								
l	GENE 2 PROTEIN	CANCOL ACTUAL STREET	2						-		
۱	HVPOTOETICAL GENE IS BEOTEN	STANDARM VINUS 4	146-173	3.30	362-310				H		Ī.
PVG3 RSVI	HVPOTARTICAL ORDER 19 NEOTRIC	MUNICIPALITY OF THE PROPERTY O	5.111								Γ
ı	KVECTION CENT TO BE OF THE TOTAL TO THE TOTA		443.469						H		Γ
1	MACHINE ILANGORIA PROJECT		249-159	§111-1401			-	l	\vdash	T	Ī
ALM PROTE	ATTO INCIDENT OF THE PROPERTY	AMENDA MODIFIED ENTORIONOMYRUS	62.5					\vdash	ŀ	T	I
1	UCAS J MUIEIN	SPROPLASMA VIRUS SPVI-RIAZ B	62-51		L			l	l	İ	İ
	DEMB 3 PROTEIN	SPROPLASIAA VIRUS 4	16-51	89.148				I	t	t	T
ا	MYPOTHETICAL GENE 45 PROTEIN	HERPESVEUS SAMON (STRAIN !!)	131-165						t	t	T
-	MORABLE MAJOR OLYCOPHOTEIN	ICTALUMO HEAPESYIRUS I	42.168	346.333	10.68	973-1807			\dagger	İ	İ
ANGLE SAN	NYPOTHETICAL DEPTS 48 PROTEIN		360-394		Т		-	\parallel	t	t	T
1	OR TAULDIN	RUS	187				-	\mid	t	1	T
1	UEAR & PROJEIN		16-146				-	-	t	t	Ī
PUNIT URDER	WASHINGTON OF THE SHOOTS		34-61	17-114					ŀ	l	l
אטר מנאו	DOSANGERICAL COME CONCRETE	MEANTS VILLE SAMOOU (STIJAIN !!)	47.74								Ι
MAR ROAD	CENT S PROTES		Ş							-	
200	OENE S PROTEIN	Called Author Control	2								
L	HYPOTHETICAL GENE AS PROTEIN		3								
l	KYPOTIGITICAL CROSS & PROTEIN	INTERIOR DESCRIPTION	2000						Н		
PVC#S HSW11	HYPOTHORNICAL GRIDGE AT PROTEIN		Š						Н		
l	HYPOTHETICAL GENE AS PROTEIN		121-121								
L	HOPOTHETHEAL GENE 67 PROTEIN					1		1	1		
	HYPOTHETICAL GENERA PROTEIN.	ICTALUME HEAVES WALLS 1	341.384			1		1	1	1	
PVOTE HSVNI	HYPOTHETICAL GENE 72 PROTEIN					Ī	+	+	1	1	1
	HYPOTHETICAL CENES 75 PROTEIN		617111	Ī		T	+	+	1	1	
_	HYPOTHETICAL CENE 76 PROTEIN		120	T		1	1	1	1	1	I
	OEMS 1 PROTEIN	SPINOFLASMA VINUS 4	7	Ī		T	1	\dagger	\dagger	1	1
WG DA			1336-1366	2404-1435		T	-	+	\dagger	+	Ţ
TACT CAR			No.	62.676	1022-1064	1271.136S		1	+	\dagger	T
West Cyan	E. CL. TCUPICITED PRECINCOR		399-436		1022-1084 1278-1305	27. JOS	-	ŀ	t	1	T
YOU CYBEY	•		~	Г	1023-1094 1278-1305	134-1365	-	ł	t	t	T
1	EL GLYCOPPOIETA PRECINCOL		368-456	643-676	1023-1084	278-1305	-	+	ŀ	t	T
	IS OCTUMBLED PRECURSOR	BOVING COLUMNATION (STRAIN QUEBEC)			1022-1064	278-1305	l		t	t	T
1	TECURSON .		399-436	2,72	1023-1084 1278-1303	24-183	-	1	t	\dagger	T
1	TECHNOR		П	209-875	1056-1113		-	\mid	+	t	T
1	TECHNOR		-	1030-1093			ŀ	┞	t	t	T
SALE PARK	ES CELVOSPACITOR PARCINICAL	MINISTER CONCRAVINGS MANY (STRAIN ASS)	ा		978-1040		7.			\vdash	Τ
1	RECURSOR		Т	1000-1002				H	Н		
ı			3		1		-	Н	Н	H	
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200	107117814	(All Virgin) (as bestering bugs)						
THANK	NOTE IN THE PROPERTY OF THE PAR	ASTROENTERITIS CORONAVIRUS (STRAIN FS??)	3	101.100 101.000	1073-1143			
VOL CYNA	EL OLYCOROTEM INSCLUSION	PORCING TRANSMISSIBLE GASTROENTERITIS CONGNAVIRUS (STRADI MILLES-110	911-69	(11-20)	104-1145		Ť	+
VOLU CVIII	E3 OLYCONIOTEDI PRECINSON	POLICINE TRANSPOSSIBLE CASTROENTERITYS CORONA VIRUS (STRAIN PURD) 69-107	\$	10.00	1067-1143		Ť	\dashv
WG CYMV	ET OF ACCOUNTS INTO A DESCRIPTION OF A D	PORCINE RESPIRATORY COROMAVIRUS (STRAIN BA/137004 / BKITISI) ISOLAT	461.309	1869	1129-1165		H	\sqcup
1	III OLYCIANOTEM IMECUASON	7	64.309	126-678	1129-163		t	+
	NORWING METON COACOA TO ET	TENTIS CORONAVIRUS (STRAIN NED)	107	20-731	(P11-1801	100001	Ť	4
	PROBABLE MEMBRING CLYCOPROTEIN		100.23	7.5	3	1007-114	Chi layer	희
VOLUMENT OF	E3 OF ACCUMULATION MECCANON		19.4V	SX-W	1037-1011	-		<u> </u>
	NOTACIONALIZADA PARECINACION	ETTE)	101-101	173-902	1036-1090		t	Ļ
	E3 GLYCOPROTEIN PRECURSOR		90	3	1037-1091	T	t	1
	ET CTACOMOTERA MECONSON			2	10001-000		\dagger	1
PYOLE BYM	ELI GLYCOPHOTEIN PRECURSOR	US (STRAIN MI)	-101-101	204-613	1900-1970	Ť	†	1
	CLYCOPHOTEDI CP110 PRECURSOR		9.12	101-034			\dagger	1
	OF ACCUMULATION IN INTECNITION		6	1			†	1
L	OLYCOPHOTEN B PRECURSOR	STRAIN TOWNES		1			†	1
L	OF ACCIDING TO A SECTION		1					Ц
L	OF ACCUMULTURE BY LATER CONTROL		¥ B	20.00				Ц
A A COLOR OF THE A	CIL YOUR AT THE PROPERTY OF	P 34A4 SMEASTAIN THEODS	411-313	616-643			H	\perp
ALC BY	GLYCOPILOTES I PRECURSON		ST.	24.38		T	f	Ļ
WASH CTOAL	OLYCOPACTED & PRECURSOIL		8	2	T	T	t	1
TAB(COA	OLYCOPROTEN B PRECUDIOR		3		1	1	†	_
WOLL KIND	OLYCOPROTEIN & PARCUNSOR		301	441475			Н	Ц
TAGE STORY	OF ACCOUNTS OF STREET		469-310		П		H	Ц
WOL KINK	OLYCOPILOTEDI C PRECLILIGAL	HELVEL SOMPLIX VIRUS (TYPE I / STRAIM KOS)	40-310		Ī	T	t	L
PVOLC JUVES	OLYCOPHOTEDIC PRECURSOR			Ī	Ť	†	1	1
AAZA 2 DAA	CLYCOPIOTEDI OPY	VALUE BLA-203 IER VIGUE (STRAIN SCOTT)	19332	T	1		H	Ц
ACC VE	OT ACCIDITATION IN MACHINESON		111-14	П		H	Н	Ц
WELL TOWN	NOSINU SELECTION POLICE IN THE CONTROL OF THE CONTR	HOVEN REGISTRATION SYNCYTIAL VIRUS (STRAIN ASINGS)	SP1C	ž.	216-20	\$43.48 8	1	٢
WILL TIME	PLESION OF ACCUMENTATION LANGE TO ACCUMENT	L	į	ž	Ž			15
WITH STOM	PUBLICATION OF ACCOMPANION AND CONTRACTOR	BOYDER RESPERATORY SYNCYTIAL VIRUS (STRAIN RESA)		120.00	21924	1	1990	٤
MOD TOW	FUSION GLYCOPROTEIN PRECURSOR	1	II A	100			†	1
IADM (TRAA	LITTION OF ACOUNT LEGISLATION	1		2		1	1	1
VATION / DOA	PURCH CLICOPROTEIN PRETTEINSON	STRAIN LONG)	ž L	154-202	214-243	4447	41-315	
TATO CON	NOSERVILLEN METOROOFY OF TON	1	71-45	194-303	213-243	HIL	481-31	Ē
1	PUMON GLYCOPHOTEN PREJUSSON	VAD HYTTE)	1	T	T	Ì	\dagger	1
	FUSION CILYCOPROTEIN PRECURSOR	INGASTIS VIRUS (STRAIN DOCACA)	278.263	T	1	†	+	1
YUNG VENY	PUSION OLIVERATION THE PROPERTY OF THE PROPERT		쫉	114		1	1	Ц
	PURSON OF ACCOUNT AND APPLICATION	JAJA VACCINE)	16-02	447-486	П		Н	Ц
	WOTEN OF ACCUMANTAL PROPERTY OF THE PROPERTY O		ž	47-486	T	T	H	L
WOLV KLINGS	NOTATIONAL MINITERACIONAL DI MONSOLA		3 3	426-51	T	t	t	L
AND FON	NOTIFICATION OF LOUISON TO MOISON	DEWCASTLE DISEASE VILUS (STRAIN AUSTRALIA-VICTORIAGE)		1	T	T	\dagger	ļ
NOV YOU	NOTION OF ACQUARTOR WEST AND TO VIOLENCE	NEWCASTLE DISEASE VIRUS (STRAIN BEAUDETTE CA)			t	t	\dagger	1
DAGN (TDA4	NOSIDIA OF LOCATO BITAL METERNATION OF LOCATION OF LANGEST AND STATEMENT OF LOCATION OF LO	NEWCASTLE DESEASE VILUS (STRAIN READS)	i i		T	t	ł	L
140 GA	FUSION OF ACTIVITIES INTEGRATED INTEGRATION	NEWCASTLE DISEASE VIXIS (STRAD) DI AUTCHMEN(1)	100	P S	T	t	t	ļ
PA COV	MOTION OF ACCOUNTS LESS AND STORY	NEWCASTLE DISEASE VIIIUS (STRAIN (TALLENAS)	1	2		T	ł	ļ
WO LOW	PUSION OF ACCAMPAIGN LATER AND TO VICE AND THE COMPANY OF THE COMP	NBWCASTLE DISEASE VOLUS (STRAIN LAVAS)	i	_	100	t	\dagger	L
SVCL BWI	FUSION OF ACCULATIONARY MIRCHARDS	NEWCASTLE DISEASE VIRUS (STRAIN ADVANCAVS))			T	t	\dagger	1
PVOLV JOVO	FUSION OF ACCUMPATION MINICIPATOR	NEWCASTLE DISEASE VINUS (STRAIN QUEENSLAUGO)			l	t	ł	1
IVOU DAY	FUSION OF ACOUSTICITION SAFECTIVES	TOTAL CHARGE THE STATE OF THE S						_
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	10717214	(All Merses (se bertyriophages)									
MON NOW	FACTOR OF COMMERCENT STREET	Vinus	ARFAI	AWFA 9	7487	1	7.407		П		
WALL BEAN	FUSION OF TOTAL I EN PRECUESOR	MEWCASTLE DISEASE VIRUS (STRAIN ULSTERIOR)		20.513			4	1	4	4	1
A PART	PUSION CLYCOPROTEIN PRECURSOR	PHOCINE DISTRIANCE VIRUS	3	1	1	-	i		:	•	•
	PUSION OLTOPROTEIN PRECURSOR	HUMAN PARADIPLUENCA I VIRUS (STRAIN CS9)	121.00	10.364							
	FUSION CL. TOUTION PRECURSOR	HUBAAN PALADIFILIERIZA I VIRUS	9		316.344					1	
	FUSION CLICOTAGES PRECUESOR	HUMAAN PADAINFLUENCEA I VIRUS (STRABA CREER)	g		1	12					1
	FIRM OF COMMENTS OF THE COMMENT	HENCAN PARAMPLUENCA I VIRUS (STRAIN TOSHIBA)	1 2		311.364					1	4
	STRING COCCESSION THE UNSOR	BOVINE PALAMPLIENCE SPIRIUS		177.00	5						
	MANAGE OF COMMENTERS OF THE COMMENT	MINAM PARAPOLLENCA I VIRUS (STIVAIN NII ANNS)		207.34	107.637				İ	Ì	-
WED THEFT	INTERNATION OF COMMERCIAL STATES	AUNORAGET VIAUS (STRAIN KABETE O)	24.765	1							
	POSICION OF TOWNS THE PARTY OF	RINGERPEST VIRLIS (STRAIN L.)	724.765	5							
	FINANCE CONTROLLING PRECURSOR	SENSON VICUS (STRAIN 27 HOST MUTANTS)	133.140		147						
L	HUNCH CA YOMEGIEN PRECINSOR	SENDAL YOULS (STRAIN PUBLICAL)	1			1					
	PUSION OF TOPROTEIN PRECURSOR	SENDAL VIILIS (STRAIN HARLIS)			À		·				
	FUSION CLYCOPROTEIN PRECUISOR	SENDAL VITUS (STICKIN INV)			Ŕ						
SE SE	FUSION OF YCOPROTEIN PRECURSOR	SENEAL WRUG (STIAME)	27	2	\$ 5 5						
PVGLP SV4	PUSION OL YCOPROTEIN PRECURSOR	SPACKA WALDE AT	122-149	211-245	180-501					T	
PVCL SVS	PUSION OLYCOPROTEIN PRECURSOR	SPACE VRIES (1978 AND WILL	144-115	241-269	967-657					Ì	Ī
CL TRIV	PUSION OLYCOPROTEIN PRECURSOR	TURKEY BURNING ANDERS UP 10	1137-171	417-444		L			Ī	İ	T
OLO BEPY	SPIKE OLYCOPROTEIN PRECIPEOS	PANA BEOMINES A TRANSPORT	134-161	002-061	127.53				T	T	T
WILL BULK	MAJOR SURFACE CL. VCDPROTEIN	PANTAL BETTER TOTAL PRIVER VIKUS	\$23.537			ľ			1	T	Ī
PYCLO HOLSY!	MAJOR SURFACE OF VESTIGATE IN	CHAIN STANDARD STACTION VINUS (STAAIN COPENHAGEN)	62-133						T	1	
CLO JOLEVA	MAJOR STREAMENT OF COMPANY	THE STRAIGHT STRUTTIAL VIRUS (SUBGROUP BY STRAIN 1855)	63.03						1	1	
WEST DES	INA IN THE LOCK OF UCOST METERS	HUMAN KESPIRATORY SYNCYTIAL YIRUS (STRAIN RSB3857)	66-103						1	1	
PVCB A MARVE	MANUAL SURVEYOR OF TOURSOLE IN G	HUMAIN RESPIRATORY SYNCYTIAL VIRUS (STRAIN RSB6190)	20.23	T						1	
CLA MOEA	Of Underweight A LEASE AND LEIN G	HUMAN RESPONTORY SYNCYTIAL VIRUS (SUDGROUP BY STRAIN 240)	2						1		
A Mades	ACTUAL EN G MECURON	EQUING NEXPESSION TYPE A	201.70	T							
Wa C LAN	CONTROL EN UP PLECUISOR	EQUING HEAPESYTHUS TYPE I (STILATIN ABAP)	97								
AND VIEW	HALL WE COME SEED THE CURSOR	RADIES VICUS (STRAIN STREET)	486.516		Ī						
1	CONTRACTOR OF THE CURSOR	VESICULAR STONATITIS VIRUS (SENOTYPE INDIANA / STRAIN GLASCOW)	477.499		T				1		
1000	CE LEGITICAL CONTRACTOR CONTRACTO	EPSTEIN-BARR VIXUS (STRAIN 845.1)	1	177 919	Ī						
THE WAY	ON COMMON REPORTED TO THE COMMON	KUNKAN CYTOMEGALOVRUS (STRAIN AD169)	_	20,703				1	1		
WENT HEVE	Ca vonement une die de	HUMAN CYTOMEGALOVILUS (STRAIN TOWNE)	1						1	1	
WELL LEWIS	CA WASHAM U TANAMA	PEACES SIMPLEX VIXUS (TYPE 6/ STRAIN GS)	1	107-09					1	1	
A MONA	OF CA WOOD OFFICE SECTIONS	PEARESYIRUS SAIMIBU (STRAIN 11)	507-100		T					1	
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VOLLA DYSV	M POLYPROTEDIN		75-103						t	\dagger	I
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1		1		EFIZOOTIC HEMOREGACIC DINIANI: VINCO (MINOT TITLE)		AGIT SAN
		·	!	BLUETONOUE VIRUS (SENOTYPE 1 / INN. A IE. SUNTH AFAN A)	OUTEN CAPMO PROTEIN Y77	SIA18 14A4
	!	Ţ		BLUETONOUE VIRUS (SEROTYTE 1/130LATE AUSTRALIA)		YIAL IAM
1	-	7	1000	ONTO MONTH ADMINISTRATION OF THE CONTRACT OF T		TIVIT TWA
_L	1	4		AFRICAN HOUSE SECONDS VIDES (SEAULTRE 47 STACIN VACCING		PASKY LAA
207.934	10-417 612-662	4		HENDER STANDS (STRAIN (I)		VEASH PERM
	1	+		EQUING HELICATION TITLE (STANCE)		CLASH MAN
		+	Ž	TEAT BY THE PROPERTY TYPE I VITE AND A DUE	DIEM YPZ	WASH CEAN
		-	249	CHAIL OF CALL AND VIN CONTRACTOR		PWP19 TBSVC
	1	+	3.18	CALLED STREET STREET CONTRACT		PVP19 AMCY
		-) 8	THE WATER OF THE PROPERTY OF THE PARTY OF TH	WIENLUM ION	NAIN SIGN
		H	101-10	WOLKE TIMOS VIELS (STRAIN NI)		ALM ELANA
		H	11-10	WAS TIMOLYTUS		AGE 11444
-		Н	53-60	ICH DWALF VALUE	THE PERSON AND PARTY OF THE PE	ALM OLIVA
-	234	221-154	131-161	WOLFE TIMOS VISUS		ACONT OLIVA
-	-	Ш	305-232	BICH GALL DWALL VILUS	PROTEIN A PROTEIN PARTS	THE PLANT
		L				

PCCENE	1167411944									
FILERAME	PROTEIN	YARDS	ABFAI	4074	1,19	, , , , , ,	44.	т	Т	
1	OUTER CAPSED PROTEIN VP4	BOVING ROTAVIRUS (STICKIN C416)	3		7	1	2000	4	AKKA	
WA ROTH	OUTER CAPSID PROTEIN VPA	BOVING ROTAVILLIS (STIAIN UK)	59,63			Ì	+	-		T
ı	OUTER CAPSID PROTEIN VP4	EQUINE ROTAVILIS (STRAIN H-2)	13:146	335.269	629-636				1	
_	OUTER CAPSID PROTEIN VP4	ROTA WALLS (GROUP B / STRAIN IDIR)	=			\mid	1			Ī
	OUTEA CAPSID PROTEIN YPA	HUDLAN KOTAVIAUS (SEKOTYPE I / STRAIN 10%)	ŝ	17521		l	1	-		Ţ
ı	OUTER CAPITO PROTEIN VPA	HUMAN KOTAVRUS (SEKOTYPE 2/STRAIN RV-3)	Г	279.306	129.58	\dagger	ł	<u> </u>		Ţ
ı	OUTER CAND PROTEIN VP	HUMALM KOTAVIKUS (SEBOTYPE I / STRAIN 69M)	l	6(1711	029		+	 -		ŀ
TANK MOTHE	OUTER CAPSID PROTEIN VP4	INDAAN ROTAVIALIS (SEROTYPE I / STRAIN 69M)	ŝ	374,306	129-595	l	+		1	-
١	COLEK CAPAD PROTEIN VIN		3	274.KM	5.542	•	:			
1	OUTER CAPSID PROTEIN VN	HUMAN KOTAVIRUS (STILAIN KS)	- SE-	11:11	:		· :	_		
TANK AND THE	OUTEL CASID PROTED VA	HUMAN HOTAYILUS (STRAZIN KU)	ĩ	23:18	335.366	129.678		l T		T
1	OUTER CAND PROTEIN VIA		l	279.306	Т		1	+		Ţ
TAN MOUNT	COLEK CANDING FINANCE	HUMAN ROTAVILUS (SEROTYPE I / STRAIN MIT)	Γ	372-610				-		T
١	COTEN CASIO PROTEIN VA	HUMAN ROTAVIRUS (SEROTYPE 3 / STRAIN MONI)	<u>≅</u>	573-628				-	1	1
1	OUTER CAPSID PROTEIN VP	HUMAN ROTAVIRUS (SEROTYPE) / STRAIN P)	1	577.431			<u> </u>		-	:
ŀ	OUTER CAPSID PROTEIN VP	HUMAN BOTAVIAIS (SEROTYPE 3 / STRAIN RRV)	1	105.114	1			+		
PWN ROTH	OUTER CAPSID PROTEDI VPA	HUMAN ROTAVISUS (SEROTYPE 4/8TILAIN ST. THOMAS 3)				1	$\frac{1}{1}$			
١	OUTER CAPIED PROTEIN VIN	HULLAN ROTAVIALIS (SEROTYPE 4/ STRAIN VA 70)	1	78.104	6198	\dagger	1	1	1	
PVP4 ROTHW	OUTER CAPSED PROTEIN VPM	HUMAN ROTAVIAUS (SELOTYPE 1/ STRAIN WA)	1	17.631		\dagger	1	1		
ı	OUTER CAPSID PROTEIN VP	PORCHAE ROTAVRUS (SUROTYPE 37 STRAIN OSU)	13.44	16771		\dagger	1	+		
PWN AGTAC	OUTEA CAPSID PROTEIN VIN	PORCEME ROTA VIRUS (GREAUP C./ STRAIN COWDEN)	Т		301.130	\dagger	1	$\frac{1}{1}$		1
	OUTER CAPSID PROTEIN VPA	POLICINE ROTA VIRUS (STRAIN COTTFILED)	Τ	18743		t	+]	1
١	OUTER CAPED PROTEIN VP	POACING ROTAVIRUS (STRADA YNS)	ŀ	Т	16770	1	1	1		7
1	OUTER CANSID PROTEIN VPA	INESUS ROTAVIAIS	Γ	Т		1				1
AL ROLL	OUTER CAPID PROTEIN VIN	SENDAN 11 ROTAVIAUS (STIAJN SAIL-FEA)	Γ	72		\dagger	1			
ı	OUTER CAPSID PROTEIN VPN	ISDACAM II ROTAVIRUS (STRAIN SAIL-SEM)	Ī	T	14.633	\dagger	+	+		
1	HONSTRUCTURAL PROTEIN PASA	WOUND TURKOR YALUS	3	Т		\dagger	1		1	I
1	NOTES CASE PROTEIN VIS	AFTECAN HORSE SICKNESS VIRUS (SEROTYPE 47 STRAIN VACCINE)		31.216	T		l			T
SIATE CAA	COLEA CAND PROTEIN VIS	ELLETOWOUR VIRUS (SEROTYPE 1871SOLATE USA)		98-126	T		-			T
ı	COTHE CARETO PROTEIN OR	BLUE UNGUL VINO (SEROTYPE II / ISOLATE USA)	П	92-126						T
PVPS BTVIA	OUTER CAPSID PROTEIN VPS	BUTSTOACH VALLE (SAND) THE 13 TRAINE USA)	2							Γ
ı	OUTER CASED PROTEIN VPS		T	7				Н		
	OUTER CAPSID PROTEIN VPS	BLUETOWOUR VALUE (SENOTYPE 27/SOLATE (15.4)	T	921.28	2		-			
ı	OUTER CAMED PROTEIN VPS		T		,,,,	1	+			
١	OUTER COAT PROTEIN PS		19			1		1		
f	VN PROTEDI	PE 10/150LATE USA)	101:101	I	T	1	1			1
PVPS: LOUV	PROB NOVSTRUCT 41.6 KD PRO	MALKE ROUGH DWALV VIRUS	153-202			f	1			T
1	IN TACTOR	OSIS VIRUS	5.6			-	-			T
T	VA PROJEM		137-119	Ī	T	-	1	\downarrow	1	T
T		UND THE PROPERTY AND THE PROPERTY VIEWS	12:45					-		T
PWK BTVII			=							T
	VIN PROTEDI	BLUETOWOUS VINUS ISENOTYPE 137 ISON ATTENNA								
	VN PROTEIN	BULDETONGUE VINUS (SEROTYPE 17/1SOLATE USA)		1		1				
1	VP9 PROTEIN	BLUETONGLE VAUS (SENOTYPE I / ISOLATE SOUTH AFAICA)	191	Ì		+	+			
₹		BLUETOWOUR VIXUS (SEROTYPE 2/150LATE USA)	33.17	T	T	\mid	+	1		1
٦	STRUCTURAL PROTEIN PA	NCS DWALV YBUS	12	15.5	†	\dagger	+	+		T
T	ry Moteur	AUTOGRAPHA CALEGRINCA MUCLEAR POLYNEDROSIS VIRUS	\$ 140 140	Ī		+	1			I
2000	TRUBABLA MEMBRANE ANTIGEN 73	346	101-306	646.624	l	ŀ		-		T
T	WAS PAULED.	TRUS	П	70.397	r	ŀ	+	+	1	T
T	MONETH FILES BOTTON BACK	EVECUTION PERMONUNAGIC DISEASE VIRUS (SEROTYPE 1)	3			-	-	-		T
ı	CAPED MOTERN PER		7							
1	CAPSED PROTEIN 197		7	140-241						Ī
WH BIVIS	NONSTRUCTURAL PROTEIN PS	BELIEFONOUS VINCE SEROTYPE 1071601 ATRICAL								Γ
l	EN VIN PLECURSOR		271-6		1	\exists				Γ
l		,		1	1	1	$\frac{1}{1}$			

CCPHE THOUSE		(A Verson (as becarrisghager) VIIII VIIII TANCO VIIII			ARCAL	AREA	ARTEL	AREAS AREAS AREAS
	N PAGE	DOS DWAAF VISUS	191424		T	T	Ī	+
	STAUCTURAL PROTEST PS	WOLFD TURION VIRUS	22.19			П	П	H
ALL PART CASE	N PAT ANGROUP TO SEASON AS ANGRESS ANGRESS AND SEASON AS	STRUCTURAL PROTEIN P	186-32				T	+
	VIETONG PROTECTION TYPICALLY TO COLUMN	ORGYTA PEEUDOTSUBATA MULTICAPSID POLYHEDROSIS VIKUS	200	234-60	T	T	T	+
	BYZIONOGRA	MOUSE ADENOVINUS THEY VIEWS TYPE I (ARVISE) ISOLATE		1	1			\dashv
	APO PROTEIN	INDIAN BANGACOEFICIENCY VIRUS TYPE I (III IIO AMD IIXII) ISOLATIS)	111		i			H
AN HAIR	NR109A DA	HIDAAH BAAUNOORI KIENCY VIRUS TYPE I (BIII ISOLATE)	Ĭ	T	1	T	T	t
	AND PROTEIN	MUNITURE BEACH-CONTROLLED CONTROLLED		T	1	1	1	t
	AMANOMEN	HOWAN DOMESTICKENCY VINUS TYPE (COC-631 ISOLATE)	ij					Н
	APO METON OAA	HIDALAN DOMINOCEFICIENCY VIRUS TYPE I (EL TISOLATE)	£33					Н
	J PROJECT	HADAJA BARDHOOFFICIENCY VIRUS TYPE I (IXXX ISOLATE)	3.4					-
	ALC LYOURN	HUKAN BARINGGENCIENCY YIRUS TYPE I (INI ISOLATE)	2.29					+
	ALO LOCATION	HUMAN BANDHOORFICURICY VIRUS TYPE I (INCSF ISOLATE)	22-49			T		H
1	AND MOUNT	HUNGAN BANDNOSEFICIENCY VIAUS TYPE I (MAL ISOLATE)	3.32	Ī		İ	T	+
WIND WA	WU PLOTEIN	HUMAN MANORING AND A STANK AND STANK (1801 VIR.)	٤	T	1	T		+
1	VPU PAGISIN	HUMAN BARDNOOTSKEENCY VIRUS TYPE I (PVZ2 ISOLATE)	Ĭ	Ť			1	+
HV181	VYU PROTEIN	HUMAN BANDNOORFICIENCY VIRUS TYPE I (SF 162 ISOLATE)		1	1	1	1	+
٦	AND MICHELL	CHARACTE PONDAMENTAL ELEVATION OF THE	Ē	1				Н
AN YAN	ALY LONG TO A LAND A LA	SUMP BUILD ATTIVE	1051-107			Ī		+
1	NE PLOTEN	BOYEM NOTAVBUS (OROUP C / STRAIN SHINTOKU)	Ē	T	1	T	t	+
1	AM LEGITOR	ROTA VOLUS (GROUP II / STRAIN ADRV)		1		T	1	+
Ц	WHO PROTEIN	ROTAVILUS (CROUP II / STRAIN IDUR)		T	1	1	1	+
	VIN PROTECT	HUMAN ROTA VIBITA (28 XIV C / STRAIN COWDEN)	Ī					H
ľ	AND MANAGEMENT AND	(P-NX NEVELS) SIDERA VEOL	229	H		H		H
Wild Market	HOMETIMAL PROTECT NEVEL	BOYNU 107KYBUS (STRAN UK)	91-16	32.2	t	T	t	+
	NONETHINGTOWN PROTECTION NO. 177	PORCONG NOTAVIAUS (SEROTYPE S / STRAJN OSU)		101-10		T		+
Ц	HONSTRUCTURAL PROTECT MCV73	SOMEON IN THE PROPERTY OF THE ADMINISTRATION OF THE PROPERTY OF THE ADMINISTRATION OF TH	2					Н
	MONITORINAL PROTECTIONS OF THE	(II NOTAVIJUS (STRADA SAII)	164-301	217-251				H
Tribu Misi	A COMPONENT AND	BOVING ROTAVINUS (SENOTYPE 6/8TRAIN B641)	2.3	T		T	T	1
1	OLYCOPICOTION VP1	BOWING ROTAYOUS (STIMIN AS)	1	T	1	T		+
	OLYCOPIOTEDI VIII	BOYING NOTAYOUS (STRAIN UK)		1	1	1	1	+
MOTO	OLYCOPIO THE OTHER OFFICE OF THE OTHER OFFICE OF THE OTHER O	HIDAAN ROTAYDUB (SEROTYPE 4/STRAIN RV-1)	2.39					Н
TO POLICE COLVA	OLYCOPIOTED ALL	HUMAN ROTAVISUS (SEROTYPE 2 / STRAIN HUS)	2-29	H		T		╀
	OL YCOPILOTEDY VP1	HUMAN KOTA VIRUS (SEROTYPE O / STRAIN BJ7)	i i	t	t	T	t	+
	OLYCONIOTED YET	HUMAN BOTAYONUS (SEROTYPE 2 / STRAIN USI)		t	1	Ì	1	+
	PCOPILOTEDI VP1	HUMAN ROTAYEAU (REPORTED 1 1975 AN MIT)	al:	1		1	1	+
	GLYCOPILOTEDI V77	TOTAL AND A VINCE STREET AND AND STRAIN DI	3	1	1	1		4
Ĭ	OLYCOPION ATT	MANAY BOTAVIAUS (SEROTYPE) / STRAIN P)	ž	1	1			Н
L	OL YCOPROTEDI VY7	MANAY BOLY AND (SEBOLADE 1/21/17/17/17)	2	1				Н
PYSON MOTHS CI	CLYCOPROTEDI VP7	MAJAN BOTAVILLE (SEAOTYPE / 17.AAN WA)	ä		į.			4
	OL TOPROTEIN VET	PORCING ROTAVILLES (SERIOTYTE) / STRAIN AT/76)	ž	1			H	Н
L	OLYCOPKULBIN VYY	POLICINA BOTAVIAUS (SELOTITES) / STAAN CAW-1)	2-29					H
L	CLYCOLNOISTA ALL	SALAH II KOTAYOUS (STUARI SAII)	ä					
L	A AMERICAN CONTRACTOR OF THE PROPERTY OF THE P	HOYDER ROTAVISLIS (CHOUP C / STRAIN SHINTOKU)	125-152	H				
PASIO NOTAS	THE COURT OF STATE OF	PSISSEM ILLIOTA VICUS (SIDAM SALI)	113-146					ŀ
L	CAN DESTRUCTION CONTRACTOR	ANNIA CATALO PROTEIN BOYDIS NOTAYOUS (STILAN UK)	5	114-145		f		1
TOTAL DESCRIPTION OF THE PERSO	MULDING CYMPO MOLEDI	POWER BOLYADERS (SLEWA NOVI)	Ę	114-145	t			ŀ
_	MUNICIPALITY CALLS CANCELLE	ALL THE STATE OF T	04-10	1	-		8	

MCCENE	10711761	All Virgos (se barteriesh ers)								-	Γ
THENAME	PROTEIN	VIRIL	H	IJ	AREAZ	AKZA	AKEA S	AREAS	AREA 7 AKE	AKEA! AR	AREAS
PUELL BREECH		HUMAN ROTAVIRUS (SEROTYPE 27 STRAIN RV.5)	2	<u> </u>							
200	MANUAL CASE PROTEIN	HUMAN BOTAVILLE (PEKOTYPE 1/STRAIN DS!)	<u> </u>	11:13							
TOTAL STATE	MINOR OUTER CAND PROTEIN	HUMAN ROTAVIRUS (SEROTYPE 1/STRAIN WA)	111-145							\vdash	Γ
Y	MINOR OUTER CAPITO PROTEIN	KABBIT ROTAVIRUS (STRAIN ALABANA)	11:13							 -	Γ
ISION INC.	MINOR CUTER CATSID PROTEIN	SMIAN II ROTAVIRUS (STRAIN SAII).	111.146							_	
A MOROL	SALL HYDROPHOBIC PROTEIN	MADACH WALLS	ž						-	ŀ	ļ
- 1	SAALL HYDROPHOBIC PROTEIN	MCMO'S VIRUS (STRAIN MATSUYAMA)	13-41							-	
1	SALL HYDROPHOSIC PROTEIN	MCIACYS VIRLUS (STRAIN) BELFAST)	7						-	┞	Γ
	SMALL HYDROPHOBIC PROTEIN	MANGES VIBLIS (STRAIN ENDERS)	***							H	Γ
- 1	SHALL, HYDROPHOBIC PROTECT	MUSING VIRUS (STRAIN BEAYLALYNN)	99,			Ŀ				-	
	SMALL HYDROMIOBIC PROTEIN	MUM-5 VRUS (STRAIN KILIAM)	g				ļ				_
	SAAALL HYDACOPHOBIC PROTEIN	MUNICE VIRLE (STRAIN BRISTOL !)	į	I					1	$\frac{1}{1}$	Ī
L	SHALL HYDROPHOBIC PROTEIN	IMUNOS VIRLIS (STRAIN MOYAHARA VACCINE)		I					1	1	T
ı	SALAL HYDROPHOBIC PROTEIN	MUMPS VILLE AFTERDO INV		T						+	T
Ł	SAALL HYDROPHOBIC PROTEIN	MARAPE VILLE ACTE AND DE VACCING A LOS								1	1
ı	SIGMA I PROTEIN PRECIESOR	BEOVER REPORT A CHEAN THE AND THE AND THE	1		Ţ					-	1
PVSII RROVI		PROCESS TO STATE S	Ī		2					_	
Men acou		SECTION (11 TE 47 STRAIN DOVONES)	_	2							
TOTAL MEDIA	SAME I TROIEM TRELUKBUR	REDVIAUS (TYPE 1/ STILAM LANG)		15-104	113-160				ŀ	l	
TYPE MEDING	NORA I PROTEIN	REOVINUS (TYPE 3 / STRAIN DEALING)	150-324						-	ŀ	Ι
**************************************	SIGNA J PROTESIA	REOVINUS (TYPE 1/ STRAIN DAYONES)	289-316					Ŀ		\vdash	ľ
TAILS MEDVD	HOMA IN PROTEIN	REOVINUS (TYPE) / STRAIN DEALING)	6	Γ						+	Ī
PVSIS REDM.	SIGMA 1-5 PROTEIN	REOVINUS (TYPE I / STILAIN LANG)	30.77				,		-		T
PYTIA CAPVI	PROTEIN TA	CAPLIFOXVIALE (STRAIN INE.)	134-151	İ					-	1	!
PVTS_SPVKA	PROTEIN TS	SHOPE PIBROMA VIRUS (STRAIN KASZA)	110 000	T						1	Ì
WISK LBV	PROBABLE DNA PACKAGING PROTEIN	EPSTEIN-BALL VIRUS (STRATN BOS.E)	500, 716	I						1	I
ž	PROBABLE DNA PACKAGING PROTEIN	HIDRAN CYTOMEGAL OVIETS ISTRAIN ABILDS								1	į
FVPER TIBUM	PROBABLE DRA PACKAGING PROTEIN	HINEPOS STAMPLES VIETE STVPH A FET BAIN THE AND A LINE.			:	:				•	_
PYTER H3VII	PROBABLE DNA PACKACING PROTEIN	ICTALIBED MEDPECYBLIST								-	1
PVTEK VZVB	PROBABLE DNA PACKAGING PROTEIN	VARICHTA-20STER VIRUS (STRAIN DIDIAS)	1	I					1	+	T
VIVI ITVIV	VIRAL PROTEIN THE	THER INCOME OF THE YEAR YOURS I SET AND VITE	2	Ī						-	1
PVTPX TTVI	VICAL PROTEIN TPX	THE BLOPE OF TENAX VIRIS : (STRAIN KRAI)	2 4								Ī
WY PART	VMOTEN	HOMEN BARABUT LIFTON AL VIRILE PETRAIN POSITION	8							-	-
l	HYPOTHETICAL 10 1 KD PROTEIN	SUFFICEUS VINUS. LIKE PARTICLE SCVI						j		1	i
L	HYPOTHETYCAL 16.8 KD PROTEIN	SULFOLOBUS VIRUS-LIKE PARTICLE SSVI			1			Ì		1	Ī
		SULFOCORUS VIRIAS, INCR PARTICIF COVI	,								Ī
Ł	HYPOTHETICAL II 2 KD PROTEIN	TOBACCO YELLOW DWARF VIRUS (STRAIN AUSTRALIA)		T					$\frac{1}{1}$	+	1
PYIJK NEVAC	HYPOTH 13,1 KD IN 39 KD STEGION	AUTOCIAPHA CALIBORNICA NACTUAR POLIVIEDADALI VIRITE		T			\int			+	1
PY13K SSVI		SUBSCHOOLS VIRUS, ITE PARTICLE SEVI		1						1	1
PYICK LIVI		SULFCLOBUS VINUE LIKE PARTICLE SSVI		T	T				+	1	Ī
PYIGK MPVAC	HYPOTH IN 39 KD PADTEIN STEDION	AUTOCALMY CALIFORNICA NUCLEAR POLYNEDROSIS VIRIS	191.00	Ī	T					-	1
PYICK 15VI	HYPOTHETICAL 15.6 KD PROTEDA	SULFOLDBUS WAUS LIKE PARTICLE SSVI		Ī	J					-	1
PYIN SIVI	HYPOTHETICAL 17.8 KD PROTEIN	SULPOLOSUS VIXUS LINE PARTICLE 33VI	T	5	T						1
PYIGK MSVN	•	MALZE STREAK VIRUS (MICERIAN ISOLATE)	I		T					+	1
PYIR MSVS	INTOTHERICAL 113 KD PROTEIN	MAJZE STREAK VIRUS (SOUTH-AFRICAN ISOLATE)	3	Ī						1	1
PYZOK LIVI	HYPOTHETICAL 38.4 KD PROTECN	SULFOLCOUS VINUS-LINE PARTICLE SSVI	1 P	1					1	1	-
PY14K SIVI	HYPOTHETICAL 24.5 KD PROTEIN	SULFOLOBUS VRUSLING PARTICLE SSVI	1	T						-	1
772 SOON		MOYBEAN CALCACTIC MOTTLE VOLUS		T	Ī						
PYDIK BIVI	INTOTALTICAL 31.3 KD PROTEDY	VI.		T					1	-	7
PTUK KIVI	12									$\frac{1}{1}$	1
PYLIK NOVAC		N VARDED SECTION IN									٦
PYS SOCIAL	. ~	MOVIECAN CIC OROTIC MOTITIE VIRUS	9	T	Ţ		1	1	-	+	
VACOOS 171			A 1777	1	T			1		H	
WHITE LEVI		(V)	1	Ŧ							
V 100 14	INVESTIGATION A		_	Ę	92:30					H	Π
×	HYPOTHETICAL BANGEOUF PROTEIN		Ţ	т						H	П
	HYPOTHETICAL BANGE ORPS PROTEDY	FOWLOX VILLE RICK THE 18-ASSISTANCED	B) -57	132-179	14.21			1	$\ $	Н	Π
PYBIO FOUPM	HYPOTHETICAL BANGE CHUTO PROTEIN		2	100,000	T	Ī	1	1	$\frac{1}{1}$	+	П
					1		1	1		+	٦
										ļ	ĺ

ANG VAC				WAS AVE	DOON HYANG	PANA AVCC	PYN TUTT	PULL POLLS		No.	DAYS CAME	DANSH LINE	ACTIVE COAL	MAN TOWN	TWAM HOUSE	777	NA AV COLLA			100						No.	1	100	TOTAL PROPERTY					LIPTO CITE	777.	1100	71700					TV.	II.	EAST NEWS	AMO DEM	MAMO! CIECA	PLANDS EIRLS	DIVITION	KCENE
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TABLE VII

107 X 178 X 4 SEARCH MOTIF RESULTS SUMMARY

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TABLE VIII

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A CONTRACTOR	IN VACUAL PROTECT	BACILLIS THURINGIENSIS	111-231	154.)14	101.721	775-602						
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E I	CHAIRM CHASTAL PROTECH	BACELUS THURINGENSIS	116-772	866.00)	2 2						1	
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10 P	PLABILE ENTEROTOXIN IL CITATIN PRECTIRSON	CLUSI RIDIUM TEATRIFICA CO.		-	İ						
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(3Y) 71030	HYPOTHETICAL MOTERN IN EPIA STREETIN		1								١
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PETCI STAN		TRANSPORTER ATTRICTED		155-206							
DAAR CO	TEXTELLIBRIES THE C. ! PRECURSOR	SIAMILLOCULOS ACRECIO	T	10.7							
		STAPPILLOCOCCUS AUPLEUS	T								
	THE PROPERTY OF THE PROPERTY OF	STAPHYLOCOCCUS AUREUS	7		1						
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	ACCUPATION OF A SAME PROPERTY AND RACE	ESCHENICHIA COLI	٦	╗		Т					
100 A	PUINITE INCHES INCHES	SENTENCIAL COLI	_	249.276	4)1-4X	526-151	× 1.4.2				
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	SUCCEDENT	ETHERTOCOPOLIS PARTIMONIAE	211-254								
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TOTE SQV	FATTY OXIDATION COMPLEX ALTHA SUBURIL	ESCALATION COST	130,363								
1	INTELLIFICATION THANKSPORT PROTEIN PRECURSOR	ESCRETARA COLI	T.		101.441						L
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FAOR PSETA	FATTY OXDATION COMPLEX AND SECTION OF	WAY DOLL A SUCCINOCENES	16-14								1
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SPENS SCOLL	FONALTE DESTEDA OCENASE	BUREALINACIO	Т	101.44				L	L		
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	т	ESCIENCIA COLI	-							L	L
		ESCHENICHTA COLI	331-361					1			l
16CA 500L		PECHERICIGA COLL	116-217								1
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15K E8	FERRIC ENTEROBACTON TRANSPORT PROTEIN FENCESCHERICHIA COLI	ESCHERICHIA COLI						,		
PFEPE ECOLI	FEALC ENTEROBACTIN PRANSPORT PROTEIN FEPE	ESCHENCHIA COL!	113-234	281-306						
PEN ECOL	<u>Peralc enterogactin transport protein percescheuchia col</u>	ESCHENICHIA COLI	131-155							
PFERK ANASP	FEATEDOXIN, HETEROCYST	ANABAENA SP	67-7							
PFELLY ANASP	FERTLEDOXIN-LIKE PROTEIN IN NIF REGION	ANABAENA SP 1	स ंद							Γ
PHAS BORDE	FILAMENTOUS HEMAGOLLITINEN	BORDETELLA PER TUSSIS	1121-1156 1359-1386	1359-1386	2063-2114 2841-2868		1051-1065 3167-3194			
PHAC BOLD	MAEMOLYSINLIKE PROTEIN FHAC PRECURSOR	BOADETELLA PERTUSSIS	343-369				10.			
TIC CO.	FORMATE HYDROGENE YASE TRANSACTIVATOR	ESCIERICHIA COLI	36-63	350-314	401-428					!
PFHUA ECOLI	FERUCHTOME-INDM RECEPTOR PRECURSOR	ESCHERICHIA COLI	431.485							Γ
PHUB ECOLI	PROTEIN FHUB PRECURSOR	ESCHENICHIA COLI	227.254			-				
PFINA ECOLI	OUTER-MEMBRANE RECEPTOR	ESCHERICHIA COLI	\$19-614							
PFIB SPICE	FIBRIL PROTEIN	SPIROPLASMA CITIU	161-195	136-367						
PFIC ECOL		ESCHERICIUA COLI	131.13							
PFIC SALTY		SALMONELLA TYPHINNUNI	181-138							
PINC BOLLE		BONDETELLA PERTUSSIS	\$68-308	140-563	616-445					
PFINC ECOL		ESCHENCIHA COLI				-			Ī	
MAD ECOL	FIND PROTEON PRECURSOR			11-111	534-361	\$63.590				
100	TYPE I FINDRIAD REGULATORY PROTEIN FINE		165.192							
PIDAY SALTY	FINERIAE Y PROTEIN	SALMONELLA TYPHINURIUM	14.76					_		
PIDAZ ECOLI	FINGRIAE Z PROTEIN	ESCHENCHA COL	43-64	162-192	196-230					
PERC SALT.	FINDRIAE & PROTEIN	SALMONELLA TYPHIROURICKI	175-209							
Provo Ecou	PING PROTEIN	ESCHENORIA COLI	14171			-				
PERIA RICH	FIRA PROTEIN	NCKETTSIA NCKETTSII	162-189							
HIXC AZOCA		AZORHIZOBIUM CAULINOBANS	179.156			L				ľ
HIXT ASOCA	SENSOR PROTEIN FIXE		247.274							Ī
PEIXE, BRAIA	SENSOR PROTEIN FIXE.	BRADYIMIZOBIUM JAPONICUNI	×	253.280			-			Ī
PICAL BONDO	PLAGELLAR FILANENT 41 KD CORE PROTEIN	BONNELIA BURCDONFEN	5.3	271-298						T
PELA! HALHA	PLAI HALHA BLAGELLIN AI PRECUNSOR	HALOBACTERUDA HALOBUTH	5-6	19 184			L			Ī
PILA! METWO	PLACELLIN BI PRECURSOR		£.3	3).160		-				
PILLY METYO	PLACELLIN BY PRECURSOR	METHANOCOCCUS VOLTAE	38-66			-				
PELM MUSA	PFLAJ NALJNA FLAGELLIM BI PRECURSON	HALOBACTERUM HALOBIUNI	36-63							
35	FLAGELLIN BY PRECURSOR	METHANDCOCCUS VOLTAE	15-16							Γ
4 X	FLAGELLM BY PRECURSOR	HALDBACTERUDA HALOBIUNI	36.90	133.184						
ALAN ALAN	FLAS HALHA FLAGGLEN BY PRECURSOR	HALOBACTEMUN HALOBIUNI	16-63	156-181						
PFLAS BACSU	FLAS BACSU FLAA LOCUS 22.9 KD PROTEIN		13.149	131-186						
2	FLAGELINA		<u> </u>	14.191	497-535					
3	TAN CAND PLANELIN A	CAMP TLOBACTER JEJUNI	8	10.37	Š					_
2	PLACELLIN A PRECURSOR		1				-			
	A LOCAL DA				× 1.1.2	1				
1710		714		771-70)	2	+	+			
PRIAT AND	FLACELLAR FOLANCINT PROTECH PRECURSOR	TREPONEMA MYCOYSENTERIAS		310.384	Ī	1			1	T
PILAA TAEPA	PLACELLAR PILANENT CUTER LAYER PROTEIN	TIEFONGMA PALLIBUM	0.1.5		T	+				I
PIT AS CAMES	PLACE LINE	CAMONIOSACTER COLL	Т	107.4116	Ī	1				T
11/15 CAUS.	FLACELLOVB	CAMPYLOBACTER PERINI	Т	1111	500-5110	\dagger	-			T
PILAB NOG	FLAGELLIN	NAZOBRUM MELLLOTI	=	117.310	1	160-101	1			Ī
PFLAV CLONG		CLOSTRUDIÚM MP	2		+			Ţ		1
PILAY CAUCK		SCENTUS	=	21:538	Ī				1	T
PFLA BACSU				128-255			-		T	Γ
PFLOO BACSU	FLAGELLAR BASAL-BOOY ROD PROTEIN FLOG	BACELUS SUBTELS	63:49				_			I
PRIOK SALTY	FLAGELLAR HOOK-ASSOCIATED PROTEIN I	INDUN	П	133.360	456-540					
EOC.	FLACELLAR MOOK-ASSOCIATED PROTEIN 3		\Box	997-627		H				
ALC: SALIT	PLACELLAR HOX-ASSOLIATED PROTEIN J	SALMONELLA ITPI WAUSIUM	Ţ	92.4.		1				
THE PERSON	PELIA PSEAE FLAGELLAR OPERON RNA POL SIGMA FACTOR	PSEUDOMONA'S AFRICANOSA	196.313	T	1	+	$\frac{1}{1}$		1	T
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		ORCANISM		1	Т	1	_				۱
L	N 1937 19		۲	T	Τ						
	71 187 18	SALMONELLA CHOLERAE-SUIS		Ī	Т	211.111	395,300	107.			
	The state of the s	SAL MONELL A MUENCIEN	ž	7	٦	Т	T				
	LAGELLIN	CAT MONET LA PARATYPHI-A	175		3					I	
	FLACELLIN	A LICENSEE A RESPECTAN	7		36-14					Ī	Ì
K JALRU	FLACELLIN	TO THE PERSON OF	Ī	36-135			7				
K SALTY	NTRONI	ALEGERIA LITERITORIO	I	Γ	\$5.49	103.130	137-164	215-321			
PRI IC SERVA	FLOSTIN	SEULATIA MANUELLING	17.		11191	16.791	386-445				
-	FLACETIAL HOOK-ASSOCIATED PROTEIN 2	SCHEMICHAN COLL			Т	167.00					
	EL AMEST AS LANCE ASSOCIATED PROTEIN 2	SALMONELLA TYPHINDULINI	822		Т						
1 TV 0 TV	TANGETON TOOK TOOK BE OF IT	BACHLUS SUBTILIS	-3		1					Ī	
_	LAG HOCK-BASAL BOOT TRO-EM CEST	P. A. P. C. 1 14 C. 18 T. 1. 15	135.361	= 7							١
~	PLACELLAR M.RING PROTEIN	BACKLES SOUTHER PROPERTY	34.51	197.124	361.368						
PEL CAUCK	FLACELLAR MAING PROTEIN										
+	STATES AND AND PROTEIN	HINDRIGH	.75	Ī							
7	LAUGHTAN MACING TO THE PARTY OF THE	PACIFILIS SUBTICIS	Ĭ								١
PILIO BACSU	FLAGELLAR SWITCH PROTEIN FLAG	CONTRACTOR CONT	2	ŀ							
1	FLACELLAL SWITCH PROTEIN FLIG	Bachadonin	١		ĺ			_			
•	PROPARIT REIN PROTEIN	BACILLUS SUITICIS	2								
2	CALLES IN CONTRACTOR	BACILLUS SUBTILIS	1.57								
	LAUGLIAN THI PROTEIN	TAT SAMELL A TYPHINITRIUM	35.410				:	:	:	:	:
HI WIT	FLAGOLLAR PLU PROTEIN	14 - 74 T 17 61 61 Pt 14	20.00	1							1
PFLIX BACSU	PROMABLE FLIK PROTEIN		16.0	30-105	109-136	L					
II BACSU	FLIL PROTEIN	BACRETOS SUBTILIS						L	L		
7	FILL MOTEIN	ESCHENICKIA COLI									
Ŧ	Ct is Becare	SALMONELLA TYPHIMURIUM	101								L
т	P. L. P. P. C.	BACH US SUBTILLS	146-173								
J	FLIM PROTEIN	Proceedings Out	251-278								
FI BY ECOL	FLIN PROTEIN	EX REACTIN COL							<u>.</u>		
	SI ACELLAS MOTOR SWITCH PROTEIN	CAULOBACTER CRESCENTUS							L		L
	EL LOS: 1 AR PROTEIN PLIS	ESCHENICHIA COLL	2								
2	TACAS AND	SALMONELLA TYPHIMURIUM	9.46	8							
LIT SALTY	FLAGELLAL PROTEIN PLIT	BEETITOAADMAS AFRUGINOSA	(\$-00	10-11							
MII PSEAB	DOMINE PROTEIN PRELUASUR	Percentage Chi I	35.5								
DOG VIN	TYPE. I FEMBLAL PROTEIN, A CHAIN PRECURSOR	ESCHEDISTRA COL	1	L							
PHIC ECOL	TYPE I FINDALAL PROTEIN, C CHAIN PLECURSON	ESCHENCIA COLL	341.312	152.379	19-444						
MI ACIVI	PRESENT SUBURIT TYPE I PRECUISOR	ALIMORITES VINCOSOS	17.7				L				
10/1	FRANKLAL PROTEIN 9177 PAECINSOR	ESOGNOMA COLI							L	L	L
	TATAL BACKET PROTEIN PRECURSOR	SACTEROLDES MODOSUS				1					L
	THE PERSON AND PORT OF STREET	BACTEROIDES NODOSUS	107-174								
WY BACK	PURILAL PROJECT PACKS WITH	MACTER OIDES MODOSUS	107-134								l
MAZ BACHO	PIALL BACHO FEDGRILAL PROTEIN PRECUEDUR	A Presonne MODOSIV	100						1		1
TAN BACK	THAT BACKO FENDRIAL PROTECT PRECUISOR		131.169			L	L				
VAA BAOK	PINGELL PROTEIN PRECURSOR	BACTEROIDES POUGSUS								L	L
	TENCHALA MOTEIN PRECUSOR	BACTEROLDES MODOSUS							ļ		L
	PERSONAL SECTION SERVINGS	IBACTEROIDES MODOSUS	32-123						-		
MAH MACK	I PAGE AND FROM CONTRACTOR	PRACTEROIDES NODOSUS	1111-145								1
DAM BACHO	PRIMI BACHO PROBLAL PROTEIN PRECINCIA	NACTE CODES NODOSUS	100	L	Ц						1
PACA BACK	FOR LAL PROTEIN PRECURENT	TATEL PRODUCTION OF A COLUCTANOSA	18.63	L			_				
HICH PANE	FEMILIAL PROTEIN PRECUASOR	Paulumenta Achiomosa	77 74	11111				L	L	L	L
SAME BACKET	SPOSTION R FORBILL ASSEMBLY PROTEDY FOOD	BACTEROLDES MODUSUS								L	L
	PERSON REPORTAL ASSEMBLY PROTEIN FOWD	BACTEROIDES MODOSUS	3					ļ		L	L
To the second	PATER AND IN PROTECT PRICE MADE	BICHERICIAN COLI					1		1	ļ	ļ
	THE PERSON NAMED IN COLUMN NAM	NEISSEALA MENTACITIDIS	10-03					-		1	1
PALI NEDO	I DURING THE PROPERTY OF THE PA	MERKSTRIA CONCILINOEAE	66-99			_					1
Photo Mildo	FEMILIAL PROTEIN MECURSON	LONG A VET 1 A LUTAGE BOTTE BACTIFIES	95.146		L		L				
PLAN MORNE	FEMILIAL PROTEIN PRECURSOR	MUNICIPAL STREET	10.61	101	L		L	L	L		
PICO PSEAB	FEGINAL PROTEIN PRECURSOR	PSEUDUROPAS AERUGINOSA	5		-		L		L	_	L
ALC: NAME		PSEUDOMONAS AERUGIMUSA			1	-		1	L		
1000	-	ESCHENCHA COLI				1	-	-			L
THOUSE CONTRACT		ESCHEDICHIA COLI			1	1	1	-			ļ
TO THE PARTY		HAEMOPHELUS INFLUENZAE	2			37		117.177	37.3%		
112 100	FIREDAKETIN BINDING PROTEIN PRECURSOR	STAMPLOCOCCUS AUREUS	2		ĝ	Т	т	Т	т	\downarrow	l
THE VENT	EN WIND VOLUMANATE SYNTHASE	ESCHENICHA COLI				1	4	1	-		ļ
		LACTOBACELUS CASE	<u> </u>	_	_	_					
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PCGENE	163:170.4										
TILE NAME	PROTEIN	т	1			П	г				
PFADA ECOLI		ESCHERIORIA CHE I	4	3	7438	SEC	7717	AREA & SAREA ?	П	AKEAI	ARCAS
PENDA WOLSU		1	Т	1					j		
PFRZE MYXXA	GLEDING MOTILITY REGULATORY PROTEIN	MYXOCOCUS XANTHUS	T.								
PFTMS CLOTH	FORMATE-TETRAHYDROFOLATE LIGASE	CLOSTEIDITE THE SUCKESSION	7	Q.							
	FORMYL TRANSFERASE	ALTOTOPOPULIC	2								
PFTSA BACSU			î	1	7						
PITEN ECOL	CELL DIVISION PROTEIN PTSA		Τ.								
200	CELL DIVISION PROTEIN FTS		7								
	CELL DIVISION PROTEIN FISE.				1					-	
	CELL DIVISION PROTEIN FISH				7						
PFTSX_ECOL	CELL DIVISION PROTEIN FTSX		=							l	
PFTSY ECOL	CRIL DIVISION PROTEIN FIRM		271-305							İ	T
PEUCH BOOL	L-PUCOSR OPERON A PTIVA TOR		236-360							T	Ī
PFUNA BACK	FINARATE INVESTIGE CLASS 1		245			Ī	T				
	FINANCIA INTURA I ASE CLASS I, AEROBIC	HERMOPHILUS	15.05		I	Ī	T				
	FUNCTION OF THE STATE OF THE ST		10.15	Ī	T	Ì				j	
Ŧ	FEMAL OF I AKE REGULATION PROTEIN		÷	:	:			:	. :		_
302	GLTC 3-PHOS DEHYDROGENASE A		91.14								
		Bit is		1				,			
POIPS ANAVA	GLYC 3-PHOS DEHYDROGENASE 3			1							
POIN ECOU	OLYC 3-PHOS DEHYDROCENASE C		104-157	1						-	Γ
٦.	GLYC 3-PHOS DEHYDROGENASE		Ţ						•		T
POSE BACK				117.211							Ī
L	CLYC LPHOS DSWYDGOGENARE	BACKLEUS SUBIRLIS	49-76				Ī		İ	T	T
Т			259-236		Ī		T	Ī		t	Ī
Т			290.328			T	Ī			1	
1000		SHE	Г	241.268	Ì	T	T	Ī		1	1
NAME OF THE PERSON	ONE WALK OF TAXABLE PROPERTY IN THE STREET		30.38		T	Ì	Ì	Ī		1	
	CCCCASE-PROSPICATE I-DENYDROGENASE		100	Ì	T	1	1	Ī			
TO THE PARTY OF TH	CTANDS CONTROL PROTEIN	PSEUDOMONAS FLUORESCENS	12.705	1	T	1	1	1		1	
	MALMALI UNUMARI		1	T	T	1	1	1			
	CALLI-PROS UNIDITALITA CASTELLA SE		L	219-260	Ť	1	1				
	GAL-1-MGS UNIDIT. YL TRANSFERASE		7	1	T	1	1	T	1		7
	WALACT USE OPERON REPRESSOR		- E		T	Ť	1	1	1	1	
	UALACTOSE OPERON REPRESSOR		25.20	T	†	1			1		
7	DE D-GALACTOSE 1-DEHYDROGENASE	DORESCENS	251-278	T	1	1					
П	dir cyclorrokolasi il		39.103	T	T	T	1	1			
_	UIP CYCLOHYDIOLASE II	LEIOGNATHI	L	246-273		1	1	1	1		
	A CONTRACTOR SYSTEM H PROTEIN		Т	1	T	Ì			1		
	CL TCDG DEMYDROGENASE		92.31	T	\dagger	1	1		1		
100	WILLIAM ULLAYAGE SYSTEM TRANSACTIVATOR	ESCHENICHIA COLI	2 3	ł	T	1	1	1	1	1	1
	PROJECT AND		 	T	t	\dagger	1	1	1		7
-	APORT CENTRALION PROTEIN		100	115:216	330.384	1	1	1	1	1	
-	AND DESCRIPTION TRUITING PRECURSOR		L	т		T	†	1	1		7
-	JECHNINA PROJEIN GENE		940	t	T	t	T	1	1		1
_	ANIBACIEMAL PROTEIN 2		3		t	1	1	1			
_	ANIBACIBADA MOIEM J	ALEMOLYTICUS	23	t	t	t	1	1		1	Ì
_	OLUCIONE INPUBLIED DEVISION PROTEIN A		286.42	\dagger	T	T	t	1	1	1	
-	ACUCASE DAMBITED DIVISION PROTEIN A		533.566	t	T	T		1	1	1	
	LLUCUSE INSIGNED DEVISION PROTEIN A	γg	319.366	t	t	1	1	1			
	ULUCOSE IMILBITED DEVISION PROTEIN B		1976	1	1	1	1	1			
	OLUCOSE DOMBITED DIVISION PROTEIN B	VQI	25.55	Ì	1	1	1				
GCC SWW1	GLUCOSE TRANSPORT PROTEIN		211.322	\dagger	†	1	1	1			İ
_	GLYCEKOL DEHYDROGENASE	THE RANDPHELUS	E S		†	1	1	1			П
TOTA ECOL			285.20	\dagger	\dagger		†	1	1		
	GLIACUSE I PHOSPHATE ADENTLY, TRANSFERASE		1 2 2	\dagger	t	†	†	1	1		
777	CLUCUSE-1-PROSPHATE ADENT THANSFERASE	ואטעטאו	12.	1	t	\dagger	1	1	1	1	7
	TOURS ECOLO COLOR TWO DESTRUCTOR CONTROLLORS ELONG		200.30	t	\dagger	1	†	\dagger	1	1	7
MEN MEN IN	ACRECIONE TROITERS I	METHANOCOCCUS THEINHOLITHOTACHICUS 158	36-15	\dagger	t	\dagger	\dagger	1	1	1	1
					1	1	1	1	1	1	٦

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FILE NAME	PROTEIN		ARGAL	AKEAJ	AREAL	AREAG	ARGAS	1	7	1	4
PGLNA ANASP	P OLUTAMINE SYNTHETASE		10			1				1	1
PCLNA BACSU	U GLUTAMINE SYNTHETASE	BACILLUS SUBTILIS	1:3								
POLNA CLOAS	B JOLUTAKINE SYNTHETASE	TOBUTYLICUM	413-440						1		۱
POLNA ECOL	CLUTALONE SYNTHETASE	ESCHENCHA COLI	=				1		1		
PCLNA METVO	O GLUTALANE SYNTHETASE	METHANOCOCCUS VOLTAE	97.00			1	1	1	1		١
PG NA PROV	U GLUTAKIME SYMMETASE			Ī	Ī		Ī	1	1	Ī	١
NAME OF THE PARTY		PTROCOCUS FUNDAUS		Ì		Ì		1	Ì	Ī	۱
MAN WEN	CLUTAMINE SYNTHETASE		-	:	į	:	:	:	,		:
SULVA STRCO	GLUTAMINE SYNTHETASE	STREPTOMYCLS CORLICONOR	7					:	:		•
TOTAL PROPERTY.	A TRIPACOR ACCOUNT TACIBLY THE			1	T	Ì	T	T	Ì		l
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	LINE COCK BECOM A 100 V BEOTE IN F. I.		8.6		T	T	Ī		T	Ī	l
ייים פריי	THE TRINGS OF THE LANGEST AND THE		19.41	11.17	Ť	T	T	Ť	Ī	T	
	SALVO ELCA CON UNDITLE INVANTENASE		2		Ť	Ť	T	T	Ť	Ī	
TO SECURITY OF THE PERSON OF T	THOUSE IN THE AMERICA A PE	CATANGER A TITUTORIO	Ī	174.117	9	Ī	-	1			•
	CITTO A CAME BINDOWS BIOTEST BEEN INCOM		т	Т		Ì	Ī	Ť	Ī		
PCI NO LACK	CLITAMINE PERMITAGE OPERON PROTEIN GLNO	DIHERMIOPHILUS	÷		Ī	T	Ī	T	Ī	Ī	İ
POLYD BACK	POLYD BACEU IAEROBIC CLYC.1-HOS DEHYDROCENASE	BACELUS SUBTELIS	94.330		Ī	T		T	Ī		
Mache Itea	AEROBIC CLYC.) PHOS DEHYDROCENASE		410-437								
PCLIF EACSU	OLYCEROL UPTAKE PACILITATOR PROTEIN		235-274					Ī			
PCLPK BACSU	J CLYCEROL KINASE	BACALUS SUBTILIS	44.93								
POLPK SCOLL		ESCHENCHIA COLI	26.90								
PGLTA ECOLI	GLYCEROL 3 PHOSPHATE REGULON REPRESSOR	ESCHERICHIA COLI	2			1					
ZG X		ESCHENDRIA COLI	20.724								
See.	GLPX PROTEIN	SHIODLLA FLEXNERI	200		Ì	Ì			Ì		
PG ECO	CLUTARLDOXIN		2		Ì	Ī	Ī				
12 EX	GLUTAKATE SYMPKASE	ESCHEMONIA COLI	5	İ	1	1		1		1	1
1	PROJECT (ACTIONS IN STRUCK I PROJECT				1	Ì		1			
TOLY ELUI		The Action Control of the Control of		1	T	1			Ì	ŀ	
	R TORRING MYTHONY WAS THE ANGRES AN	CARPYI ORACTER ISHINI	100	1	T	Ì	Ī	آ	Ť	-[
POLVA HVEGE		IY.LOVORUM	L		T	Ī	Ī	Ï	T	Ī	
POMO? BACSU			7	122	Ť	Ī	I	Ì	Ī	I	
POPTIX BACK	U OLUCOMOKIDIASE		Ŀ		Ī	İ		İ	Ī		
PCPID CHETE	VACULARICA PROTEIN POPILIO	CHLAMYDIA TRACHONIATIS	11:31						Ī		
NOTE CALTE	VIKIA ENCE PROTEEN POPS-D		111.6			П					
rcess crem	I VIRILAZINCE PROTEIN POPS-5		26-32								
2000	VALLENCE PROTEIN PORTO		8	2.5		Ì		Ì			
10 mg	VALUEDICA MOTEDI POPTO	COLANTOIA I RACHEMIA IIS	8		1			1			
	WALLEY OF THE IMPORTATION FACTOR CARA					1	Ī	Ī	1		1
POINT PACE	CAPELINE PROTEDI	SACELUS SUBTELIS	<u> </u>		T	T	T	T	T	T	
DENG BORD	CAPELINE PROTEIN	UEN	9.		T	T	Ι	T	Ť	Γ	
PCAPE GOAL	I CAPACIDA PROTEIN	CLOSTNIDIDA ACETOBUTYLICUS	17.2		Ī				T	Ι	
KALL MACH	A CALACEDRY SYNTHETASE	SACELLYS BREYS	143.572	790-126	20.05	1035-1082		Ī	Ī	Ī	ı
PORTS BACK	R. GRANGCEDEN S SYNTHET ASE IS	SACELLUS BREVIS	\$4.33		M-383	136-1133	13.1340	1215-1240 2162-2119 2559-2516	330-3316	3116.3144	1604-143
POSHI ECOLI	CLUTANATE CYSTEDIE LICASE		139-366	174-501						Γ	
PCSHR, ECOL	OLUTATIBONE REDUCTASE		100-134	170-311							
POSING POEAR		UGINOSA	10.00								
POSIA BACKU	I STARVATION-INDUCTALE PROTEIN A		14.101	П							
MOSPO EXINCA	A PROTEST D PRECINIOR		150-285	П							
POSTO DAVO	OSPO EXWCH PROTEIN B PRECURSOR		150.302	107.538	811.538	999-669	П				
2 CH CH	4 PROTEIN D PRECURSOR	KLEBSTELLA PYEUPONIAE	239.206								
POSPE BAWC	A PROTEIN &	ERWORLA CAROTOVORA	136.361	1	1	1	1				
FGSFR EXWON	H PROTEIN I	ELWING CHAYSANTHEM	28-36	1	T	1	1	1	1	1	
5	TACITED E	12	137.76	037.11	1	1			1		
	I INDIENE	FACULTATION APPROXIMENT	451.77		•	•				ĺ	

LE PROTECTION WEL MOTERN FREGUESCA FREGUESCA WELCH FREGUESCA WELC	PCGERE (185417844										
A PATIENT A PATIENT	_	Prohoryatic Sequences	-								
		ORGANISM	AKIAL	AREA	AKA.	ARTA			1.		
PRINTENT CONTRICTORY PRINTENT CONTRICTORY	ŧ	AANTHONONAS CALIPESTAIS	130.33					7	7	7	1
MINISTER PROTOCOL PRINCE	COSM AERRY PROTEINTER CHARAC	PSEUDONONAS AERUGINOSA	95.91				Ī	Ī	1		
WEIGHT ACCOUNT WEIG	CONTRACT PROTECT PROTECT	AEROMONAS HYDROFIFILA	17.5				Ì			-	
	COLUMN TACOMONIA	ERWINIA CAROTOVORA	3			Ī	1				
PATRICE PATR	CARLO MANUELLA PACCIASON	KLESKELLA PYEUMONIAE	140.143								
	USTA LAWLA PROJECT I	ERWINGA CAROTOVORA									
MORTOR MUSICAL MATCHES M	WATER CHARLES IN THE STATE OF T	EAWORLA CHAINSANTHEALL									Ī
	ONE ALEY PROTEIN K	KLEBSIELLA PNEUMONIAE									Ī
PROTECT PROT		PSEUDOMONAS AERILOIMOSA									
CHARDEN LANGE LA	USPL EAWCH PROTEING	FRESIDA CITA CALCALITATION	5								Ī
CHOCKIN LANGE LEGISTRATE THE PROPERTY THE PRO	SIM, XAMOP PROTEDUL	VANDALA CIGATANA		241-21n	131-35	İ			İ	ļ	
CHESTIFUS PRECISES TANDECCEL DOWNER 19-19 19-1	SUM ENWEATHERING	AND INCHIONAS CAMPESTIUS	Г	7			I	Ī	1		
GUCGOTT, TANGELEGATE FACTAGE F	COOD EAWON PROTEIN IN DREPARAGE	ERWEGA CAROTOVORA	L	Ī		Ī		1	1		
GUCCOST NATIONAL STATEMENT 111-10 111-11	The second secon	ERWINA CHRYSANTHEAN	1.		T						
QUECNITAMINITALIS TREFFECCUS TOWNS TAY	THE CLASS OF THE CLASS OF THE CLASS OF	STARPTOCOCCUS DOWNER	П		7	7				ľ	
A CACOMY INVESTIGATE	THE STAND COLOROSTITIONSFERASE I PRECURSOR	STREPTOCOCIUS DOUGOS	7	2	_			405-1529			Ī
QUECNOTIVADE LALIS RECURSON TREPPOCOCCUS SOLVANS 424 104.17 161.18 104.29 10.20	ITTA STRUN (QLUCOSTILTIANS) ERASE.S	Checker of the control of the contro	7	28	_			Ī	İ	-	:
QUEORITY TANGE LAST STREETINGS THE PROCESS BUTTAND THE PROCE	1779 STRAND GLUCOSYLTINANUSERATE FEERINGS	SHELL TO COLCUS PROTANS	297.350				i	Ī		i	İ
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PAICHD METYOL COENTYNE NI NEDUCTASE	METHANGCOCCUS VOLTAE	247.274				-	
PRICAC ECOLI INCRC PROTEIN	ESCHENCHIA COLI	\$1.15					
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POUTB BACSU	SPOKE OUTGROWTH FACTOR B	BACILLUS SIMPHUS		1	1					
POUTO ERWCA	LEADER PEPTIDASE	ERWINGA CAROTOVORA		1	1			Н	-	-
TICK STRA	_	STAEPTOCOCCUS PARASAMOINS		1	+	1	1			
THE STISA	IS KD PROTEIN IN SSAB STREGION	STREPTOCOCCUS SANCINS	Ť		1	1				
יייי דייי	PI. I YPE PROTEINASE PRECURSOR	LACTOCOCCUS LACTIS	Ţ							
PP 26 MYCHO	PROTEIN P19	NYCOPLASMA HYDRHINIS	2	-	ह्य	2000	1466-1496 162	1625-1655		
7	MI-TYPE PROTEINASE PRECUISOR	LACTOCOCCUS LACTIS	200	+						-
V. CACA	PILTYPE PROTEINASE PRECURSOR	LACTOBACILLUS PARACASEI	Т	200	B) - (10			5.1649		-
The Eco.	PJO PROTEIN	ESCHERICHIA COLI	T	+		0521-727	96-1498	1628-1655		
2	PROTEIN PA	NCKETTSIA NCKETTSII	T	15.7	1	1	1	$\frac{1}{1}$		
ALC:	PROTEIN PJ7 PRECURSOR	MYCOPLASMA HYDRHINIS	I		+	1	1	1		
TA LACIC	MILTIPE PROTEINASE PRÉCURSOR	LACTOCOCCUS LACTIS	E	974-946	1631150	11000		-		-
	A KO PROTEIN	PSEUDOMONAS CHLORORAPHIS	Т	•				1032-1633		
5	PAS PROTEIN PRECURSOR	ENTEROCOCCUS PAECIUM	Ŧ	41.300	1	t	+	1		
N. 1. 1994	MOTERN AND PRECURSOR	LISTENIA GRAYI	T	Т	300-334 411	117.117	\dagger	+	$\frac{1}{1}$	
71517	PROTEIN PRO TALCURSON	LISTERIA INNOCUA	Ī	Т	1	†	\dagger	+	+	
P 60 LISMO	PROTEIN PAR PRECINGOR	LISTERIA IVANOVII	101-160	33.339	\mid	t	\dagger	+	$\frac{1}{1}$	-
PPed LISSE	PROTEIN PAOPAECLA SOR	CISTEMA MOMOCYTOGENES		1	Г	ŀ	\mid	ł	1	-
Г	PROTEIN PAS PRECURSOR	LISTERIA WEI GLANAGE	П	П	П		l	-	-	1
Γ	PROTEIN POS		7			-	-	-	+	1
г	ADC SYNTHASE		5	421-464 48	489-519 544	\$44.595	-	1	-	1
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	4-AMINO-4-DEOXYCHONISMATE LYASE	EKHENCHA COLI		1	+		H	-		
7	PROTEIN Y	SEUS	01.50	\dagger	+	+				
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	PENICALIN ACYLASE PRECURSOR	SUS	Ŀ	111.141	107.163			+		
Т			Т	Т	Т	+	1	$\frac{1}{1}$		
Т		TIAMS	T.	261-465 516	311-465 136	136.410	1011			
+		BACILLUS SUBTILIS	61.0	Т	1	+		10111011	3	
۳		2	145-172		H	1		1	1	1
┮	MINOR FIXIBILIAL PROTEIN PAPE	SOUTH COLI		16-123	-	\vdash	+	1	-	Ţ
_	FINGSTALL PROTEIN PAPO PRECURSOR		₹				L	-	-	Ţ
Ī	PARA PROTEIN	TIMESACIENS	916-214	-			-			I
PAN ECOLI	PLASMID PARTITION PAR B PROTEIN		т		1					
	TOPOISOMERASE IV SUBLINIT B		7	195.70	1	+			-	[
_	TOPOISOMERASE IV SUBUNIT B	KILON			$\frac{1}{1}$	+	+	H		I
T	PROTECTIVE ANTIGEN PRECURSOR	CIS	T		Т	П	-			F
7	PENTCALIN-BINDING PROTEIN 2		I		200.00	630-684	3			
-	-		L	Т		+	1			
PORPS CTREAM	FEMALICIAN BINDING PROTEIN 2		027.6	+	+	+	+	1		
Т	104 01 123	NEUMONIAE	144-183 216	216.243 235	259-216 605-612	+	+	+	+	
1	1	ESCHERICHIA COLI	Т	1		+	+	1		
					1	$\left\{ \right.$	$\frac{1}{1}$	$\left\{ \right.$	$\frac{1}{2}$	

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TEN BACSU	PENCINE IN PROPERTY OF SECURIT		136.363	Ī	T	T	Ī	Ī	Ī			
	ACCOUNT OF THE BROKEN OF THE CONTROL	ECCIRETCHIA COLI	155.13	Ī	T			T	Ī			
1000		CENTRE INCIDENTIAL CONTRACTOR	3 57	17.30				ı	l			
TECO.	PENCELLING TO PROPERTY OF	SACREMENT COST			T	T	Ī	T	Ī	Ī		
NA STREET	PENCILLINGINGHO PROTEIN IA	STRETTOCOCCOS PREDMICATAS		f	1	50.69	Ī	T	T	Ī	l	
L STAKU	PENICELLIN-BINDING PROJEIN	SIATHTLE UCCUS AUREUS		Ť	7		T	T	Ī	Ī		
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PELI ERWCA	PECTATE LYASE III PRECURSOR	ERWINIA CAROTOVORA			1	1	Ī	1	1	Ī		
PELA ERWCA	FECTATE LYASE A PRECURSOR	ERWINIA CAROTOVORA	2			1			1		1	
PELB ERWCA		ERWINIA CAROTOVORA	10-11							1		
PELC ENWCA	PECTATE LYASE C PRECURSOR	ERWINIA CAROTOVORA	110-133									
HUMUS SISS	PERTATE VACER PRICINGE	EDWIND CHRYSANTHEN!	40.67	(12.402		l		l				
ELS ENWINE	BERTH ACAD BOTH A TO THE BERTHANDER	ENVIOLE PARTICIONAL	(97)		Ī	T		-		Ī	l	
CLC ENTINE	CANTENDER COLORIDA CONTRACTOR STATEMENT OF S	Canada and Anna Anna Anna Anna Anna Anna		I	Ì		Ī	İ	Ī	Ī	l	
ELP TERUS		TENSINIA PSEUDO I UBERLULOSIS				1		1	1	I	١	
ELX ERWCA		ERWINIA CAROTOVORA	2.		1	1		1	1	1		
PELX ENWOH	EXOPOLYGALACTURGNATE LYASE PRECURSOR	ERWINA CHRYSANTHENI	466-492	_								
FPD ECOLI	ANDVOACYL-MISTIDINE DIPEPTIDASE	ESCHERUCHIA COLI	264-314									
г	X-PRO DIPEPTIDASE	ESCHENICHIA COLI	251-278									
TET BORBE	PERTACTIN PRECURSOR	BOADETELLA BRONCHISEPTICA	617-644					l				
A BOOK	PER TAPTA PROFITE SOR	RORDETELLA PARAPERTUSSIS	628-655	Ī				T	Ī	I	ļ	
т	PERSON AND PROPERTY OF STREET	SOB DEPELLA PERMISSIS	1		T	Ī		l	Ī			
2000	SUPPRESENTA VICE ATE RIVARE	CORVINERACTERIE			Ī	Ī	Ī	Ì				
3000	PATOCEACTION OF THE PRINCIPLE	RACKERITAIN TOR	116.314		Ī	T	Ī		Ī	Ī		
3	TROSTROGE CENTRE ANTONIO	S. A. S. A. A. A. A. B.	MEI DANOBACI EROM BATANIII		1	1	1		1	1	I	
_	PHOSPHOCALYCE KANASE	TREMANS AQUAINEDS	77777		1	1		1	1			
	ENDO-POLYGALACTURONASE PREGURSOR	ERWINIA CAROTOVORA	27.77		1	1		1	1		I	
ORE SALTY	OUTER MEMBRANE PROTEASE E PRECURSOR	SALMONELLA TYPKIMUNUM	56-93		1	1						
HAI FREDI	C-PHYCOCYANIN-1 ALPHA CHAIN	FREMYELLA DIPLOSIPHON	21.48									
HAZ FREDI	C-PHYCOCYAMIN-3 ALPHA CHAIN	FREMYELLA DIPLOSIPHON	21-48									
PHAN PSEOL		PSEUDOMONAS OLEOVORANS	364.79									
		ANABÁENA CYLINDRICA	7			1						
_		ANABAENA VARIABILIS	=			1	1					
HAB FREDI		FREMYELLA DIMLOSIPHON	9			1						
HAB MASLA		MASTICOCLADUS LAMINOSUS	14.43			1		1				
PHAS SYNYS	ALLOMYCOCYANIN BETA CHAIN	SYNECHOCOCCUS SP	=	1	1	1		1				
MIAC SYNDS	ALLOPHYCOCYANIN ALPHA-8 CHAIN	SYNECHOCOCCUS SP	9									
TING FREDI	ALLOPHYCOCYANIN GAIGAG CHAIN ;	FREAMELLA DIPLOSIPHON	5							_		
	C-PHYCOCYANIN-1 BETA CHAIN	FREMYELLA DIPLOSIPHON	2									
	ACETOACETYL-COA REDUCTASE	ALCALICEMES EUTROPHUS	2				7					
PIICA SYNYI	C-PHYCOCYANDI ALPHA CHAIN	SYNECHOCYSTIS SP	<u>=</u>									
PPHCB SYMP6	C.PHYCOCYANTN BETA CHAIN	SYNECHOCOCCUS SP	£								İ	
HICE SYNP!	C.PHYCOCYANIN BETA CHAIN	STATECHOCOCCUS SP	26-55									
PHCE SYNY!	C-PHYCOCYANIN BETA CHAIN	SYNECHOCYSTIS SP	21-33									
HEA ECOU		ESCHERICHIA COLI	16-37									
HEA ERWICE		ERWINIA KERBICOLA	16.37	159-116	152-216							
HEA PEET	PIGNOL 1-MONDOXYGENASE	PSEUDOMONAS SP	171-201	115-514	137-464							
PIEB MASLA	PHYCOERYTHOLOCYANIN BETA CITAIN	MASTICOCLADUS LAMINOSUS	21-62						Γ			
PHEB PSESP		PSEUDOMOKAS SP	24.51						Ī			
PARC STAPY		SYNECHOCOCCUS SP	138-115					l			ŀ	
MED ECOL		ESCHELUCHIA COLI	284-311		F		I	Ī	Ī	ſ	+	
PHEI CLOSA		CLOSTRUDIÚM PAŠTEURIANDA	1077		F			Ī	Ī		ľ	
PHELI BACKE		BACR.LUS CEREUS	*			Ī		ľ				
PHO.2 BACCE	SPHIMOOMYELINASE C PRECURSOR	BACALUS CEREUS	*:					T	Ī	Ī		
PPIG BACCE		SPYCETOS CEREUS	1.36									
PHLC BACCE		BACOLUS CEREUS	12.59	17 306								
PPIG. CLOB!	PHOSPHOLDASE C PRECURSOR	CLOSTUDIUM BIFERMENTANS	5	13.75				Ī				

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ANEA!	T		T	1				47-109		64-91	4-103	20.21	1	\dagger	107	201.34			411-515		1	1	1	939.660			152-102		1	1	\dagger	\dagger	\dagger				2		\dagger			260-287 369		\dagger	1	¥ 5	+	\dagger	+	
AMEAL	200	3	39.70	П	96:362	78-205	<u> </u>		3.40		\neg	╗		234.246	T	r	Τ	•		8		00-01		7	П	156-188	П	~ ~	57.73	216-263		341-270	2		1	T	٦,	171.205		11:11		П	<u> </u>	+	100.110 411.440	Ţ	+		E.	190 236-203
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Prelatricie Sequences PRGANISM LISTERIA MONCYTOOENES	PSEUDOMONAS AENUGINOSA	STAPHYLOCOCCUS AUREUS	BACILLUS CEREUS	LEPTOSPIRA INTERROGANS	ESCHERICHIA COLI	COUNTRICATION CONTRIBUTION	SCHEMENIA COLI	CHINOBAL IEA FREUNDII	ESCREPCHIA COLI	KI ERSIELLA DATIOCA	ALEBSIELLA PREUMONIAE	BACH LIS SIRTH IS	ESCHENCHIA COLI	SALMONELLA TYPHINDINIUNI	BACILLUS SUDTILIS	ESCHENCHIA COLI	SYNECHOCOCCUS SP	SYNECHOCOCCUS SP	EXCIRATION COLI	NEISCERIA COUCERNE	PSELDOMONAS AFRICANOSA	PSEUDONOMAS AERUGINOSA	NEISSERIA CONORRINDEAE	PSEUDOMONAS AERUGINOSA	PSEUDONIDHAS AERUGINOSA	ESCHENCIAL COLI	MOLACELLA BOVIS	MACH LIS CERSIS	BACILLUS THIRINGIENCIC	LISTERIA MONOCYTOGENES	ESCHERICHIA COLI	ESCHERICHIA COLI	ERWINIA CAROTOVORA	ESCIENCHIA COL!	ERWINIA CHRISANIHEMI	2 YNOMONA & KIONII IS	ESCHERKCHIA COL.	SALMUNIALA TYPHIMURIUM	BACTEROIDES SYNORIOSUS	PSEUDOMONAS SYRINGAE	PSEUDOMONAS AERUGINOSA	CECUE MOUNTS AERUGINOSA	ESCHERICULA CIVIL	ESOR NORTH COLI	BACILLUS SUBTILIS	BACILLUS SUBTILIS	ESCHERICHIA COLI	ESCHENCHIA FERGUSONII	LAYODACTERIUM MENINGOSEPTICUM	FLAYOBACTERUM MENINGOSEPTICUM
	7	THOSPHOLIPASE CPRECURSOR	т	+	Ŧ	+-	N OUTER ACEMBRANE PORE PROTEIN B PRECINGEN	OUTER MEANE PORE PRINTEN E PROTECT	X OUTER ACKIDICANE PORE PROTEIN E PRECIMION	N OUTER MEMBRANE PORE PROTEIN EDERTHEOR	Y OUTER ACMBRANE PORE PROTEIN E PRECIPE CO	U ALK PHOS SYNTHESIS TRANS REG PROTEIN	1 SENSOR PROTEIN PHÓG	Y VIRULENCE SEMSOR PROTEIN MIDG	U ALK PHOS SYNTHESIS SENSOR PROTEIN PHOR	THOUSENING PROTEIN PRO		Т	1	₽=		-	4	7	PI PACIFON	_	PILIN GENE INVENTING PROTEIN	PHOSPHODIESTERASE PRECUNSOR	PHOSPHODIESTERASE PRECURSOR	PHOSPHODIESTERASE PRECURSOR	ACM TRANSFERASE	PLAK PROTEIN	MAN PROFESS	PECTINES TRACE PERCINARIA	PHOSPHOGL YCENATE MUTASE	PHOSPHOOLYCERATE MUTASE	POLYRIBONUC MIKT. EOTIDYI, TRANSF	THE PROPER	A HE LANGE LE BOLL DE STEEL	POUNT O PRECURSOR	POALN P PRECURSOR	BINDING PROTEIN PRECURSOR	PUI KISCINI; UKMIIIME AKTIPOKIEK	PYAUVATE DEHYDROGENASE	ALKALINE PHOSPHATASE III PRECURSOR	ě	ALKALING MIOSMIATASE PRECURSOR	ALKALINE PIOSPHATASE PRECURSOR	PROLYL ENDOPERTIDASE PRECURSOR	PHOSPHOENDI PVERIOR FRECURSOR
FCGFNE FILE RAME PPGC LISMO		2000	700	PPIND ECOL	PPINK ECOL	PPHINA ECOLI	PPHOE CITTR	PPHOE ECOL	PPINOE KLED	PPHOE KLEP	PPHOE SALTY	PHIOP BACSU	THOS ECOL	PHIOD SALTY	THE BACSU	A THE	PPICA SYNDY	PHSO ECOL	PPHSM ECOL	PPILA NEICO	PPILB PSEAE	PPILC PSEAE	S	200	100	PPIV MORBO	PPIV MORLA	PPLC BACCE	PILC BACHU	PLC LISAED	FFLSC ECOLI	PHY VO FEWER	PAUL ECOL	PPICE ENWOR	PPKOY ECOLI	PPMGY 2 YOU	PPN ECOLI	THE SALITY	PORT PERSY	PORO PSEAE	PPORP PSEAF	POTO ECOL	Profit ECOL	ויסאם פטרו	LL BYCON	PPPS BACOU	TOTAL SECOND	PPCE FLAME		PPCK FC011

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THE MANIE PROTEIN	ONVACATION OF BEINGENS	Г								
PROTEIN A PRECURSOR		19.76								
COBMYNE POO SYNTHESIS PROTEIN IS	SACETICUS	10.34								
PROTE ANAVA I CALCILLA DEPENDENT PROTEKSE PRECURSOR	ANABAENA VAIUABILIS	171.391		1			1	1		
PADTEASOME ALPHA SUBUNIT	FHERMOPLASMA ACIDOPHILUM	:= := :=					1	1		
TAIL-SPECIFIC PROTEASE PRECURSOR	ESCHERICHIA COLI	28.182	100				1	1		
PLASMID RECOMBINATION ENZYME	STAPINGOCCUS AUREUS	<u>.</u>	33.13				1	1		
PLASAILD RECOMBINATION EN2 YNG		41.75	111.70	10.361	2			1		
PLASAID RECOMBINATION ENZYNIE	7	11.11	291-318				1	1	-	
REGULATORY PROTEIN	BACILLUS LICHEMIFORMIS	2.40					1	1		
PLASMID RECONDINATION ENZYME	BACILLUS SP	181-224								
BI ACKLIN BETTACKETON FINZ YAS	STREPTOCOCCUS AGALACTIAE	215-219	933-159	150-021						
LESCONDIA VON BROTEN	LISTERIA MONOCYTOCENES	36-110	7.70							
PARTICIPATION OF THE PROPERTY OF THE PARTICIPATION	ESCHEDICHTA COLI	111.145								
Transfer to the second of the	BACH LINE CHATH IS	11711								
UNA FRUMASC	¥ 100	3	262.319							
	1410114									L
		90								L
DNA PRIMASE		247.407		7	107,757					
PPRIM RICPR DNA PRIMASE	AKKETTSIA PROWAZEKII	2	97.50	2	2 P. 73					
	DESULFOVIBATO DESULFURICANS	30-53								
	ACHROMOBACTÉR LYTICUS	11344								
BELLEN DETALL VINC NOT ALL DENDOPEPTIDASE	LYSOBACTER ENZYMOGENES	111-161								
	LISTERIA MONOCYTOGENES	111.145	175-310							
ALTO ME INTERNATIONAL PROPERTY OF THE PROPERTY	PETERIA MANAGENTA	59:15								L
	THE PARTY OF THE P	71, 90,								L
ROA SERMA GANDAA-GLUTAMYL PHOSPHATE REDUCTASE	SERVATIA MARCESCENS									
PROTEIN A PRECURSOR	STAPHTLOCOCCUS AUREUS	2								
OLUTAMATE S.KIMASE	SERVATIA MAKCESCENS	3								
PROTEIN STRAC PROTEIN B	STREPTOCOCCUS AGALACTIAE	31-13								
	PSEUDOMONAS AERUGINOSA	141-132								
	AACH LUS SURFILIS	200.237	L							
TOURSE TO THE PROPERTY OF THE	ESCHERICHIA COLL	460.483								L
TACLING INVITAMENT	Cocyce Con 1	3								
PERIPHERAL MEMBIRANE PROTEIN PROV.	SACREMENTAL COMPANIES IN COMPAN									
PERIPHERAL MEMBRANE PROTEIN PROV.	SALMONELLA I IPRIMURUM						I			
PRAB PROTEIN	ESCHENICHIA COLI	2								
ANTICODON PUCLEASE	ESCHERICHIA COLL	200								
PARD PROTEIN	ESCHESUCHIA COLI	116-105								
PROTEIN EXPORT PROTEIN PRSA PRECURSOR	BACILLUS SUDTILIS	11:45	651-56							
BECOME A SECTION	STREPTOMYCES GRISEUS	36-110	L							
TALK SINGE SECTION OF THE SECTION OF	ELWINIA CHRYSAMTHEMI	8				L				L
SECONDISCO PACIFICATION OF THE SAME	PORPHYROMONAS GINGLYAL 15	215-312								L
TAIL TOKOL COLLACEATA PARCONAS BENTERA BEST	BENEVIA CHRYSANTHEMI	126.155								L
	DA PER BUILDING MODIFICATION	2	210.241	144.184					L	L
	ES CANALA CHIND STATE ST		1	11.700						
	SATISTICAL PROPERTY.									
PRITE ERWCH PROTEASES SECUETION PROTEIN TRIF	ENTING CAN I PROFILED									
PATH LACLA PROTEASE MATURATION PROTEIN PRECURSOR	LACTOCCCOS PACIES			91.						
PROTEASE MATURATION PROTEIN PRECUISOR	LACTOCOCUS LACTIS	ê								
PRIM LACPA PROTEASE MATURATION PROTEIN PRECURSOR	LACTORACILLUS PARACASEI		2	1						
PRIN SERMA BYTRACHELLIE AR SERING PROTESSY PRICHMSON	SERRATIA MARCISCIANS	Ē	S PACE	# · ·	_					
PERTUACHLILIMAR SERVING PROTILASE PRECONSOR	SILVRATIA MARCIECLINS	3	### ###	1007-1041						1
PPATY ERWCH ISECULTED PROTEASE C PRECURSOR	ERWINDA CHRYSANTHEMI	114-341								
CHECK ON ONLY A APOPROTEIN A!	SYNECHOCOCCUS ELONGATUS HAEGEL	130-147		•						
CHARGOPHYLL A APOPROTEIN A I	SYNECHOCOCCUS SP	105-136	376-356			L				
DEAN CYLING CHOPHYLL A APOPROTEIN AL	SYNECHOCOCCUS WALCANUS	130-10								
	SYNECHOCYSTIS SP	<u>-</u>	130.143	31.36	L				Ŀ	L
CHAMESONE MOTERN PEAN PRINTEGO	VERCINIA PESTIC	34.33								L
TOTAL TEXT CONTRACTOR TOTAL TOTAL TEXT OF THE STREET STREE	SYNECHOCOCCUS SP	-								L
-	VERENIA BEETIE									
			_		L	L	L	L	_	_

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OBGANISH MACESTIS HIDUANS ESCHENCIA SUCCISMENS	П	\Box		11	48.44	AREA	1 1	1
ANACYSTIS MIDULANS ESCIEDOFIN COLI WOLINELLA SUCCISINGANS	Г			1	1		1	
POLINELLA SUCCINAZINES				-			1	1
WOLINELLA SUCCINTRICINES	19-65		_				Ì	
	10.51		-				1	
E.SCHEAKHUA ('OI.)	20.24	İ			T		Ť	Ī
MACHLUS SUBTILIS	9		<u> </u>				1	
ESCHENCITA COLI	29-51	140.4%	-				1	Ī
SALMONELLA TYPHINERIUM	1	927-626	-				1	Ī
STAMINLOCOCCUS CARNOSUS	144	-	-				1	Ī
STAEPTOCOCCUS SALIVARIUS	10-50	14:332	-					
ERWINIA CHRYSANTHEM	23:12	-	-					
JACILLUS SUBTILIS	670.697						1	Ī
ACTOBACILLUS CASEI	537.364	-		-				1
ACTOCOCCUS LACTIS	т	1010		\prod				
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STREPTOCOCCAL ACID GLYCOPROTEIN STREPTOCOCCUS PYOGENES 194-331 185316		PACCA COMMISSION ANTICOMINATOR	BACH (IIS CIRTH IS	Т	16.314	Ī	\dagger	T	T			
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SECRETICAL COL 1-33 408-470 1-34 408-470 1-34 408-470 1-34 408-470 1-34	CD ECOLI	_	ESCHERICHIA COLI	П		F						Ļ
PRECURSON 12-15	N ECOL!	_	ESCHERUCHIA COLI	273		155-510		Ī				
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STIATE INDIAGLASE INTESTIGECUS MILANS (1915)			KLEBSIELLA PNEUNIONIAE	┰	Т		1	1				
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Preharyade Seguences	SALMONELLA TYMUDALBERY	KLEBSIELLA PREIMONIAR	SALMONELLA TYPHIMURUM	BACALUS SUBTILIS	ESCHENCHIA COLI		1		1	1	METHAMOCOCCUS VANHELII	STAPHYLOCOCCUS CARNOSUS				7	R SERBATIA MARCESCENS	ESCIENCIUA COLI	ESCIERCINA COLI	ESCHERICHIA COLI	ESCHERICITA COL.	ESCIENCIIIA COLI	ESCHERUCHIA COLI	ESCHERICHIA COL)	BACILLUS LICIENIPORXIIS	BACILLOS SUBTILIS	ALE I UCERTURI KINUI	ESCHERICHA COLI	ESTIMATION OF I	CALICALCHIA COM	SYNECHOCOCCUS CO	COXIELLA BURNETII	ESCHENCIIIA COLI	METHANDRACTEMUM THEMMONUTOTACHICE	PHOTOBACTERIUM LEIGGNATHI	PROPIONIBACTERNIMI FREUDENKISICIIII	ESCHERICHIA COLI	ESCHENCINA COL	BACKLUS SUBTILIS	BACILLUS MEGATERIUM	BACILLUS SUBTILIS	BACILLUS LICHEMIFORNIS	BACILLUS MEGATERIUM	MACHINE THE PROPERTY.	BACELUS SIMILIS	T	T	П	BACILLUS SUBTILIS	BACILLUS SUBTILIS	BACKLUS SUBTRIS	STREPTOCOCCUS DOWNE	21 22 E 10 C 11 EV 10
ISTAITAS	FRUCTOKINASE	SUCROSE PORIN PRECURSOR		т	PACTACLE IN TRANSLOCASE SECA SUBUNIT	-			PRESENTE INCIDENCE SELT SUBURIT	PARE PROPER TO AND DOCASE SECT SUBURIT	Pare partie and octate and a second	SEEF PROTECTION OF CHARGOS SECT SUBURIT	A LAUSSIANI SPECURSOR	CENTROL TELEVA IN DER YDROGENAS	SLOAD PERMITTING SUBURIT PALLUASOR			SUBSION PROTEIN A	State on People in	SPILIFIE ON PROTEIN B.	SHUFFLON PROTEIN	CIDECI ON PROTEIN C	SKIPS ON MOTERA	SIMI PROTECT	SING PROTEIN	CELL SURFACE PROTEON PASCINGS	PROPHAGE CPA-(1) INTEGRACE	SAIF PROTEIN	SMALL PROTFIND	SNIP PROTEIN PRECURSOR	TRANSCRIPTIONAL REPRESSOR SMIB	SUPEROXIDE DISARUTASE	SUPEROXIDE DISARUTASE	SUPEROXIDE DISARUTASE	SUPEROXIDE DISARITASE	SOMO PROTEIN PRECINSON	SOPB PROTEIN	SOXX PROTEIN	STACE O SPORULATION PROTEIN !	STAGE I SPORTE ATION PROTEIN AA	STACE IS SOME A FIGH PROTEIN AA	STAGE IS SPORTE AT THE PROTEIN AN	STAGE II SPORIGATION PROTEIN IN	POSSIBLE ASPARTM. PROTEASE	STAGE II SPORULATION PROTEIN J	STAGE III SPORULATION PROTEIN D	STAGE III SPORULATION PROTEIN I PRECURSOR	STAGE IV SPORULATION PROTEIN A	STAGE IV SPORULATION PROTEIN B	STAGE IV SPORUGATION PROTEIN FB	STAGE V SPORULATION PROTEIN AF	SUBTILINI BIOSYNTHESIS 117 P.D. SECTION	
PCGENE FILE PANE	PSCRK SALTY	PSCRY RLEPN	PSCRY SALTY	TACA BACSO	100	200	PSECT POOL	PSECY PCB	PSECY LACIA	PSECY AGETVA	PIECY STACE	PSEFC SALEN	SEEK ANDER	PSCAA FCOLL	1024 AS 24	PULL SERVA	1003	PSVIUS ECOLI	PSI(U) ECOL	PSHIM ECOL	PSIND ECOL	PSIAM ECOL	PSWC ECO.	PSINA BACLI	PSINK EACSU	PSLAP ACEK!	PLPA ECOL!	PSVE COLI	PSVIPB ECOLI		SYM	1500/ COXBU	200	TO STATE OF THE PARTY OF THE PA	7		1		PSPOJ BACSU	7	1	1	-			П	_		PSP-0 SACU		Т.		

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PSPAK BACSU	SEMSOR PROTEIN SPAK		- 1		7		170	1000	X177 .11.	\dagger	I
UNTE CARE	CELL SURFACE ANTIGEN MI PRECURSOR	UTANS	2	7	2	ROO	201-101		2	1	Ī
PSPAR BACSU		BACILLUS SUBTILIS		122.199				1		1	
PAPAT BACSU	-		7775	136-367					-	-	
VANTA TABLE	EXOTORIN TYPE C PRECINIOR	OCENES	11.34							_	
12102 01030	(breve hy		± ±	155-102							
10 CHANE	COLD AT IN	JERUN	195-222						-		
1000	CHAM. P. S. B. C. C. C. C. P. V. P. V. D. P. I. O. P. I. O. I. V. D. B. C. L. A.		199-(69						-	H	
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PSRS ECOLI	⋍				,			T		\dagger	T
PSRPS MYCMY			┪	Т	27					1	I
PSSA1 PASHA	_		151-17	38-35	465-512	29.570	2	1		1	
PSSAB STRPA	•	STREPTOCOCCUS PARASANGUIS	13.39							1	
ATT THE	-		85-12	101-138						_	
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	COLC. E. CTR A MANAGEMENT PROTEIN		61.10						-	-	Γ
	AND THE PARTY OF THE PROPERTY.	203,	100		Ī			T	-	l	
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PSTA ECOLI	STAEPTOTHUCIN ACETYLTRANSFERASE		2							1	I
PSTC1_STANU	STAPHYLOCOACULASE PRECURSOR		٦	-	20.0					1	1
PSICE STANU	STAPHYLOCOAGULASE PRECURSOR			264-29						1	7
1000	L. TRANSD TRANSC CONTROL PROTEIN	CLOST ALDIUM BEITENINCKII	17:19								
10/18 10/18	STPA PROTEIN	ESCHERICHIA COLI	19.60							-	
1000	+	USEUS	e≅:≘						L	┞	
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	STRETIONINGS A PRECONDOR		Т.	281.308					-	\mid	Ī
21.5			Т	135.561	9(9-500					l	Γ
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FEURY BACK			Τ						+	†	Ī
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PSUCP AGAM		AUTOCOLOGIC BANGO CONTRA		Ī					+	\dagger	T
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PSYE BAONU	_		9. %	31:38						1	
PSYE THETH	~	THERMUS AQUATICUS	Ž		-					1	-
PEYFA BACSU	-	BACILLUS SUBTILIS	ヿ							1	1
PSYFB BAESL		BACILLUS SUBTILIS	- 1	403-441						1	
PSYFB ECOL!	PHENYLALAMYL.TRNA SYMMETASE BETA CHAIN	ESCHERICHIA COLI	_1	7.7	741.331					1	1
PSYCO ECOLI	GLYCYL-TRNA SYNTHETASE DETA CILAIN	ESCHENICHIA COLI		41.514						1	
MYH STREQ	HISTIDYL-TRNA STYTHETASE	STREPTOCOCCUS EQUISIONILIS 176-403	9							1	1
PSY1 METTH	ISOLEUCYL-TRNA SYNTHETASE	METHANOBACTERIUM THERATOAUTUTRUPHIRLY	1010-1017						1	1	7
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PCCENE	1107217124	Probaryotic Sequences					ſ				
THERM	PROTEIN CONTINUES OF THE PROPERTY OF THE PROPE	ORGANISM	ARCAL	AREAL	ANEA	AREAd	AREAS	ARIA 6 AREA!		AREAL	TAILS.
PAYES ECO.	I YSYL TRMA SYNTHETASE MEAT INDUINE	ESCHERICHIA COLI	7	211.12	1		1				
rsy. ECOL	LEICYL-TRNA SYNTHETASE	Estruceations (No.)	77.4	200							
PSYM BACST	ATETHIOMYC-TANA SYNIIGETASE	BACILLUS STEASOTHERAIOPHILUS	2 2	Ī	Ī	T	1	T		1	
PINA ECOL	ACCTHIONYL-TANA SYNTHETASE	ESCHERICHIA COLI	767-10	1			T	T	T	T	T
1377 ECOL	PROUYL-TRWA SYNTHETASE	ESCHERICHIA COLI	28.5						Ī	T	Ţ
1270 ECOL!	CLUTANINYL-TRMA SYNTHETASE	ESCIERCHIA COLI	1	Ī		Ī		Ī	Ī	T	Ī
PSYRD PSESY	SYAD PROTEIN	RINGAE	(17-67)								
PSYR ECO.	PRODUCTIONA SYNTHETASE										Ţ
200	VALVE TEMA CYMPICS ASE	BACILLUS SUBTILIS	Т	\$0.436 \$0.436							
PON ECO	VALVE TRIAL CONTINUES	SACILLUS STEARUTHER MOMILLUS	7	7							
PSYW BACST	TAYPTOPHANYLIANA SYNTHETAKE	A A CHILL THE THE AND THE STANDARD COLOR	Т	7	924-931						
PIYY! BACSU	TYROSYL-TRNA SYNTHETASE I	DACHEUS STEAMOINERS AND THE CO.	7	87.66			1				
PSYY2 BACSU	TYROSYL-TAMA SYNTHETASE 2	BACH LINE EINSTILLS	1	8		1					
PSYY BACCA	TYROSYL-TRMA SYNTHETASE	MAX	11110		1	1	1				
PSYY BACST	TYROSYL FRMA SYMTHETASE	HOPHILLIS	1		Ī	1		Ī		1	Ţ
PTIMI ECOLI	ENZYME ECORISM IN PROTEIN		T	Т	445.513	Ī	1	1		Ī	
PTIRE ECOLI	ENZYME ECORIZUI A PROTEIN	ESCHENCHIA COLI	65.00	Т	Т	761.701	8,5.17	WA. JAM		1	I
TIR ECOLI	ENZYME ECOK I A PROTEIN		Т	Т	1	Т	т		Ī	1	Ţ
113 ECG.	ENZYME ECORIZATI SPECIFICITY PROTEIN	ESCHENCHIA COL!	10.00	Ī		Ī	T	T	Ī	1	
PTISA ECOLI	ENZYME ECOA I SPECIFICITY PROTEIN		278.306			Ī		Ī		T	T
200	EXCYME ECOS I SPECIFICITY PROTEIN		238-312						T	Ī	T
71130 ECUT	ENCYME ECOD I SPECIFICITY PROTEIN	ESCHEMICHIA COLJ	349-303						Ī	Ī	T
	ENCINE ECOCIONES INCIDENTE		279-308								Ī
2 17	ENZYME CHECKLISTY BACKEN		_	П							Γ
PTS/ FCOL	17 VPE 115 LAST PROTEIN ENZYAGE ECOCH		2	┑	7	7	lł				
PT2A ACICA	TYPE II RESTRICTION ENZYME ACCI	ACRETORACTER CALCOACETICIE	_	62.60	200	639-612	27.72	25.65			
PTZBF BACSU	TYPE II NESTRICTION ENZYNG BSUF!		Τ	100	314.366	1	1	1	1	1	
	TYPE II RESTRUCTION ENZYME BSURI		T	Т	7	13.53	1	T	1	Ť	
PIX: CITA	TYPE II RESTRICTION BIRZYNG CFILB!			Т	7		T	T	Ī	T	T
PTXC HERAU	TYPE II RESTRICTION ENZYNG MOICH		176-2115								T
PT201 DE CON		DECLI FOUNDING AUTAMIACUS	£ .							İ	T
PIZOI STIUN			21:5	1	1						
P 12E1_ECOLI	TYPE II RESTAICTION ENZYNG ECON		3 8	1		1	1	1	1		
P12E2 ECOLI	TYPE II RESTRICTION ENZYME ECORUI		35.56	T	T	1	İ	†		1	1
1755 (COL	TYPE II RESTRICTION ENZYME ECORY		П	214-241			T	T	T		T
NATE OF THE PERSON NAMED IN	1 TTE IIS RESINCTION ENZYME FORI	KOITES	2								T
FORTH HAFFA	DATE DESCRIPTION FRANCISTS	HARMUTHIUS INTLUENZAE	3	9							
PT312 ILÁBILA	TYPE II RESTRICTION ENZYMETIIIAII		9	1	Ť	1			1		
PT310 HAEIN	TYPE II RESTRICTION ENZYME HINCH		97-138	T	T	T	1	1	1		
PT3K1 KLEPN		ONIAE	٦	178-205	T	T	T	1	†	1	T
PIZMI MORBO	TYPE II RESTRICTION ENZYME MOO!		Ī	T	111-151		T	T		\dagger	T
OBJOW TWI	1 TE IIS RESTRICTION ENCYME MEGII			151-185	337-364				l	T	T
COISM DNCL		METHAMORACTERUM THERMOFORMICICUM							ľ	T	T
7.10 ETR.			3	_							Γ
PT2S1 SHBSO			77.7		93.46						
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TINE PALLE	3 7 3 1 EM ENG TIME NES	BACHLUSCEREUS	61.69	136-285				ľ	r	T	T
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-	Protection Sequences	1 7887	1 74.17	ABEA S	A N. P.A. A.	AREAS	AREA AREA AREA	1	L	Y KEY
FILE CAPIL AT THE COMMON ANTICON PRECIDENCE	TREPOVEMA PALLIDUM	16.53								
PARTY THEORY IS NO MEMORANE ANTIGENA PRECURSOR	TREPONDALA DEMTICOLA	94-136	216.379							
	BACELUS ALVEI	111.101	374-401							
	CLOSTNORUM PENFINACENS	276-311	372-434							
•	LISTERIA IVANOVII	13-120	5	7						
PTACY LISHO LISTERIOLYSIN O PRECURSOR	LISTERIA MONOCYTOGENES	98-123	16.1%	т	20.66					l
	LISTERIA SEELIGEN	92-126	2		1					
j	STREPTOCOCCUS PREUMONIAE	174-373		9,				1	Ī	
	STREPTOCOCCUS PYOCEMES		- 1	2			1	Ī		
PTAGE BACSU TECHOIC ACID BIOSYN PROTEIN B PREC	BACILLUS SUBTICUS	1,00							I	
PTACE BACSU TECHOIC ACID BIOSYNTHESIS PROTEIN C	BACILLUS SUBTILIS		19, 77,		100	117 007				
PTAGE BACSU TECHOIC ACID BIOSYNTHESIS PROTEINE	PACILLUS SUBTILIS	34.43		2	Ž					
7	BACILLUS SUBTILIS	10,501	777 161	161.150	170.010			1		
7	PERSONAL VORUMENTS	1	71.11	17(-60)						
PIBUD PSEM (PREMOL 2-HOMODATOUNASE	CALLONGER A TVERMARETAL									
TOTAL MALE INCOME AND PROPERTY OF PRECING	VIRGIO CHOL ERAF	Ş		11.11	25.280	344.335	987489			
-1-	VIBIUD CHOLERAE	24:36	11111							
	VIBRIO CHOLERAE	32-66	211-134							
Y BCK	VIBRIO CHOLERAE	95.123								
1	VIBRID CHOLERAE	25-51	234.261	75-306	366.)78					
PICPH VIBOR TOP PILUS VIRULENCE REGULATORY PROTEIN	VIBRIO CHOLERAE	5.3								
	VIBRIO CHOLERAE	230-237								
7	VIBRIO CHOLERAE	131-14								
-	VIBRID CHOLERAE									1
PTCN2 BACSU ITETRACYCLINE RESISTANCE PROTEIN P	SACILLOS 209 III.IS	137.567								
PICE BACSI TETRACTCUMB PESISIANCE TAURIN	STAPHY OCOCCUS ALMEUS	17-100								
۴	STREPTOCOCCUS AGALACTIAE	422-453								
۴	STREPTOCOCCUS PREUNIONIAL	422-455								Ц
+	ESCHENCIIIA COLI	210.339								
Н	ESCHERICHIA COLI	134-36	1	97, 987						
-	STREPTOCOCCUS PTOCHARS	2	2							1
PIECE ECOL TETACTCINE REMESSOR MOTERN CLASS B	ESCRIBING COLI	101.310								
7	ALCALICENTS IP	97-57				L				L
PARKE KECK LACY COA THOUSTERASE II	ESCIENCIA COLI	Ę	L			L				L
PIETS ENTER TETRACYCLINE RESISTANCE PROTEIN TETAL	ENTEROCOCCUS FARCALIS	1.36	130-130	139.306	215.344					
	ENTEROCOCCUS FAECALIS	2.36	130-150	217.244	196-36)					
PTETC ECOLI TRANSPOSON THIS TETC PROTEIN	ESCHENICHIA COLI	12:106	2							
PTETM STRLE TETRACYCLINE MESISTANCE PROTEIN	STREPTOMYCES LIVIDANS	13:109								
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PYEND ECOL		ESCHENCHIA COLI	126-151					Т	т		
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T XX BILLIA	HYPOTHETICAL PROTEIN	BRADYTHIZOBIUM JAPONICUM	100-150								
YON BACK	E HYPOTHETICAL 31.1 KD PROTEIN	BACELUS MEGATERUM	40-63					l			l
YGFD ECOLI	HYPOTHETICAL 29 4 KD PROTEIN	ESCHÉNICHA COLI	214-241			Ī	Ī	l	Ī	Ī	
103	HYPOTHETICAL 10 9 KD PROTEIN	ESCHOLUCIDA COL!	31.46			T	T	1	Ì	Ī	I
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DISTRICT OF THE PARTY OF THE PA	_	PSEUDOMUNAS PUTIDA	145-172								ĺ
	_	ESCHENCHIA COLI	123.164				l	l			
PYGL4 BACST	_	BACELUS STEAROTHERMOFHILUS	15.3				l	İ	Ì	I	l
YOLS BACST	HYPOTIGETICAL PROTEIN	BACILLUS STEAROTHERAIOPHILUS	163.300				Ī	l	İ	Ī	١
PYGLN BACCE	HAYPOTHETICAL 15 KD PROTEIN	DACH LUC CRESUS	1			Ī	Ì	1	1	Ī	1
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GR. CLOA	HYPOTHETICAL 38 B KD PROTEIN	CLOSTRIDIUM ACETORUTYLICUM	160-210					l	Ī	Ī	İ
YGT2 STRUNU	HYPOTHETICAL PROTEIN 3	STREPTOCOCCUS MUTANS	9	100	20.50		l	T	Ì	Ī	
NAME (COL	HYPOTHETICAL TO 4 KD PROTEIN	BSCHENCHIA COLI	79-62 20					l	T	Ī	l
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NA ECOLI	HYPOTHETICAL PROTEIN	ESO/EXICHIA COLI	16.3				T	t	1	Ī	
ראושם נכסנו	PROBABLE ABC TRAMSPORTER	ESCHERICHIA COLI	136.301				1	Ì	1		I
THIS PSEPU	PROBABLE ABC TRANSPORTER	PSELECTIONAL PUTIDA	10.15	į			1	1	Ì		ı
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TOP ECOLI	HYPOTIGETICAL 35 4 KD PROTEIN	ESCHERICHIA COLL	100		T	1	1	1	1		1
PYMEM BACSU	HYPOTHETICAL 310 KD PROTEIN	BACKLUS SUBTILIS	1		I	Ì	1	ı	1		
THE ANASP	HYPOTHETICAL PROTEIN	ANABAENA SP	11.00			T	T	t	1	1	ĺ
HIIA ECOLI	HYPOTHETICAL 16 6 KD PROTEIN	ESCHERKINA COLI	3		Ī	1	1	1	1	1	
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\ \ \ \ \	HYPOTICAL PROTEIN	LACTOCOCCUS LACTIS	167.194				l	l	l		
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MSA CLOAL	HTPOTMETICAL 10 6 KD PROTEIN	CLOSTAIDIUM ACETOBUTYLICUA	121-14					l	l	T	l
	HYMITHTAL 42 4 KO PROTEIN	CLOSTADIIM ACITIONULYI, KTAK	23-53	13.E	34.310	ļ	İ		t	Ī	l
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HYA PSESY	IIYPOTIETICAL PROTEIN	PSEUDOMONAS SP	31.34	ı	1	1	1	1	1		
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PYIDK ICOU	HYPOTHETICAL 42 I KD PROTEIN	ESCHERICHIA COLI		1	1	1	1	1	1	1	1
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PYIEC ECOLI	HYPOTHETICAL 40 6 KD PROTEIN		7	13.	1		1		+	1	7
PYIEC ERWCH	HYPOTHETICAL PROTEIN		T			1	1	1	1	1	1
PYIED ECOL	HYPOTHETICAL 14 9 KD PROTEIN	ESCHERICHIA COLI	1	Ť		T	†	+	+	†	1
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PYIEN ECOL	HYPOTHETICAL 24 7 KB PROTEIN		2:3			T	\dagger	ł	1	\dagger	T
LIEM ECO.	HYPOTHETICAL 13 9 KD PROTEIN		27-105			T	T	+	+	t	T
PYIED ECOLI	HYPOTHETICAL SI SKD PROTEIN	ESCIERICHIA COLI	Г	100-001	Ī	T	I	-	+	\dagger	T
PYIFC ECOLI	HYPOTILETICAL 19 6 KD PROTEIN		135.202		Ī	T	ľ	\dagger	+	+	T
LYIG ECOL	HYPOTHETICAL 140 KD PROTEIN		21:07			T	T	ł	+	+	T
L COL	HYPOTHETICAL 31.7 KD PROTEIN		261261		T	T	l	-	+	t	T
LUGN ECOL	HYPOTHETICAL 34.3 KD PROTEIN		307-234		l	T	r	l	+	t	T
200	HYPOTHETICAL 28) KD PROTEIN		83.50				T	-	+	t	T
	HTPOTIETICAL 21 3 KD PROTEIN S		133.300		Ī		l			+	T
PYOT ECO.	HYPOTHETICAL 27 1 KD PROTEIN		132-159			T		l	-	t	T
	HYPOTHETICAL 21.3 KD PROTEIN	2	13-40					-		t	T
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	HITCHELIKAL SA LKUTKOILUM	ESCIENCHA COLI	300.576					-	\mid	H	Τ
PYDE SCOT	MYDOMOTOR ALARD BEOTEN		13:138	1						-	Γ
PYHON ECOL	HYPOTHETICAL 16 9 KD PROTEIN		7	7							
PYING ECOL	HYPOTHETICAL II I KD PROTEIN	B COMBRONIA COL		Ž.	201.724	1	1				
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PYHZ ECOLI	HYPOTHETICAL 15 9 KD PROTEIN		1	T	†	1	\dagger	1	1	1	Ī
PVIIP CCOL	HAPOTHETICAL 32.4 KD PROTEIN		2	İ	T	I	\dagger	+	+	1	T
THE PERSON	HYPOTHETICAL 9.6 KD PROTEIN		18-71		l	l	l	+	+	t	T
TOTAL BLOCK	HTTOINETICAL 18 & KD TROTEIN		136-163					+		+	T
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1 0 1 0 1 A	HANDING TICKE 13 1 KG BEGTER	ESCHENCHIA COLI	2						-	┞	T
PYLLP ECOL	HYPOTHETICAL ALA RO PROPRIM		7						L	ŀ	Γ
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PYISP BACE	HYPOTHETICAL 43.1 KD PROTEIN		912-339	t	F	t	\dagger	\dagger	+	+	I
PYIAG ECC.	HYPOTHETICAL 23 6 KD PROTEIN			T	t	\dagger	\dagger	\dagger	+	7	J
TAIN ECO	HYPOTHETICAL 20 4 KD PROTEIN		1111		t	t	t	\dagger	+	†	Ŧ
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TOUR PLAN	AMOUNTAIN AND PROJECT		10-51					-	-	+	T
PY/BO ECOLI	HYPOTRETICAL 15 3 KD PROTEIN	ESCHERONIA COLI	\$				Н			-	Τ
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PYKS ECOLI HYPOTHETIKAL 11.1 KD PROTEIN		346-396						
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PYLPA YEREM YLPA LIPOPROTEM PRECURSOR	YERSINIA ENTEROCOLITICA	164-231			-	-	-	L
PYLTS ANAVA HYPOTHESICAL 23 6 KD PROTEIN	ANABAENA VANJABILIS	177-199	-			-	L	-
PYLUD LACLA HYPOTHETICAL 39.7 KD PROTEIN		27.0			-	ŀ		-
PYNEZ BACSU HYPOTHETICAL 151 KD PROTEDY		2:3	_		-			-
PYMOS MYCCE HYPOTHETICAL 114 4 KD PROTEIN PRECURSOR	ION.	16-03 159-193	3 420-445	941-1001	t	-		-
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PYOND ECOLI INTROTHETICAL 31 4 KD PROTEIN >	ESCHERICHIA COLI	17.5	-			-	_	L
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PYOTA ECOL! HYPOTHETICAL 150KD PROTEIN		13.44						
PYONE ECOLI HYPOTHETICAL 93 SKD PROTEIN	ESCHENCHIA COLI	231:348			-			Н
PYOR ECOLI HYPOTHETICAL VIND PLOTEIN		43-62	-					Ц
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PYORA LISMO MYPOTHETICAL 25 6 KD PROTEIN :-	GENES	11:11			ŀ	\mid		ļ
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FILENAME	PROTEIN	ORGANISM	14334		LABEAL	17.10	AREA S AREA 6	ASEA	AREA! A	ARTAI	AREAs
PYTOK BACSU	4 ×	BACBLUS SUBTILIS	244-271	179-106							
PYTHE LEPBI	HYPOTHETICAL 23 KD PROTEIN	LEPTOSPIEA BIFLEXA	(11.11)								
PYTE LACIA	HYPOTHETICAL 13 3 KD PROTEIN	LACTOCOCCUS LACTIS	36-112								
PYTH BACSU		BACILLUS SUBTILIS	15-44								
PYTSF SPICE	1	SPIROPLASMACITIU	102-149								
PYX04 BACSU	τ	BACKLUS SUBTRUS	13-64	\$6.69							
PYX06 BACSU	7	BACKLUS SUBTILIS	142-169								
PYXIJ BACSU	1	BACILLUS SUBTILIS	11.51								
PYXIS BACSU		BACILLUS SUBTILIS	165-169	697-798							
PYXII BACSU	KIN BACSU HYPOTIGHICAL 66 8 KD PROTEDY	BACILLUS SUBTILIS	1.10	19-96	94.143						
PYXIS BACSU	HYPOTHETICAL 31 J KD PROTEIN	BACILLUS SUMTILIS	\$6-03	15-112						Ī	
PYX30 BACSU	HYPOTHETICAL 1) 1 KD PROTEIN	BACKLEUS SUBTILIS	34.58								
PYXII ANASP	HYPOTHETICAL 18 9 KD PROTEIN	ANABALNA SP	13.104								
PYXTE CALITY	LINYPOTHETICAL IN THE PROTEIN	CALDOCELLUNI SACCILANDLYTICUNI	9.39								
PYKYC CALSA	NYPOTHETICAL PROTEIN	CALDOCELLUM SACCITAROL PTICUM	41-94								
137E1 ECOLI	HYPOTHETICAL 16 9 KD PROTEIN	ESCHENICHIA COLI	16:31								

WO 96/19495 PCT/US95/16733

TABLE IX

107 X 178 X 4 SEARCH MOTIF RESULTS SUMMARY

FOR ALL HUMAN PROTEINS

PCT/US95/16733

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PASH'S HUMAN ASPANGENE STRINGTASE (OLUTAKING-HYDROLYZING) (EC 4.3.5.4) (15)	CELL 311.338	347.334							
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PATPE HUNAN JATP SYNTHASE & CHAIN, HUTOCHONDAIAL PRECURSOR (BC.) 61.34).	139-163				Ī		Ī	1	
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PBIAL MINAN BETALLADRENERGIC RECEPTOR	202.310	1111			Ī			Ī	
ſ	1111-1001 (71CON)				ľ	Ī	Ī	ŀ	
		535-362	969.69		Ī	I	I	F	
PBANT MIMALN EXYTHROCYTE BAND 7 INTEGRAL MEJABIAANE PROTEIN.	104-146	Į –						Ī	
PRASO MONAN BASOMICION.	130-141	16.31	13.103			Ī	I	F	
POCID HUMAN ITLANSFORKING PROTEIN DCL.4:BETA	118-205					Ī	l	Ī	
PECER MINERAL BACELL GROWTH FACTOR PRECURSOR (PCGF-12 KD);	1143							ŀ	
PBCN HUMAN BREAKPOINT CLUSTER RECKON PROTEIN	104-025								
	346-350	504-53						F	
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PCAP RUMAN CALLAM PS, LARGE CATALTICS SUBURIT (EC.) 4.23 (7) CALCIUM.	674-701							H	Π
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PCCEME	103.178.4 Motif Storeth on All Houna Protein Commen									
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PCATA INDICAN	M CATALASE (BC 1.11.11.6)									
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THE PARTY OF THE P	LAMBOATPETIDASE B PRECINSON (EC 14.17.1) (PANCREAS-SPECIFIC PROTEIN)	1	191.161	¥7.				1		
	LANGUATION OF THE PRECURSOR (EC.) 4.17 (9) (CANBOXYPEPTIDASE E) (CPE)	18.58			Ī				•	
	LUCE HOWOLOG (PLCCCI) (FRACIABIVE)	3	Ī		1					
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PCD4X HIBAAH			113-217	İ	İ	İ	İ	T	Ì	
NAMA ACT	12 CHI T THE LY CHI WASHINGTON THE CURSOR (CDAVE) (PHAGOCY TIC	136-155			T	Ì	1	1	7	
PCDS3 HEMAN	LETHOCYTE LIBEACE ANDICES AND CONTROL STATES AND CENTROLING OF CHILD STATES AND CENTROLING OF	46-31	26.367	T	ľ	T	t	1		T
PCD7 HENAN	BATTI MERENDA VICE AND LANGUAGE CO.	17:114			İ	İ	İ	Ì	Ì	1
PCDKJ HUBAN	CELL DIVISION PROTEIN PRIVATE SPECIAL	118-177			İ		\dagger	1	1	
PCDK! HILLAN	CFL DIVISION PROPERTY OF A SEC.	22			T	T	t	T	1	Ī
POEM HULLAN	CCAATOWAANCE BROOM SECTION (KINASE PSSALRE)			İ	T	Ť	\dagger	1	1	
PCENTE HISLAN	MAJOR CENTROLOGIE ALTONATION BEIN (CERT BETA) (NOCIEAR FACTOR	394-330				T	1	†	+	
PCIDIC HUMAN	CRATROMENT PROTEIN C (CRAP.C) (CENTRALAGE LIPELINE) (CENT.B)	36.30				T		1	†	
PCENE HUMAN	ENTROMENC PROTEIN E ICEND E PROTEIN	┪	٦					T	T	Ī
,			493-520	13.407			650-654	8.00	1007190	1 1 V
		2	36.23	1179-1239 1250-1277 1340-1367	100-1301		1466-1555 1646-1620 1550-1574	46-1640		1 9 Ce . 1 6 A C
PCERU MOMAN	CERULOPLASADY PRECURSOR (EC. 1 16 1) INFERENTIALES	1832-1883 1890-1917 1940-1988	200	940-1988 20	2021-2048 2	2300-2310	2440-2476 2498-2963	11.2361		
PCETP HUMAN	CHOLESTERY, ESTER TRANSPER PROFEIN PRICINGOR							t	\dagger	Ī
NOTE HOME	CYSTIC FIREOSIS TRANSMENDRANE CONDUCTANCE REGULATOR (CFFF)							l	t	I
PCOCC HUMAN	COMP-CATED CATION CHANNEL PROTEIN (CYCLIC MUCLEOTIDE	7	т	7	243.1370				ľ	Ι
ACC. HERVA	CYSTATIONING CANDIALLYASE (EC 4.4.1.1)		1					ŀ		
DOL HOUSE	CALCADECONG MEDUCTASE (EC 1.1.1.223) (CDA).		1	1			-		T	T
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MAN HONO	CHOROLDEIA ANOTEIN (TCD PROTEIN)		т							Γ
A ROLL	SOUTH CHANNEL PROTEDY, CANDIAC AND SKELETAL MUSCLE ALPHA-SUBUNIT	Т	80.18	1	1	1		H		
A Mark	CLATHOLD LIGHT CHADY A (BRADY AND LYAPHOCYTE LCA)	Т		\dagger	1	1	1			
A HEAVE	CLATHOLIN LICHTI CHAIN & (BILAIN AND LYNCHOCYTE LCB)	100	t	\dagger	†	1	+	1		Γ
A HOME	CALCYCLEN (PROLACTEN RECEPTOR ASSOCIATED PROTEIN) (PRA) (GROWTH	2	t	1	†	1				Γ
	CLUSTEUM PRECURSOR (CONDITENENT: ASSOCIATED PROTEIN SP-40,40)		23.150	191.18	1	1	1			
THE PERSON	CHROMOGRANDIA A PRECIDENA (COA) (CONTAINS PARCHEASTATIN AND WE IS	L	╁	+	\dagger	†	1	1		Π
NAME OF TAXABLE PARTY.	CILLAKY PRUKOTKOPIOC FACTOR (CNTF).	7		\dagger	\dagger	1	1	1		
	NATIONAL MATERIAL ANTIGEN COATS	2	-	1	\dagger	1	1	1		Π
		242.276 59	Ī.	197:163	\dagger	\dagger	1	1		
PCOS HIDAAN		292-1319	T	t	t	\dagger	\dagger	1	1	
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PCD1 HUMAN		367.398				\vdash	t	t	\dagger	T
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PCOX! HIMAN	PROTEIN COMBANDER FOR VERPTIDE LIKELI 6 1 11	ARCAL	PER	AKEA	3	Ž V	4		т	
PCP WILLIAM	CYTOCHROAD PARK VILOURIES RATEROL 1. AL PILA MONDON VIENA CEN		166.491				Ī		1	
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		231-238								
A NOW AND A SECOND	CARBANOTI, PHOSPHATE STATHASE (AMONTA) MOTOCHONDRIAL PRECURSOR	3	Ž							1
	_	410-437	•							
POT MINA	CYTOCHOME PAIN APILA! (MADCIT) (EC 1.14 99 9) (STENDID 17-ALPHA.	186-255								l
PCPVI HUMAN		125-271								
PERS HILLIAM	CONDITIONER RECEPTOR TYPE 3 PRECURSOR (CRJ) (COMPLEMENT C1D RECEPTOR)	(101-106)								
PCACH HOMAN	COLONECTAL MUTANT CANCER PROTEIN DACC PROTEIN	1	376-230	11.4%	3,4,3	61.76			ŀ	
POLES HUMAN	ICAMP RESPONSE ELEMENT BINDING PROTEINS A AND BICCUEB. A AND CRED. BY	1							1	١
MANN CARD	TALE BROKENER RESERVE BROKEN PROTECT CRESSE								1	l
77777	CONTRACTOR DESCRIPTION OF THE PROPERTY OF THE								1	
200	Charling Motern Precurator			i	!			1		
TOWARD TOWARD	CLEAVAGE SIGNAL I PROTEIN (CS-1)	203-233							•	
PCSF1 HUMAN	_	143-170								
PCST3_HUMAN	CLEAVAGE STRAULATION FACTOR, SO NO SUBLINIT (CSTF SO ND SUBLINIT) (CF.)	1(-9)								
PCTNA HUBAAN	ALPHA-CATENIN (CADMERIN-ASSOCIATED PROTEIN)	114:11		İ				I	ŀ	ļ
PCTRK HUMAN	ALPHA-CATEMIN RELATED PROTEIN (CATEMIN ALPHA-1)	610-717								١
POST REPORT	DAP AMETION BETA-2 PROTEIN (COMMEXIN 26) (CX26)	100.130						Ţ	Ī	l
PCX12 HUMAN	PCKUS KUMAN IGAP MACTION BETA-1 PROTEIN CONNEXIN 331/CX331/GAP LUNCTION 31 KIS								Ţ	
CX1) HIMAN	GAP INCTION ALPHA - PROTEIN COMMEXIM 331 (CX 57)		Ī						·	
KANIS KUNAN									I	
TANK IN		٦.	177	30, 00,					1	l
	CONTRACTOR AND THE PROPERTY OF	1		B. (-).						
STATE STATE	WANTEN CTELASE SULUBLE, ALPHAS CRAIN (EC. + 0 1.2)									
CYGA MUMAN	RETINAL GUANTLYL CYCLASE PRECURSOR (EC 461.2)	25.5								
CYRO HUNAN	CYTOKINE RECEPTOR COMMON GANDA CHAIN PRECURSOR (GANDIA-C)	26)-130								
CYTA HOMAN	PCYTA MOMAN CYSTATIN A (STEFIN A) (CYSTATIN AS)	_							-	
DEL HUMAN	PROTO-ONCOCENE DBL PRECURSOR (CONTAINS MCF2)		485-524	164-79)	841-101					
PDESM MUMAN	DESAID	133-110	112.312			_			ŀ	
DESP HUMAN	DESNIOPLAKIN I AND II (DPI AND DPII) (FRACAIENT)				115.465	115.434	497-469	331.331	¥5:19%	6)6-654
		167-734	118-710	1436-1493	1506-1515				F	
DKA HOMA		11-50							F	/
DAD MAKK	DYSTROPHEN		138-365		111.110	976-1003	1013-1030	1201-1021	1	
		1838-1888	1150.2105	211.2343	2752.2779	2786-2830	37.47.	10(4.)041	111111111111111111111111111111111111111	١
PDNU HUKKN	ı	2.5							I	l
PONT HUMAN		18.50 18.00	35.391	951.55			Ī		Ī	l
POPOA HUMAN		2.5	99-1037	1100-1137			Ī	Ī	† 	l
POPOD HUMAN		25.32					Ī	Ī		l
POPE RULLAN	DEPETENT PEPTENSE IV (EC. 1.4 14 5) (DPP 11/) (T-CELL ACTIVATION	r		Ī				Ī		l
PORN! MILLAN	DEDXYPLOONUCLEASE PAECINSON (EC.) 11 11 (DMASE))	T		I			Ī	Ī		l
POSCH MIMAN	DESMOCULLO JAMA PRECURSOR (DESMOSOMAL OLYCOPROTEIN II AND III)	L	146.18						1	
HANN IOSON	DESARCE BIN I PRECINCO (DESARCOMA). CLYCOPROTERA IL MICH	Т	Т	401.411		I	1			
POSOS RUSKAN	DESCRIPTION OF PERSONALING ND PRACHICALS VILIDARIS ANTICENTIVAL	Ţ.	Т						1	1
NYMEN CHO	DIVERGENT IPSTREAM PROTEIN (N.P.)	1		1					1	
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STATE OF STA	IRAC AMERICA SEATER AND RESPONDENCE OF CENTS		I							
ATTENDED TO SELECT			1							
	ELUNCATION FACTOR FACTORIAL	2								١.
PEND MONEY	ELONGATION FACTOR (-OELTA (EF-1-DELTA).									
TEGTA MUMON	EPIDELMAL GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112)	5	140-467							
TEGT RENAM		47.74							Ī	
PELFI HUMAN		1187166						l	Ī	ŀ
PENOR, HUMAN		1	100				Ī	Ī	Ī	
PENVI KUMAN	ARTROVILLELATED ENV POLYPROTEIN.	383.470							T	
FERC MUNICIPAL IN	IS BYSILON CHAIN C'REGION.	101-101						Ī	Ī	ľ
PEPIND RUMAN	POROLHOIC			249-283					Ī	
YEATH MENAN	PROTEIN DISTALIDAE ISONGRASE RELATED PROTEIN PRECURSOR (ERPT)	28.83	143-160	\$87757					l	
PREFIT MEDIAN	DAM BYCHON BEAM PROTEIN BECC.						1	1		

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THE PERSON NAMED IN	FACESCAN REPAIR PROTEIN ERCC-6	50.00					4	4	1	3
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THE PARTY OF	EMECINE DES PRECINSOR (ET.2)	35.58	Ī	Ī				1		
NAME OF THE PERSON NAME OF THE P		182,300	Ī	Ī	T		1		-	
FEYZA MIRAN			1	1	7					
PEZZI HUMAN		┪	Т	ı						
TAS JUMAN		-	200	4776	525.53					
PFAL HURLAH	ı	=1								
PLAS HOMEN	COACILATION PACTOR IN DESCRIPTION CONTINUED TO	$\bar{}$	1007-1034 1194-1230	194.1230				Ī	I	
PFASI HILLAN	т.						T	Ī		T
PLASA HOMAN	A POPTONIE MEN AND FINE FOR	<u>=</u>				Ī	Ī	1	T	1
7777	CONTROL MAN SURFACE ANTIGEN FAS PRECURSOR (APO-I ANTIGEN)	Г	249.301	100					-	
TANK TO SE	LOW AFFIRMTY PROMUNICAL OBULLIN EPSILLON FC RECEPTOR (LYAPHOCYTE IGE	T	+						~	0.00
NO.	HIGH AFFORTY BOARDOCLOBILIN EFSEION RECEPTOR ALPHA-SUBLINIT JECERTI		Ī	1						
PICK HUMAN			1							
PEBA MIDAN	FUNDOCEN ALPHA CHADA PRECURSOR	7							1	
PERSONALAN	PIDALMOGEN BETA CHAIN PRECURSOR	Т	2					Ī	1	
PFIDG HUMAN	FIBRINGOEN GANDIA-A CHAIN PRECINSON	٦						Ī	-	T
PERH HUMAN	PIBRINGCEN GANGNA-B CHAIN IT BIRTHOCHN CALALAN	1	8					Ī	ŀ	
PEINC HUMAN	FIBRONECTIV PRECURSOR		32.2				l		1	I
PLI HUMAN	FLL-1 ONCOCENE (SECOR TRANSCERPTION SACTORS)	2101-2199					ĺ	Ī	1	T
FIAD) MILLAN	DOG THALAND DE MONDONYGENATE ALANING FALLINGS SEE	┪					T	T	ļ.	1
FOS HADALAN	PSS-CAOS PROTO-CONCOCENTE PROTECTAL	┪	28-210	301-328		T		Ī	T	I
PILA I HUMAN		6:30					T	T	T	
THAS RUBERT	POSABLATED ANTIGEN 3	23-166						T	I	I
FUEL HONON	FEMULIA KEANY BUAN	169-180				T	T	T	I	I
THE MINN	FEMILIAN DAM	2					T	T	1	T
TSHE HUBLEN	FOLLICLE STIMULATING NORMONE RECEPTING DEPONDENCE AND	-					l	l	Ť	I
PUCO HUNAN	1000	364.393						T	t	I
FLACH HUMAN	ACOSIDA SE		1					l	t	I
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DIPP HULLAN	PROTEIN KINASE C SUBSTIANTE, SO KO PROTEIN, HEAVY CHAPS PRECEDI			1					ŀ	T
POST MINAN	GLUCOSE G-PHOSPHATE ISOMERASE (OPI) (EC. S.) I 31 (PHOSPHOCL LICOSE			1						I
G732 HOMAN	MAJON CASTROPITESTINAL TUMOR ASSOCIATED PROTEIN GASSS. PRECURSOR	1	\dagger	†						
CALL RUNA	CALACTORDIASE 2 (EC 2.2.1 4).		\dagger	İ	1		1			
	CANDOL-AUDIO DE TRUC-ACID RECEPTOR ALPHA-1 SUBUNIT PRECURSOR (GABAIA)	16.33	t	T	1	1	1		1	
CASS MEMAN	CASTRIANCE CONTROL TARCACIO RECEPTOR ALPHA-3 SUBUNIT PRECUTSOR (GABA(A) 211-333	183	r		T	T	1	1	1	
	CIANNE MY EQUIDS BROWN 177E B ALCEPTOR (CCR. 8 ALCEPTOR)	15.105	-	l	T	T	1	1		1
		\$ -20	I	\mid	t		\dagger	1	1	
	CHANDE MET BOTTOS BRODES ROTES FOR ALPRA SUBURITY	22-49			l	T	1	†	1	1
COAL REPLY	QUANDE KILL TOTTO BENDEN CALL ALTAR TOBURIT (CIT) ALPHA.))	22-49				\dagger	\dagger	†	1	T
GBAY MUMAN		2				l	I	1	T	T
CBB) HUMAN	GUANDE MICLEOTIDE BINDING PROTEIN CHINGS WITH REFA THEIR AT	#	1					t	T	
UBLY HUMAN		7	Т	1			-	l		T
		10-01	22.55	200			-	l	t	T
-		1	1	1					t	Τ
S RIMAN	OCHICH SEQUENCE DRA-BRODING FACTOR (GCF) (TRANSCRIPTION FACTOR 6)	T.	Т	7	7			-		I
POCH HUNAN	DIP CYCLOHYDROLASE I (EC 1,5 4.16)	Т	291-120	ž.	196-421	647-674	-	\vdash	1	T
NA MINAN	ALLICOCORTICOD RECEPTOR, ALPHA (CA).	7	1	1	4				1	T
	T	10.00	1	1	1		Н			Τ
-	PRECURSOR (EC 1,44 2)		+	+	1					Ī
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	CERLEDIG FACTOR) (ADF)	1	1	1	1	+		-	-	T
		7	146.134		1	1	+			Γ
NAME OF THE PARTY	Ī	T	7~	-	t	1		1		
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	THE STATE OF THE S	32.59 344	144.331	ł	\dagger	+	\dagger	†	1	I
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PHELIA MANAN	UROPORPHYNDWOOLK-LII SYNTHASE (EC 4.2.1.75) (UROPORPHYNDWOOLK-III	=======================================	-				ĺ	ŀ	
PHEET HENAN	HEPABLY COPACTOR IS PLECUASOR (AC.II) (PROTEASE INVESTOR LEUSERIEM 1)	100 IN	l				Ī		
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PIEXA KUMAN	BETA HEXISTALIONIDASE ALMA CHAIN PRECURSOR (EC. 1.1.1.31) (N-ACETY).	396-343							
PICTO MUNAN	BETA-HEXIOSANDMIDASE BETA CHAIN PRECURSOR (EC. 1.1.1.1) (PLACETYL-BETA-	38415							
PIOCKS HUBANN	HOWEOBOX PROTEDN MSX-1 (NOX-7).	176-212							
PHOFA JEMAN		67.7							
PHO! KULLAN	HENG OXYCEVASR I (EC I. 14.99.3) (NO.1).	191.234	1		$\frac{1}{1}$		Ì	1	
PIETO KINA	ANDROXYMENTLYTOVATE DIOXYGENASE (EC.13.11.27) (MPPU).	111	7			77.00	1000	1	
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HIVE MINAN	IS HEAVY CHAIN PRECINSOR V-II REGIÓN (AUH-T).	101-69						r	
PHYST JUNEAN		47.74							
PICK HENCAN		261-289							
PHOOD, HOLLAN	-	135-162						-	
PAN RUMAN	-	23-40	·						
PERFORMAN	-	113-210					П		
PICE HUMAN	PLASUA PROTEASE CI IMMINITOR PRECUNSOR (CI INN).	111:31							
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PITAM HUBLAN	CELL SUNFACE OLYCOPROTEIN MAC. I ALMA GIRII INTERFERINGE CO.		310-341	793-122					†	T
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PITTE MEMAN	CELL SIMPACE ANYONING WOODS SEED TO THE COURSE BETA-1) (CD29)		154.38		l	T	T	1	1	7
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PRICO HUMAN	CRATIN TYPE CYTOSKELETAL 19 POPONER APRIL 19 ACT	┪		-	ŀ		t	\dagger	1	T
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PKZKI JRUKAN	KENATOL TYPE II CYTOKERI KTAI ACETA		346.384 390	190-060	-	l		\dagger	1	1
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AN INC.	WAAPTA CHEGION	37.63	1	\dagger	1	1	1		\vdash	Γ
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PETER MENAN	MACES UNHACE THE STANDARD AND SET OF COMMON (SET 27.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1	Т		T					T	
PKSTN HUKAN	PROPOSONE TYROSINE PROTEIN KINAGE FYR (EC. 1.1) (1954)	1	Ī	I					1	l
PKOPE HUMAN	COMP DEPENDENT PROTEIN KINASE, BETA 1502 YAG (COR) (EC 171.17)	7.5								
PKIGK HUNAY	I TYNOSDIE KDIASE VEK NECEPTOR PRECURSOR (EC 2 ? 1.112).	1	Ī							
PKENH HUMAN	KINELIN HEAVY CHAP.	125-135	435-452	471-542	633-610	619-716	872-899			
PKKT HUMAN	KIT PROTO-CNICKEDE TYROSINE KINASE PRECUNSOR (EC 2.1.).112).	235-263								
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A MANAGE	INTELLERUNGHOUSE, DOUBLE-STRANDED RIA-ACTIVATED PROTEIN KINASE	7	ê	2022						
MAN MAN	PUTATIVE SERMETROCOME.PROTEIN KINASE P71 (EC 2.7.1)	\$]						-	
PICTO, MUNA	CPC_PRIMADA PROTEIN KROASE C. STA TYPE (EC. 17.1) (MPKC-STA) (PKC-L)	┪							1	
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TATAL MARKET	INTRUVALE KENASA, MI (MUNCLE) INCETME (EC. 1.7.1.40) (CT 1050CK) THYROTO KNOWING THE CONTRACTOR OF A 1.44.	Carrier Carrier	1		I			I	-	١
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PKACK MINAN	ILOS PLOTO CONCROTOR TYROSONE KINASE (FC. 2.2.) 1131 (FLACIONIT)	197.481						Ī	Ţ	
PKSAC HUNAN	PROTO-COCENE TYROSING-PROTEIN KINASE SAC (EC. 2.) 1,112) (P60-3AC)	35.130	T	Ī		I		T	Ī	
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PLEAT HEAVEN	PHOSPHATIDY CHOLNE STRICK ACT. TAXHST EXAST PLECINSON (EC. 1.) (4))	T					I	Ī	Ī	
PLDIST RULLS	LLACTATE DENTOACCEMASE HICKON (EC 1.1.1.27) (LDH-B).	F	625.20			Ī			F	İ
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H DLA MUMAN	ILOW DEWITTY LIPOPROTEIN RECEPTOR PRECURSOR.	915-640								
A HOLL	ASIALOGLYCOPROTEIN RECEPTOR I (ABPATIC LECTIN RI) (ASOPR).	84.59							·	
TO MUNICIPALITY	PASELECTIN PILELUNGUR (URANIOLE MENERALANG PROTEIN 149) (UNDA 140) (PAUCIEM)	4.5		Ī		Ī				
NAME OF STREET	LENELANDA BAGINTINA Y RACTOR MERCHATOR (LIST RISERRANDANA).		T		T	Ī			Ī	
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PLES HULLAN	HORNONE SENSITIVE LIPASE (EC. 3.1.1) (HEL).	1	П							
PER ROAN	HINDROPAENT AN HYDROLASE (EC.) 3.24) (LTAN HYDROLASE) (LEUKOTHENE		20,24							
PLACE HOMAN	LAMININ A CHAIN PRECUSOR.				134-193	124-123	1963-1999	2026-2059	2017162	
TANK MUKAN			_	101-160	1031-1714	127-1781			1	١
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PLOXU HUMAN	TABACKEDONATE S-LIPOXYGENASE (EC.1.13.11.34) (S-LIBOXYGENASE) (S-LO).	60	T		T		Ī		T	
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PLAYS HUNAN		191 91	1676				Ī		Ī	
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PLEUZ HUMAN	MOTEDICTYLÖSENE PHOSPILATASK ZETA PRECURSOR (EC 31.).41) (PTP-ZETA).	35-587	1034-1051	1973-2000						
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### 1950/18 (#C.2.11.43)(4-0- 91-119 191-1	STEACER RC 2 1.63) (4-0-6) 13-154 15-157 51-458 15-157 51-458 15-157 51-458 15-157 51-458 15-157 51-458 15-157 51-458 15-157 51-458 15-157 51-458 15-157 51-458 15-158	AND MAKE	MERCESIN HEAVY CHAIN (LAMININ CHAIN AS) (FRAGMENT)	T								
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PAUSI HUMAN MUNCHED	П	101-18	e€.330		t	t	T	1	Ť	T
	7	_	161.318				T	T	T	T
-	(EPSTEIN-BARR VIRUS SMALL BNA ARROCKLAFE)		170-400	H						T
PALZS HUMAN 605 NBOS	Τ	Т	61776		1					
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PCCEME	107217816 Moil Search on All Homan Protein Sequences	П	H					П	П	П
DIE KAME	PROTEIN	I	AREA?	7	1	AREA AREA	1	3	AREAL AREAL	4
PRI AC HIBAN	MAS ACROSS BEING PAGE 18 P. S.	1	T	T		T	T	T	$\{$	
NEW PRESENT	19 FO BO PR. I FIN COCKER CYNDROME TYPR A ANTRONIC CAN	۳	177	T		Ī	Ī	T	F	Ī
PROV. M. PAAN		۲		T	T	Ī	Ī		Ī	Ī
PROC HUNAN	CI AND HARNE	1	T	T					I	Γ
PIOL MOVEN	т-	501-528	-							
PROU HUMAN	METEROCEMOUS ASSIGNACE SOMETHIN U.	Т	Т							
PATHE HUNAN	DNA-DEECTED INVA FOLYMENASE II 313 KD POLYMENTIDE	Г	65.789 R	106.64	1314-1341	1316-1398				
PRPB3 HOMAN	DNA-DRECTED ANA POLYMENASE II 140 KD POLYPEPTIDE	(99-989	1004-1016							
PRPD) INMAN	NAA-DIRECTED RNA POLYMERASE II 33 KD POK YPCP FIDE					•				
PREXA HUMAN	LETIMOSC ACID RECEPTOR EXC.ALPHA.	311-352							_	
PRUCE HUNAN	RETINGIC ACID RECEPTOR RXR-BETA ISOFORM I	176-403							ŀ	
FULKE HUMAN	ABTIMOIC ACID RECEPTOR EXPLIETA ISOFORM S	- F	<u>-</u>	i	:	İ			:	:
PRESS HUMAN	468 RIBOSOMAL PROTEIN SIZ	2	Ì	İ	!				ŀ	
PKS14 INDAM	46S RIBOSOMAL PROTEIN SIG	11:00	İ	Ī			Ī	Ì	1	!
PRESS INDIAN	405 RIDOSUNIAL PROTEIN \$15	:53							٠.	
PRS27 MISAN	405 RUBOSONIAL PROTEIN 327A	1	Ī	Ì						Ī
PRST HUMAN	•	8	İ	Ī] :	Ī				
PASS HIMAN		1	1	:	:	-	:	:	:	:
PRTCI KUMAN		200	!	Ī	: :		ĺ		Ī	1
PRUIA HUMAN	UP SALALE MUCLEAR ABONUCLEOPROTEIN A (UI BYRAY) A PROTEIN	1	Ì	Ī	Ī	Ī		I		
PRUZE MINAN	UT SMALL MICHEAR MINORUCI EOPROTEIN D'	1	Ī	Ì	Ī	Ī				
PRYOR MALAN	BYANDING BECKETCH SESTETAL ADJECTS	Ŀ	161.191	169.04	1110	120.2147	1104.1111	1529.1154 1012.1010	1012.1010	1007-1607
AVVIO VOI		Т	т	Т						
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2112	ANGENERAL MANAGEMENT OF THE TAIL THE ANGENERAL MANAGEMENT		İ	Ť	T	Ī	Ī	1	T	
TANK HOME	AMERICA TURORICA TOTALIA ASE (EL 1711) (PAMERICO TURORICA TOTALIA EL MANAGO DE CARROLA MANTA DE AMERICA EL TOTALIA DE CARROLA DE AMERICA DE AME		Ì		T	Ī	Ī		1	I
7777	INCIDENCE THE PARTICULAR ANTICEMACIONAL PROPERTY.		Ì	Ī	T	Ī	Ī	T	ŀ	T
NAME OF	ATEM CFIL FACTOR PARCHAGOR (SCF)	100	T	T	T	T	Ī	Ī	Ī	T
PSEAT HUMAN	EMEMOCREBY I PROTEIN PRECURSOR (SGI) (CONTAINS SEATINAL BASIC		25.74	50.00	134.368		Ī	Ī	-	I
PSENCE MENANTS	DAPAGCELIN II PRECURSOR (SGII)	Γ	Т	304.355	L	100		Ī		
PSET HUMAN	ET PROTEIN.	Γ	1	Т	Т		Ī	Ī	T	
PSG1 NUMAN	SECRETOCALATIN I PRECUNSOR (CHAROMOGRANIN B)	14:136	П						Γ	
PSG1 HUNUN	SECULTOGRAPH II PRÉCURSOR (CHROMOGIANIH C)			34.8						
PSIAL HUMAN	BONE SIALOPROTEIN IS PRECURSOR (BSP 11)	14-113	185-193	36.283					Γ	Γ
PSYLL HUMAN	POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SHF1L	101-101	148-573							Γ
PSINCE MUMAN	SKLILELATED ONCOCENE SHON									
PSPCA MUDAN	SPECTION ALPHA CHAIN.	-	370-621		8	1000-1126 1461-1502	100	148-7022	3120-2154 2323-2256	21:13
		न	- 1	-1	Т					
L L	IPECTUA META CHAIR EXTINGUETTE		060-01	026-910	200	1207.10	027-1083	1287-1324 1347-1374 (1854-186	2	2 2
TANK MANAGE	SECTION FOR THE PARTY OF THE TOTAL COLUMN TO THE PARTY OF	T	197.947			Ī	Ī		I	
MANAWA WASA	RECEPTOR ALPITA SURIDANT COLLAI PHAS	Т		T	Ī		Ī		T	
PITE MAKAN	ĺ	122	T	1	Ī		Ī	l		T
PETICA MINA	STATIONAL PHOSPHOPROFEN PLY IONCOPROTEIN PLY CLEUKEARIA-ASSOCIATED	×.:	T	T		Ī	Ī			T
PSUNS HUMAN	SINCHASE SOWALTASE INTESTINAL (BC) 2 48)/ (BC) 2 10)	1348-1735	l	İ	Ī	Ī	Ī		Ī	Ī
PSYTE HUMAN	PRAPTOBLE VIN I.	2	T	ľ			I		Ī	
PSYTO MUNICIPALITY	PSYDS HIDAAN LASPARTYC, TRINA SYNTHETASE ALPHA, 3 SUBURIT (EC. 6.1.1.13) [ASPARTATE.	16-7	l		Ī	Ī		Ī	Ī	T
PSYED MUNICIN	3	134.20	140-771	Ī			Ī	Ī		T
PSYH HUNN			464.502			Ī				T
PLYTI HUMAN	SYNATIOT AGAIN I (PSS).	140-167	130-277	Ī		Ī	Ī	Ī		Ī
PSYTC HUNAN	HOLONYLTANA SYNTKETASE, CYTOPLASMIC (EC 6 I 1.3) (THULONINE-TANA	r	519-05	T	Ī		Ī			Ī
PSYV MUNCH	VALYI-TIMA SYKTHETASE (EC 6 I I.9) (VALINE-TIMA LIGASE) (VALRS).	П	41340				Ī			ŀ
PENY HUMAN	triptomanyl-trna synthetase (EC 6.1.1.1) (tryptoman-trna Ligase)	П	196-123							
THE REAL	TA CHADA (TFITE-BETA).	7		1			1			
MAN HUMAN	PTAM HIMAN ITTANSCULTION FACTOR APA (FRAGMENT)		243.27	1	1	1	1	1	1	١

PCCENE	1971 1784 Moul Search on All Haman Presen Seguences									
THE NAME	_	AREAL	ANTA	ARFAI	AREA A ABEA 4	т	7.4.4	, , ,		
A STATE OF THE PARTY OF THE PAR	TRANSCULTION FACTOR JUN-B	1				т		1	-	
NAME OF THE PERSON OF THE PERS	THAMSCHIPTION FACTOR RUND.	291.33						Ī		
TAN MUNICIPALITY	PACK ROTUBULE - ASSOCIATED PROTEIN TAU	271.305								
TANK MUNICA	MUCKUTUBULE-ASSOCIATED PROTEIN TAU, FETAL	111:111					,			
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	I CAN'S UBALLANTIN I PRECURSOR	192-102	30.33		Ī					
1000	COMPLEX PROTEIN ((CP.1)	(14.91)						I		
PTER HIDIAN	BECEROON TOTAL MONTHE POT AND THE SECOND (TERMINAL ADDITIONENTY NEW	61.93	Н							
PTEN LINEAL	THE STANDARD THE STANDARD SET THE CASON (EC. 7.1.112) (HPK-6)	(44.671	969.04	1007-1036					i	:
7	ANALYSIA MARITALIAN PACTUR (18110)	135-162								
7	INAMELIATION PACTOR ET (PILAGRENT)	0(1)	172-149	178-226			Ī	I	ŀ	Ī
777	I MANAGAR I BON ELUNDATION FACTOR S.II.	34.76	١						F	
NO.	INSUE FACTOR PRECURSOR (1F) (COAGULATION FACTOR HI)	₹-173					T	Ī	Ī	T
NAME OF THE PERSON AND ADDRESS OF THE PERSON	TANNSFORMING GROWTH PACTOR BETA I PRECURSOR (TCP-BETA I)	1	T	Ī			T		T	1
TO SHOW YOU	TRANSFORMING GROWTH FACTOR DIETA & PRIECURSON (TGF-BIETA 2) (CI. ICHII. AN ICH	1000			:	: !	•	:		
LOA MAAN	TRANSFORMING GROWTH FACTOR ALPIN PRECURSOR (TGF-ALPHA) (EGF-LIKE TGP	1	l	Ī	Ī	Ì	İ		1	I
TOLK HIDAAN	PROTENAGLUTAMINE GAMMA-GLUTAMYLTNANSFERASE K (EC 2) 2 (1)	28.283		Ī	Ī			Ī	-	
A SECTION	THROMBOSPONDIN PRECURSOR.	L	1	Ī				T	-	
THE MOVE	3-KETOACYL-COA THIOLASE PEROXISOMAL PRECURSOR (EC 23.1.14) (DETA-	T	Ī		Ī	T	Ì	Ī	I	
LIXMB MUNCH	PROTACTIVATIVIN BETA PRECURSOR (CONTAINS: SUBSTANCE P. NEUROKININ A	=	Ì	Ī				1		-
PTLE HUMAN		100	Ī	Ì	Ī	Ī	İ		+	
PTLE2 HUMAN		200	T	T	Ī	T	1	I		
PT.E. MOAN			T	T	T	Ī				T
PIOPA HUMAN	DNA TOPOSOMERASE IL ALPHA 1502 YASE (EC 1.99 1.3)	T	201-533	T	Ī		Ť		1	1
PTOPB HUMAN	DNA TOPOISOMERASE II, BETA 1502 YAE (EC 1 99.1.1)	T		T	T	1	1		1	7
PTPM3 HUMAN		T	7	1	1	1	1	1	-	
PTPMA HUMAN		T	Ť							
PIPLO MAKAN		L	,	T	7	Т			1	
PTPINC HUMANI	Ī	T	7	101.31			1		-	
PIPE MOMAN			1_	977		T	T	1		
THO HUMAN	THIS MUNAN TROPOWYOSIN, PLBROBLAST NOW MUSCLE TYPE (THISPL)	Т	Т	Т	307.234	T	T	1	Ì	
LINE ICHAN		Τ	Т	Т		Ť	Ì	Ī	T	
NAMA MUMAN	AUTOM TOSIN ALPHA CIAIN, SMOOTH AUSCLE (FRAGMENT)	± 30 × 30 × 30 × 30 × 30 × 30 × 30 × 30	=	İ	Ì	İ	İ	Ī	Ī	
THE HOLLE	APPERTUAL-PEPTIDASE II (EC.) 4 14 10) (TPP II) (TNIPEPTIDAL	Ī	1601-100	1160-1187	Ī		Ì	Ī	T	T
DECEMBER OF STREET	I'M UNCOCANE (PRACAGENT)					Ī	T	Ì	Ì	
TANK AND A	INTERNO PROTEIN		243.269				T		Ī	T
	TOPOCHE I TABLE TARESTO TORMONE MELETICA (TAPLA) (THYROLOBELUN	14,78)						ĺ	Ī	Ī
PTRKA MENAN	MONATENETY WEST COMMENT AND A COMMENT OF THE PROPERTY OF THE P	٦							T	Ī
PTRSR HOMEN	TAKNETBERN BECEPTOR PROTECTION TREATMENT THE CARLOTTER (EC. 2.7 112)	7	13:14							
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			7	7		1	1			
PTYKI MUNKAN	NOW RECEPTOR TYROSINE PROTEIN KINASE TYKS (EC 2) 1 (12)	+	7				1			
PUBAT HUMAN	UBIQUITIN-ACTIVATING ENZYNGE ET (ALISO PROTEIN)		t	T	1	1	1		1	
PUBEL MONCAN	MUCLEOLAR TRANSCRUPTION FACTOR I (UPSTREAM BINDING FACTOR I) (UBF-1)	20.15	t	\dagger	T	T	1	1	1	
ACADA MONANA	UDP-CLUCTRONOSYLTIANSFERASE PRECURSOR, MCCROSCHAL (EC 2 4 1 17)	¥2:62	İ	T	T	T	\dagger	1	1	T
PUTO NOMEN	RECENTOR TYROSING-PROTEIN KINASE UPO PRECURSOR (EC 2.7) 112)	411-522	-	T	T	İ	1	T	T	
NAME OF THE PARTY	UPSTREAM STEAMLATORY FACTOR I.	52-152	-	l		T	Ì	T	1	1
PYAIC MUNCA	VACUOLAR ATP SYMMASE SUBURIT C (EC.) 6.1.34) (W.ATPASE C SUBURIT)		Т	T	T	1	\dagger	1	1	I
TVILL MUMAN	ישרות	136-372 42	437461	11.74	T	T	t	T	T	T
TANK MAKAN	A BACKAI IN	119-146 23	233.260	T	T	T		T	†	T
	CINCULAR SELECTION DECISION OF THE SECOND SE	101-133	H			T		\dagger	T	Ī
SUCES AND AND AND AND AND AND AND AND AND AND	AGING THE BACKET PRINTS AND EAST (SEC.)	95-134	_		l			T	T	Ī
NY NA	WEST-LOS PROTEIN LINKS (EC. 17.1.117)	354.388					l	T	T	Ī
	II Contraction	247.374					-	T	T	T
PYPAC HIMAN	MALE BALL BOLD THOU LAND TABLES OF THE CONTRACT OF THE OFFICE OF THE PROPERTY OF THE OFFICE OFFICE OFFICE OFFICE O	3.03	1	7		П	H		T	T
PXPCC HUMAN	PARCE KUMAN DINA REPAIR PROTEIN COMPLEMENTING AT CELLS (YES DIRECT) SIGNE STORES	╗	+	1			H		r	Γ
	III MARAILINE I CANTAACHO LARRA LA CONTROL I MARECA I ANDREA	7	701-726	1	1	1	1			П

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Table 20 Table 100. A Marie Course on All Homes Protots Separated							l	
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UMAN DNA: ALFAUR FROI BAT COM	215.966	1047-1081						
DHA, REPAIR FIGHER CONCLEMENTING XF-U LELLS (ACADDERMAN FIGHER 1920M								
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PZNIO HUMAN ZIM. PIMAKA PROJEM IVIEWS		100	14/41	3011.3011	12/2 12/2 1900 2011, 2007 2146, 2160.			
1851 A TRAIN SIND ENGLE PROTEIN AD BEINGE BROKENOWING HICK VINCE I THE LENITH IN 1974	1						!	١
15.00	201-128							
PERSON LINE FINDER PROTEIN SOUNCE IN THE STATE OF THE STA								
121-1-	•							

TABLE X

Search Results Summary for PCTLZIP, P1CTLZIP, and P2CTLZIP Motifs

PCTLZIP		PICTURE			1	PZCIZIF	j		
LIBRARY FILE		LIBRARY FILE			+	משאינו ביים			
PENV POAMY	401-400	PENV BIVOR	23.450			PRNV BINGO	750-070		
PENY MYTMA	439-483	PENV BIV27	463-479			PENV BIVZ7	1/9-199		
BOW LIVELES	(82.188	PENV FOAMV	461-466	094-990		PENV FENVI	25	93062	
שנית התושה	446.440	PENV HVIKB	762-768			PENV PIVE	781-708		
הפוא האנפט	188.201	PERV KVIMA	437-463			PENV FIVED	178-706		
20171 7710	192.138	PENV HV1MP	183-188			PENV PIVTZ	780-797		
PENN NAME	436463	PENY KYIRH	2113			PENY FLVCO	39-66	924-041	
76AV AV16A	360.366	PENV HV181	738-764			PENV FLVOL	606-622		
PENV HVZBE	741.764	PENV HVIAC	186-201			PENY FLVLB	026-642		
PENV AVADI	244.384	PENV HV122	123-138			PENV FLVBA	602-619		
PENV MVZG1	444 464	POINT MAIN	117.193			PENY FOAMY	710-727	967-074	
PENV HVZNZ	197:797	BOWN WATER	18767		-	PERV FBVQA	625-642		
PENV HVZRO	/10/10/	DENY INVOKE	28A. 2AR			PENV PINCE	605-622		
PENV HVZ68	747/00	PENV NVADA	341.360		-	PENV FOVBM	808-625		
PENV HVZBT	740-760	PEN DY CO.	241.3RA			PENV HVIOY	123-140		
PENV JSKV	104:30	PERM DIAM	343.987			PERV HVIZZ	410-427		
PENV MMTVB	016-033	PER DATA	361.364			PENV MV123	164-171		
PENV MMTVG	010-013	PENV NVACO	744.768			PERV MY2CA	760-767		
PERV BRAK	139-164	FENV AVOB	200			DEIN UPER	A00-817		
PENV BINMIL	139-164	PENV HVZ81	(46-(00)	. 70 . 70	-	PENV MOSES	801-818		
PHEMA CVBLY	391-409	PENV JERV	2	786.180		OCIN MI VAV	810.647		
PHEMA CYBM	391-408	PENV MOTE	307-413			PERV MEVAV	A36.649		
PHEMA CVBO	391-406	PENY MOPES	307-413		1	FENY MEYES	1		
PHENA CANOC	301-408	PENV MLVAV	427-443			PENV MLVPD	020-020		
PHEMA CYMAS	402-417	PENV MLVCB	422-438			PENV MINT	038-020		
SUFILA CVMS	817-604	PENY MLYMO	423-430			PENV MIVE	639-656		
PUEMA MRAA	286-310	PENY MLVMO	426-442			PENV MINHO	626-643		
OUEUA NUME	303.318	PENY MLVAD	424-440	-		PENV MLVKI	107-164		
PUCINA INPRO	903-308	PENV MLVRK	424-440			PENY MIVMO	629-646		
BUENA MIREN	301.318	PENV MIRTYD	016-033			PENY MIVRO	924-04:1		
PURENT BUREL	286-301	PENY MMTV0	616-633			PENV MLVRK	024-641		
DAKENA BURGE	206-211	PENV BFV1	864-850			PENV MOVED	170-187		
PHEMA INDHY	203-308	PENV BFV3L	881-877			PENY RMON	029-620		
PHEMA INDIB	288-303	PENY BIVOS	95-109			PENV BEVI	710-727	987.974	
PHEMA INBIO	299-314	PENY BIVMK	129-164	802-810		PENV BFV3L	707:724	164-071	
PHEMA MOLE	302-317	PENY BIVML	120-164	901-617		PENV BIVMS	706-783		
PHEMA MEMO	292-307	PENV BIVE&	806-822			PENV BIVINK	766-782		
PHEMA MBME	200-211	PENY SIVAP	610-626	-		PENV BININ.	764-781		
PARIA MRNA	288-303	PHEINA COVO	30-62			PENV BIVBA	709-786		
BUELLA TAROB	301-316	PHEMA CYBLY	391-400			PENV BIVEP	773-790		
PARTY WAR	201.316	PHEMA CVBM	391-400			PENV BMRVN	630-663		
THE PERSON NAMED IN	208-313	PWEMA CYBO	391-406		_	PENY BMSAV	42.59		1 1
PHEMA INDIA	204.300	PMEMA CVMOC	391-406			PHEMA COVO	30-63	200-217	
PHEMA INDUS	200	BUREAL CANALE	103.413			PARMA CARLY	301408		
PHEMA RIBVI	780-311	L'ALLE CAROL	417.07			PARMA CYBN	291-408		
PHEMA MEVK	303-318	THE MA CVMS	200		 -	PURMA CARD	907-106		
SAME ALGORE	265-301	PREMA IAAIC	23/-203			ונטפשט הגמת			

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907-190	322-330	306-323	320-337	320-337	310-333	302-310	302-318	319-336	316-332	320-337	322-330	320-337	306-323	308-323	306-123	306-323	308-323	306-323	322-330	320-337	323-330	306-323	327-330	318-332	320-337	220-337	319-336	321-338	216-312	316-332	316-332	318-332	321-338	521-556	321-338	316-332	316-232	321-236	321-338	815-332	315-332	321-336	85. <u>15</u> 6	316-332	316-332	321-338
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PHEMA CYNOC	PHEMA JAAIC	PHEMA MBAN	PHEMA IABUD	PHEMA MOKA	PHEMA LACKO	PHEMA IACKP	PHEMA IACKO	PHEMA LACKS	PHEMA LACKV	PHEMA IADA1	PHEMA LADAS	PHEMA IADOZ	PHEMA IADHI	PHEMA JADH2	PHEMA IADHS	PHEMA IADHA	PHEMA IADHO	PHEMA IADH?	PHEMA IADM2	PHEMA IADNZ	PHEMA IADUS	PHEMA LAENO	PHEMA LAENT	PHEMA WIPA	PHEMA IAGRE	PHEMA MOUZ	PHEMA WOUA	PHEMA WHAL	PHEMA IAHCE	PHEMA IAHCT	PHEMA IAHCD	PHEMA WHDE	PHEMA LAHFO	PHEMA JAHKO	PHEMA IAHK?	PENA MALE	PHEMA IAHLO	PHEMA LAHMI	PHEMA IAHNM	PHEMA LAHIN	PHEMA JAHPR	PHEMA WARO	PHEMA WHEA	PHEMA LAHBP	PHEMA LAHOW	PHEMA LAHTE
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782	90	180	147	246	7EO	263	.092	137	12)	33	5	5	5	.25	63	99	13	63	99	25	91	40	46	97	46	62	62	62	9	9	23	52	22	2	9	2	22	22	2		23		3	2	2	62
221-237	234-280	234-260	231-247	230-248	234-280	237-263	134-260	1221-237	1221-237	221.237	221.237	221-237	1221-237	1221-237	237-263	234-250	221-227	237-263	230-246	230-262	236-261	230-246	230-246	230-246	230-246	230-252	236-252	236-282	230-248	230-246	230-252	230-282	230-262	230-282	230-248	230-246	230-282	230-262	236-282	236-261	226-261	233-249	239-254	237-263	237-253	237-253
PHEMA LABAN	PHEMA (ABUD	PHEMA IACKA	PHEMA LACKO	PHEMA IACKY	PHEMA JADA1	PHEMA IADAS	PHEMA IADCZ	PHEMA IADH1	PHEMA IADH2	PHEMA IADHS	PHEMA IADHA	PHEMA IADHS	PHEMA IADHO	PHEMA IADHT	PHEMA IADM2	PHEMA LADINZ	PHEMA LAENS	PHEMA IAEN?	PHEMA LAFPR	PHEMA WHAL	PHEMA LAHAR	PHEMA WHCO	PHEMA INHC?	PHENA LAHCO	PHEMA LANDE	PHEMA LAHFO	PHEMA IAHKO	PHEMA MHK?	PHEMA IAHLE	PHEMA IAHLO	PIEMA LAHMI	PHEMA LAHNM	PHEMA IAHRO	PHEMA IAHBA	PHEMA JAHBP	PHE MA JAHBW	PHEMA JAHTE	MEMA IAHTO	PHINA IAHUR	PHEMA LAKIE	PHEMA IALEN	PHEMA LAMAA	PHENA IAMAB	PHEMA IAMAO	PHEMA JAMET	PHEMA JAMES
PHEN	MEN	PAEN	PMEN	PHEN	Ž	PREV	PHEV	PHEN	PHEM	PHEM	Z.	PHEN	Mari	PHEM	PHEM		PHEM	PREM	MEM	MEM	PHEM	Mahai	PHEK	PHEN	PHEM	PHEM	PMEM	PHEM	PASK	PHEM	_	_	PREM	Z Z	2		T E	3 2 2	된	28.2	PARR	PHEM	PHEN	PHER	Ž	E E
9:	61		8			2				_	,			7	4	8 317-332			6	8		1		9		Н				200		143-160							1							
133-148	133-148	133-148	346-360	95-80	89	368-383	7.84	7.04	7.04	12.04	42-67	99-104	72-67	242-287	169-184	210-228	164-188	685-900	134.149	183-188	163-198	109-124	81-86	466483	97-112	20-38	11-04	22-37	105-123	1263-1268	264-289	22.37	208-283		207-282	1000	22.28	234-248	22.52	234-240	204-279	264-278	204-278	204-279	264-279	264-270
PHEMA MUMPH	PHEMA MUMPA	PHEMA MUMPS	PHEMA PITHW	H27	HEMA PIZHT	PHEMA RINDK	2	PHEMA BYBCM	PHEMA BYSCP	PHEMA BYBLM	DHVIS	CAPAR	WFUE VACCE	BPP22	PVGO1 HSVES	HSVII	8PT4	BPT4	HBVII	BPPH2	BPPZA	HSVSA	BPP1	8PT4	1748	HSVII	BPPHS	BPOX2	HEVBA	BPT2	HOVE	HEVII	HBVII	EM.	HEVE!		Z	AZA	¥	¥	.VBF	:Mro	VBLY	W.	2	Ž.
PHEMA	PHEMA	PHENA	PHEMA	PHEMA P12H	MEMA	MEMA	PHEMA BV6	PHEMA	PHEMA	PHEMA	PVERV DHVIS	PVFP7 CAPVK	2	PVG01 BPP22	PV001	PVG01 HSVII	PV000 BPT4	PV007 BPT4	PVG08 HBVII	PVG10 BPPH2	PVG10 BPPZA	PYG10 HSV8A	PVG16 BPP1	PVQ18 8PT4	PV026 BPT4	PVG29 HSVII	PV030 BPPHS	PV036 BPOX2	PV036 HBV6A	PV037 BPT2	FVG37 HBVII	PYOSE HEVI	PYOSO HBYII	PV056 HBVI	PVGS9 HSVI	PVG85 KBYI	70 e 2	PYGB BPFZA	MOD BANIA	PVOF BPPHX	PVOL2 CVBF	PYOLZ CYTES	PVOL2 CYBLY	PVOL2 CYBM	MOLD CYBO	PYOLE CYBV

.1,44,	Ļ	PARTY TOTAL	221.237			THEM WHILE	041-000		
100,700	915,61	PURITY IAMES	PE.101	231.247	FEE	PHEMA LAMUR	321-338		
10.40	200	PUPMA IANTA	237.283		PREM	PREMA WJAP	317-334		
4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6		PURMA IACIU?	721.227		MIM	PHEMA JAMAA	218-336		
200		GUELLA (ABLT)	234.260		MIKE	PHEMA LAMAB	324-341		
0100		PUCUA IARES	234.260		A PHEM	PHEMA MAMAD	322-338		
200-001		DURINA IABUS	234.280		PHEM	PHEMA WAME!	322-339		
10001		ALPIA IABAA	976.00.6		THE	PHEMA IAMES	322-330		
1068-1070		PURMA IABIA	200		MEN	PHEMA JAMES	306-323		
1088-10/0		FREMA IAIAI	107.007		MEN	PHEMA LAMIN	316-333	_	
701-718		MEMA IAIKM	207-207		ממנה	DUELLA LANTA	322.330		
203-218		PHEMA IATKO	233-248		1000	THE THE PARTY	190.117	+	
475-490		PHEMA LATKA	230-246		THEM		100.000	-	
444-489		PHEMA IATKW	220-246		ž.	I	200-223		
427-442		PHEMA IAUDO	237-283		A. B. W.		/25.25	1	
440-461		PHEMA IAUBS .	235-261		7 X		320-337		
20.04		PHEMA IAVI7	238-284		E E		321-338		
70.04		PHEMA LAXIA	236-261		PHER		316-332		
000		PHEMA 1AZCO	237.263		Maha	PHEMA IATKM	320-337		
200-200		BURNA 147US	221.927		25.	PHEMA JAUDO	322-338	380-397	
207-007		BUESTA JAPUS	221.227		PARK	PHEMA LAVIT	323-340		
205-ZB0		LUEMA IALIA	727.77		200		222-238	-	
206-200		PHEMA MAZUK	207-/07	010 300	7874	I	206-323		
265-280		PHEMA INBAA	10-12	200-310	nane		206.323		
266-280		PHEMA INSSE	123-138	303-316		THE PARTY OF THE P	999.990		
265-260		PHEMA MEBO	116-122	293.308	FALM	YOU W			
9.04		PHEMA INBEN	123-138	301.318	WEW	PHEMA MUMPIN	911.101		
276-293		PHEMA INBFU	108-124	286.301	MIN.	PKIMA MUMPH	911-101		
910-000		PHEMA INSOL	110-136	200.311	X.		101-110		
741.788		PHESTA WORK	116-132	293-308	PHEN		03-110		
910.00		PHEMA DUBIB	106-124	288.303	PHEM	PHEMA NOVB	03-110		
100		PARITA MED	120-130	200.314	NEW NEW	PHEMA NOVD	03-110		
	ŀ	PARTA MAIR	123.130	302.317	PHEM	PHEMA HOVH	03-110		
7202		ON UN TRANS	112-120	282.307	X 25.		92-110		
,		MIRELL MILLE	144199	20A.311			03-110		
207		PARENT WENT	108-124	288.303	35	PHEMA NOVO	011-60		
050.170		PURILLA BURDO	125.130	301.316	X STA	PHEMA_NDVTO	011-0		
2000		PARTA DIRE	123-130	301.318	E E	PHEMA HOVU	93-110		
130.101		PHEMA MRS.	119-136	208.313	Mark	PHEMA PHODY	36-63		
200		PURITA MALIA	116-132	294.309	25.5	PHEMA PINW	486-503	_	
200 400		PURITA DARVI	116-132	296-311	E SE	PHEMA PIDB	111-120		
2000		PARUA MANT	123-139	303.316	X 25	PHEMA PIDM	111-120		
		BUSILA MINT	104.192	288.301	E E	PHEMA PISKA	111-128		
363-386		PARTIE ANGLES	1000		35		111.128		
234-248		TOTAL MORE IN			Date		111.198		-
28-40		PHEMA MUMPR	132-148			2021			
26-40		PHEMA MUMPB	133-146		N. C.	PARMA PIONO	B2 1-11		1
26-40		PHEMA PITHW	345-360		X	PHEMA PICHW	111.128		
28.40		PHENA PIZH	66-61		THE STATE OF THE S	MEMA PIENX	111-128	1	

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86-102	84-101	64-101	84-101	84-101	280-297	290-297	281-298	176-103	176-183	209-226	173-180	948-066	100-126	171-168	1262-1268	2073-3080	1084-1111	736-783	676-692	736-783	726-753	736-763	507-614	907-824	907-824	180-187	700-186	401-418	366-382	364-381	245-282	248-262	43-60	90-10	90-08	712-728	712-720	344-301	344-381	12.04	12.04	12.04	12-94	12.04	250-287	280-287
PHEMA 8V41	PHEMA BYS	PHEMA SVBCM	PHEMA BVBCP	PHEMA_BV61.N	PVF06 VACCC	PVPOB VACCP	PVF08 VACCV	PVP00 VACCC	PVF09 VACCV	PVG27 H8V8A	PV028 HSVI1	PVG39 HBV/1	PVG43 HBV11	PVG67_HSV11	PV072 HBVII	PVQF1_IBVB	FVOL2 INVO	PVOLA HSVE!	FYGLS HEVEA	PVOLB HSVEA	PYGLS HSVEB	PVOLB HOVEL	PYOLE SLTV6	PYOLD RTYS	PVGLB RTVT	PVOLC PRVIF	FVOLE VZVD	PVOLF 8V5	PVOLH KCMVA	PYOLH HCMYT	PYGLH HBV11	PYOLH HOVIE	PYGLI HBY11	PYOLM BUNE?	FVOLM BUNSH	PYGLM PUDMIH	PYOLM PUUMB	PYOLM RVFV	PYOUM RVFVZ	PYOLY LASSO	PYGLY LABBJ	PYOLY LYCVA	PVOLY LYCVW	PVOLY MOPE	FVM1 REOVD	PYM! REOV.
										_										-	_																									264-279
										_				L									į																			204-270	284-279	204-279	264-279	174-100
																			317-332												143.158			330-346		618-633	`		ī			174-100	174-190	174-190	174-190	123-130
324-340	324.340	324-340	324-340	324-340	324-340	324-340	324.340	208-283	7.94	7.04	ž	<u>2</u>	42.67	Ī	99-104	101-104	72-87	109-104	209-228	134-140	109-124	103-118	270-286	76-82	200	22-37	108-123	284-200	244.260	1244-1260	22-37	268-263	101-117	130-146	267-282	362-376	69-106	234-248	234-248	67-72	2210-2228	123-130	123-130	123-130	123-139	31-47
PHEMA PIOR	PHEMA PISH4	PHEMA PIDKA	PHEMA PISHT	PHEMA MISHU	PHEMA PISHV	PHEMA PISHW	PHEMA PISHX	PHEMA RINDK	PHEMA BVB	PHEMA BYSCM	PHEMA BV6CP	PHEMA SVBUN	PVENY DHYII	PYENY EAV	PVFP2 FOWPV	PVFP7 CAPVK	PVPUS VACCE	PV001 HBVEB	PVG01 HBV11	PVGD6 H9VI	PV010 HBV8A	PVQ11 HSVII	PVGR2 HBV11	PVGI BPVIR	PV029 HBVII	PY086 BPOX2	PV036 HBV8A	PVG37 HBVII	PVO41 HBV11	PVG46 HBVII	PV066 HBVII	PVOSS HBVII	PV059 HBVII	PV059 H8V9A	PVG69 HBVII	PVOIS HBVII	FV071 HBVBA	PVG9 BPPH2	FVOT BPPZA	PV08 BPV1R	PVOP1 IBVB	PVOL2 CYBP	FVOL2 CVBLO	PV012 CVBLY	FVQL2 CVBM	PV612 CVBQ
26-40	26-40	25-40	28-40	26-40	25-40	78-40	176-241																																			_				
PVMT2 IALE1	PVMT2 LALE2	PVMT2 IAMAN	FVMT2 IAPUE	PVMT2 IABIN	PVMT2 IAUDO	PVMT2 IAWIL	PVMTB MYXVL																																					-		

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148-168	87-104	147-164	147.164	117.164	147.164	79.67	143.164		20.11	707-001	E6-202	10.1	75	174:101	174.101	29.5	174-101	185-202	198-202	11.04	174-191	174-101	174-101	26-42	28-42	26-42	25-42	28-42	28-42	26-42	2F-42	26-42	28-42	29-42	20-42											
PVINAT COVO						Ī		Ī	T	1	1	1	1		1		٦											PVMT2 LAFPW		i			I		VMT2 IAWIL											
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264-278					1274-1200	10.00	1060-1086	1050-1088																																						
124.100		2071-7071	1216-1231	770-27	900-910	804-618	570-682	676-502	1277-1203																		1266.280	266.280	206-280		206-280	265-280	266-280	266-200			·			276.282			·			
245.44	20145		95-13	1148	442-467	440456	216-233	216-233	803-819	1066-1071	1066-1070	1066-1071	1066-1070	1056-1070	201-710	203-218	622-638	478-480	444-460	427-442	448-401	160 166	160-160	30.0	79.94	2.04	206-221	206-221	206-221	398-414	206-221	206-221	206-221	208-221	266-302	289-306	288-302	276-282	276-202	6-04	273-289	273-269	273-288	273-288	273-269	
	אמרל באפא	באמר כאאי	PYOLE CVIMAB	בישלט כישרא	PVOL2 CVPF8	ריסנט בעריט	PVGL2 CVPRB	PVOL2 CVPRM	PVOL2 FIPV	PVQL2 BV6	PVOL2 BVB	PVGL2 IBVD2	PVOL2 BVX	PVRL2 BVM	PVOLB MSVBA	PVOLD PRVP	DVAIR VZVO	PVOLC MBVBC	PVOLC HOVE	PVALC MAVES	eval C PRVIS	evale vzvo	Page Varia	EVOID MINI!	PVOID HRV2	PVALE PRVPI	EVOLF RESVA	PVOIN BRBVC	PVOLF BRBVR	PVO P CDVO	PVGLP HRSV1	PVGLF HRBVA	PVOLF HRSVI.	PVOLP HRBVR	PVOLP MEASE	PVOLP MEAS!	PVOLP MEASY	PVOLE MUMPM	PYQUE MUMPR	PVQU MUMPS	PVGL NDVA	PVGIL NDVB	PYOLF NOVA	PVOLE NOVT	EVOLP NDVTO	
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282-286	282-298	178-101	27B-293	356-371	499-616	409-615	429-515	743-788	829-809	509-525	386-371	366-371	826-842	969-866	Ī	12-04	12.94	12-84	12.94	12.94	1021-1037	821-538	191-207	136-161	136-161	169-206	189-206	111-00	118-134	118-134	118-134	118-134	116134	110-134	115-131	380-388	187-202	378-303	363-388	860-080	383-388	363-388	234-240	26-40	25-40	25-40
PYOLF RINDK	PYOLF RINDL	PYOU THY	PVOLI VZVD	PYOLM HANTS	PVOLM HANTH	PYOLM HANTL	PYDLM HANTY	PVOLM PTPV	PVOLM PUUMH	PYOLM PUUMS	PYGLM BEOUR	PYGLM BEOUS	PYGLM UUK	PVOLP BEV	PVOLY LABSO	PVOLY LABSJ	PVGLY LYCVA	PVOLY LYCVW	FVOLY MOPEI	PVOLY PIARY	PYBNM CPMV	PVM3 REOVD	PVMAT MUMPS	PVMAT NDVA		PVMAT PIZHT				PVMP CAMVD			PVMP CAMVB								PVMBA WHYB		FVMBA WHVW6			PVMT2 IAPOW
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PVMT2 WEPR			1	ł	ı				l	1												•			-	-												٠					.;;
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TABLE XI

Search Results Summary for P3CTLZIP, P4CTLZIP, P5CTLZIP, and P6CTLZIP Motifs

Pact 219	_		PACTIZIP			PBCTL21P			POCTIZIP			
I MANAY ETT			LIBRARY PRE			LIBRARY FILE			LIBRARY FILE			
DENV BINSS	147.188		PENVI FRSFV	360-300		PENVI FRBFV	360-400		PENV BINDS	47.00	626.540	
PENV CARVE	810.628		PENV AVISU	08.117		PENV2 FRSFV	380-400		PENV BIV27	47.66	147-160 564-575	564.575
DENY CARVO	ACA. 826		PENV BIV27	147.160		PENV BAEVIA	170-180		PENV FENVI	226.246	930.061	
PEND HUSBE	280.248		PENV HV12H	1123-142		PENV FIVPE	761-601		PENV FLVCS	624-645		
PENV MV201	241.780		PENV HV2D2	0.20		PENV FIVSD	779-709		PENV FLVOL	447-488	908-929	
PENV HV201	741.750		PENV HV258	778.707		PENV FIVT2	780-000		PENV FLVLS	407-488	979-979	
PENV HV2N2	742.780		PENV JSRV	641.860		PENV FLVOL	9-29		PENV FLVSA	111-108	802-825	
000AN ANSO	781.780		PENV RSVP	633.662		PENV FOAMV	265-276	924-844	PENV FOAMV	162-174	967-978	
PENV HV298	743-701		PHEMA VACCC	173-102		PENV FSVOA	0.20		PENV FOVOA	467-488	628.646	
PENV HV387	746.783		PHEMA VACCI	173.182		PENV HVICE	428-448		PENV FEVOR	447-460	906.626	
PENV JARV	376-384		PHEMA VACCT	175.102		PENV HY2CA	750-770		PENV POVOM	460-471	808-828 I	
SUCIAL POPU	116.130		PHEMA VACCV	173.192		PENV MLVF6	400-420		PENV FEVET	467.408		
DUELLA DISUT	110.130		PVENV BEV	62.81		PENV MMTVB	643.663		PENV OALV	62-73	619-640	
BURNA BUAT	KK.23		PVENV MCVI	91.90		PENV MMTVO	643.683		PENV HV28E	760-771		
PVENY THOON	473-401		PVENV MCV2	91.60		PENV OMVVS	76-95		PENV HV201	741.702		
PUDIA 89922	83-101		PVFUS ORFIVE	29-49		PENV RSVP	42.02		PENV HV2NZ	742-703		
PV024 RPT4	116.133		PVOOL MSVEB	100-166		PENV BEVI	024.944		PENV HV2RO	781.772		
PVOTA HEVRA	344.362		PV001 VACCC	376-396		PENV BEVOL	021-941		PENV HV26T	745-766		
פאסאס הפאונ	14.37		PYGG! VACCV	316.334		PENV SIVMI	766-780		PENV MCFF	600-621		
MANER MANAR	1.07		PVGO! VARV	376.306		PENV BIVME	165-788		PENV MCFF3	601-622		
0106 apt4	18.0		PVOD8 BPT4	827.846		PENV BIVML	764.784		PENV MLVAV	630-661		
אישר הפייו	A4.102		PVG10 H6VII	36.64		PENV BIVS4	769-789		PENV MLVCB	825-546		
MAN TONG	166.173		MG11 H9VII	103-122	160-160	PENV SIVSP	773-703		PENV MLVFB	639-600		
PVOG ASTI	2789-2808	3374-3302	PVQ! BPPH2	31.60		PHEMA COVO	403-613		PENV MLVFF	639-660		
PVOL3 CVM22	1063-1071		PVOI BPVIR	659-676		PHEMA CVBLY	391-411		PENV MLVFP	639.660		
PVOL 9 IBVA	1056-1074		PV020 8PT4	231-250		PHEMA CVBM	391-411		PENV MLVHO	020-047		-
BVOI 3 IRVS	1066-1073		PV032 V2VD	90-109		PHEMA CVBO	301-411		PENV MLVKI	167.188		
PVOL 2 MVO 2	1066-1074		PV010 BPK1	132-161		PHEMA CYHOC	301-411		PENV MLVMO	628-650		
PVOL 2 MVK	1068-1073		PV037 8PT2	10.38	020.046	PHEMA CVMAB	402-422		PENV MLVRD	024.048		İ
PVOL 2 IBVM	1066-1073		FV017 8PT4	19-38	626.644	PHEMA IACKO	101-101		PENV MLVRK	024-645		
PVOLG MSV81	660-678	669-707	PVOSB HSVII	1038-1057		PHEMA IADMA	101-101		PENV MSVFB	170-181		
PVOLD MEVEC	692.710		PVO41 HSVII	62-81		PHEMA MUMPM	307-417		PENV RMCFV	603-624		
PVOL B HSVSA	564.602		PVO43 BPPF3	350-399		PHEMA MUMPR	307-417		PENV BEVI	067-878		Ī
PVOLB ALTVO	740-768		PVO48 BPPF1	337-366		PHEMA MUMPS	397.417		PENV BFV3L	167-170	924.93	
PVOLB ILTVE	760-768		PVOSB HSVII	142-101		PHEMA PHODV	403-613		PENV BIVA!	437-468		1
PVOLB ILTYT	760-788		PVD81 HSVII	117-136		PHEMA PINW	322-342		PENV BIVAG	442-463		
PVQLC VZVD	431-440		PVOB7 MSVII	316-337	1072-1081	PHEMA PI2H	15.33		PENV BIVAL	421-442		
PVOLC VZVS	431-440		PVQF1 IBVB	1687-1606	2108-2127	PHEMA PIZHT	13:33		PENV SIVAT	435-450		
PVOLE PISHA	12.04		PVOL2 CVBF	991-1010		PHEMA RINDL	407.617		PENV BMSAV	42.63		
PVALM MEVAG	314.332		PVOL2 CVBLB	991-1010		PHEMA BENDS	322-342		PHEMA CVMAB	402-423		
DVOLV URVEA	614-632		PVQL2 CVBLY	991-1010		PHEMA BENDE	322-342		PHEMA INDE!	206-267		
200.00	807.826		PVOL2 CVBM	0101-108		PHEMA BENDH	322-342		PHEMA MUMPM	228.246		
1 NW1 1	5.84		PVOLZ CVBO	991-1010		PHEMA BENDJ	322-342		PHEMA MUMPR	228.240		
AND MADA	676-686		PYGLZ CYBV	0101-100		PHEMA BENDZ	322-342		PHEMA MUMPS	22E-246		
				***	11115.1134	DOMESTIC AND LINES	67.46		SECTION ACCOUNT		-	

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		378-400	378.400	378-400	378-400							-		-	-	-					-	-	 - 		-							_			7						-	-		-		463-474
19-34	13.34	7.28	7.28	7.20	7.28	168-180	599-810	314-336	86.08	162.178	288.300	AK.10A	1165-1174	206.287	30.61	228.259	1868-1877	167-178	1269-1280	1269-1280	1269-1200	1269-1260	1269-1200	1259-1280	1317.1338	1265-1266	1176-1107	101.00	82.103	62.103	93-104	136-160	440-467	338-357	224-246	227-240	224.246	440-407	446-467	446-467	306-326	468-4771	15 797	480-471	460-471	Γ
PHEMA PIZH	PHEMA PIZHT	PHEMA OVE	PHEMA BYSCM	PHEMA BVBCP	PHEMA SVBLN	PYGO! HSYEB	PVGO1 MGVII	PVG25 H9VII	PVG37 8PGX2	PV043 H9VII	PVOSS MSVII	PVDES MEVRA	PVGS6 MEVII	PVG68 HSV8A	PVGEO HSVII	PVG83 H9VII	PVOF1 18V8	PVOH3 HCMVA	PVOL2 CVBF	PVGL2 CVBL6	PVOL2 CVBLY	PVOL2 CVBM	PVGL2 CVBQ	PVOL2 CVBV	PVOL2 CVM4	PVOL2 CVMAS	PVGL2 CVMJH	PVOLB HBV11	PVOLB HEVIF	PVOLB HBV1K	PVQLB HBV1P	PYGLB MCMVS	PVOLC PRVIF	PVOLF COVO	PVOLF MEARE	PVOLP MEABI	PVOLF MEASY	PVOLF MUMPM	PVOLE MUNDA	PVOLF MUMPS	PVQLF PHOOV	PVOLP PITHC	PVGI E PIZM	VOLF PIZHO	PVOLE PIZMT	PVOLP PISS
PHE	PHE	32	E	3	Z	2	DAd	DAd	970-890 PVQ	0/4	274	000	2	000	2	PVO	PVG	Ž	378-388 PVQ	,	DA	PVQ.	2	2	Ž	PVOI	PVQ	PVOI	2	₽ 2	PVO	PVG	Ž	PVQ	PVG	PVat	DA	Ma	2	NA.	Z Z	ğ	D/A	M	Ž	PVG
360-378	208-318	237-267	200-318	31.61	31.61	26.46	161-171	300-320	040-008	20.40	336-360	117.137	124-144	328-348	327.347	328.348	328-348	327-347	327-347 3	310-330	732-762	760-770	761-771	70.00	70.00	88-88	72-92	279-200	63-63	738-768	283-303	464-474	454.474	454-474	454-474	464-474	670-690	1326-1346	1326-1348	996-1018	909-1019	1000 1020	1001-1021	1001-1021	1166-1170	1000-1020
PVENV THOOV	PVG01 VACCC	PV001 VACCV	PVGO1 VARV	PVG06 VACCC	PVGOG VARV	PVGOB BPPF1	PVO12 HSVII	PVG22 HSVII	PV039 H8VII	PVG61_K3VII	PVG63 HSVII	PVG06 K9VII	PV074 HSVSA	PVGL2 IBV6		PVOL2 IBVD2	PVGL2 18VD3	PVGL2 IBVK	PVOL2 IBVM	PVGL2 IBVU2	PVOLB EBV	PVOLB HCMVA	PVGLB HCMVT	PVQLB M9V23	PVQLB HBV2H	PVOLB HSV29	PVGLB MSVBU	PVOLB HSVB2					٦				PVOLH MCMV8	PVOLM BUNL?	PVOLM BUNBH	PVOLM BUNYW	PVOLM HANTB					PVOLM SEOUR
4	٩	d	1030-1067	1030-1066 P		a.	4	771.780 P	200.789 P	Г		770 780	Γ	á	á	هَ	á	ά	467-400 Pt	487.486 PV	à	à	٩	١٩	3	PV	٩	7	٩	Ą	2	2	2	2	21	2	V	۸	3	8	2	2	1	2	2	74
800-1016	947-866	066-877	64-83	64.83	614-833	614-633	1041-1060		687.606	688.607	697-606	687.606		707-728	117-130	266-276	266-285	286-286	3.04	3.04	475.484	436.466	172-301	44.03	278-207	117-136	162-171	007-1010	166-174	156-174	830-849	630-648	066-074	99-106	1166-1104	621-640	171-180	136-166	174-103	174-103	174-103	171.100				
PVOL2 CVM4	PVOL2 CVMA6	PVOL2 CVMJH	PVOL2 CVPFB	PVOL2 CVPPU	PVGL2 CVPRB	PVGL2 CYPAM	PVOLZ FIPV	PVOL2 18V6	PVGL2"IBVB	PVOL2 BVD2	FVGL2 MVK	PVQL2 IBVM	PVOLD HCMVA	PVOLB HCMVT	PVOLB MSV6U	PVOLG RTV6	PVGLB RTVS	PVOLD RTVT	PVGLC H6V11	PVOLC HSVIK		PVOLO CHAN	_	PVÖLI HSVEB	PVOLI VZVD	PVOLM BUNDE		PVOLM PTPV	PVOLM PUUMH	9		2	7	_	1	Ì		PVMEI CVH22	PUNE! CUPFE	PVINEI CVPPU	PVME1 CVPRM	PVMEI CVTKE				
120-144			-	, i		-			•	ď	•			•	•	d			4	b	•	ď	٥.	اهٔ	٩	٠	ě.	ā	•	هٔ	•	١	٤	Σ	٤	٤	٥	ه	8	á	٤	8		-		•
101-01	227-246	227-246	14-62	100-200	190-208	183-201	183-201	103-201	183.201	163.201	103-201	160-198												_															-							-
PVM01 VACCV	PVM1 REOVD	PVM1 REOVE	PVMAT HABVA	PVMAT NDVA	PVMAT NDV8	PVMP CAMVC	PVMP CAMVD	PVMP CAMVE	PVMP CAMVN	PVMP CAMVS	PVMP CAMVW	CAMP MAA																						-								-		-	•	

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277	220-241	220-241	460-481	480-481			450-481	460-481	463-474	446-467	991-712	116-009	304.328	207.918	ACO. 470	1000		2:23	107-218	180-211	180-211	103-214	237-268	239-250	83.68	281.302	990.981	149-140	Т	T	146.183	8	201-222	100/	244-206	244-266	244-265	233-264	70-01	233-284	233-284	233.284	70.01			244-205 1	244-288	10-04	233-264	133-284
PVOLF NOW	PVQLF RINDK	PVOLP RINDL	PVQLF BENDS	PVM R BENDE		LANGE PERCH	PVOLF BEND.	PVOLF BENDZ	PVOLF BV41	PVOLF BV6	PVOLK HCMYA	PVOLM HCMVT	BVOLK MRVEA	PVOLIN MOVED	AND MOVE	AND MOVE	YASH MAA	PVQU H9V23	PYOLM FUNDE	PVOLM BUNL?	PVOLM BUNSH	PVOKIM BUNYW	PYOLY LABEO	PVOLY LABBJ	WORR CRV	PVIADI VACCO	WALL VALUE	PVIDAT MANA	PULLET BRUDE	MANAGE THE	PVMAI IKIV	PVMEI CVMDC	PVM8A HPBD8	PVMBA HPBV0	PVM0A HPBV2	PVMBA MPBV4	PVMBA HPBVD	PVM8A MPBVA	PVMBA MPBVD	PVMSA HPBV	PVMBA MPBVJ	PVMRA MPBVL	PVMBA MPRVA	011001	LAMBA NIEVO	PVMBA HPIVP	PVMOA HPBVR	PVMBA HPBVB	PVMBA HPBVW	PVMBA HPBVY
909-1019	026-048	12.32	25.21	67.6		141:101	516-330	308-328	300-320	308-328	312-332	312.332	00 430	108.118	20000			¥9.2	74-84	201-221	208-228	203-213	207-227	912-232	919,919	919.919		83.84					1										-		-		-			
PVOLM REGUS	PVOLM UUK		Ţ	Ī	Ī	1	Ţ	PVMAT NDVA	PVMAT NOVB									_	PVME1 IBVK	PVMSA HPBDB	PVMSA HPBGB				I	Τ	T	PUMBA WHYDI	T																					
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133-284	28-46	28.66	28-48	26.46	25.48	28.40	28.48	38.48	28.45	28.40	8.48	9																									7		-		
PVM9A HPBVZ	PVMT2 IAANN	PVMT2 IABAN	PVMT2 IAPOW	PVMT2 LAFPA	PVMT2 IAPPW	PVMT2 JALES	PVMT2 IALE?	PVMT2 IAMAN	PVMT2 IAPUE	PVMT2 IABIN	PVMT2 IAUDO	PVMT2 IAWIL																													
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TABLE XII

Search Results Summary for P7CTLZIP, P8CTLZIP, and P9CTLZIP Motifs

97CH 218			Ē		•					
LIBRARY PILE			LIBRARY FILE			LIBRARY FILE				
PENY BATYM	102-224		PENVI FRSFV	360-403		PENV BLVAF	303-327			
PENV HV181	486-820		PENV2 FREFY	300 403		PENV BLVAU	303-327			
PENV HV188	119-616		PENV BIVOS	176-201		PENV BLVAV	303-327			
PENV HV1BN	019707		FENV BIV27	207-230		FENV BLV82	303-327		_	
PENV HVIBA	603.625		PENV FOAMV	604-887		DEAN BIVBG	203-327			
PENV HVIEL	406-617		PENV HV123	176-109		PENV BLVJ	303-327		_	
PENV HVIH2	498-620		PENV HV2BE	3-26	761-804	PENV FIVPE	781-805			
PENV HV1H3	498-620		PENV MV2CA	760-773		PENV FIVSD	779-803		-	
PENV HVIJS	610-632		PENV HV201	3.20	772.706	PENV FIVT2	760-604			-
PENV HV1JA	490-812		PENV HV201	772-705	•	PHEMA CVBLY	301-415			
PENV HVIKB	604-B20		PENV HV2NZ	777-900		PHEMA CYBM	301-416			
PENV HVIMA	600-622		PENV JSRV	641-664		PHEMA CVBO	301-416			-
PENV HVIMP	490.610		PENV BFV1	664-887		PILEMA CVHOC	381-416	-		-
PENV HVIND	489-610		PENV GFV3t	661-004		PHEMA INCCA	442-408			
PENY HVIPY	499-620		PENV SIVMI	603-626		PHEMA INCEN	430-464			
PENV MV181	469-611		PENV GIVMK	802-825		PHEMA INCOL	430-464			
PENV HV122	123-148	406-617	PENV BIVML	601-824		PHEMA INCHY	429-463			
PENV HV126	407.610		PENV SIVS4	606-829		PHEMA INC.H.	443-407			
PENY HV128	606-627		PENV BIVSP	610-633		PHEMA INCKY	420-463			_
PENV HVIZH	488-620		PHEMA COVO	200-223		PHEMA INCM!	420-463			
PENV JOHN	276-286		PHEMA PIZH	66-86		PHEMA INCNA	429-463			
PENV NOWV	213-236		HIRMA PIZHT	65-68		PHEMA INCP!	430-484			
PENV BRVI	213-238		PVF11 VACCC	161-164		PHEMA INCP2	430-484			
PHEMA MAIC	37.88		PVF16 VACCC	26-48		PHEMA INCP3	430-464			
PHEMA LABAN	21-43		PAPIS VACCE	3-26		PHEMA INCTA	430-464			
PHEMA LADAS	17-69		PVOIL AMEPV	313-338		PHEMA NCYA	430-484			. 3
PHEMA MOH2	21-43		PVG28 HSVII	401.614		PHEMA MUMPM	101-125			
PHEMA JAOHS	21-43		PVG43 HBVII	322-346		PHEMA MUMPR	101-126			
PHEMA WOHA	21-43		PV062 HSVII	220-252		PHEMA MUMPS	101-126			11.5
PHEMA IADHS	21-43		PVG67 HBVII	722-746		PHEMA PITHW	29.63			
PHEMA LADHO	21-43		EVOL2 CVBF	10-33		PVENV BEV	02.00			
PHEMA IADK?	21-43		MOL2 CVBLB	061-874		PVF08 VACCC	280-304			8.1
PHEMA IADM2	37.66		PYOL2 CYBLY	10-33		PVF06 VACCP	280-304			10
HEMA WOMA	20-60		PYOL2 CYMS	1207-1280		PVFOS VACCV	281-308			
WENA IADUS	37.69		PYOL2 CYMA6	1216-1230		PVF09 VACCC	170-200			
PHEMA LAENS	21-43		YOU CYMAN	1120-1148		PVF08 VACCV	176-200			
HEMA IMEN?	37.60		PVOL2 CVPFB	1274-1207		PV401 V2VD	69-02		F 0 F	
PHEMA JAMAO	37-60		האסום האסום	1272-1205		PVQ10 HEVBA	366-370			
MEMA LAMET	27.60		PYOLS CYPRS	1060-1073		PVG12 MBVBA	66.62			
PHEMA LAME2	37-60		PYOLZ CYPRIA	1060-1073		PVG18 MEVIT	211.00			·
PHEMA LAMES	21-43		PYOL2 FIPY	1277-1300		PV02B HSVII	173-107		-	-
PHEMA IANTO	37.60		FYOLZ RV6	196-219		PV043 HSVII	109-133			
PHEMA IAQU?	21-43		PYOLE IBYB	196-218		PV067 HBVII	108-132	1006-1029		-
HEMA INTRM.	33-66		PVQL2 IBVD2	100-210		PVG72 HEVII	720-744			
			40.00	313 333	ľ	A.M. 400.00				

201	I TOTAL				_
DI 7.04 I	_	PVOLD RTV8	587-021		1
PVOL2 18VU1 178-201		PVOLB ILTVS	607-031		
PVB1.2 IBVU2 178-201		PVOLE ILTYT	607.631		-
PVOL2 18VU3 178-201		PVGLE H9V11	413-437		-
PVOLD HCMVA 635-658		PVOLE VZVD	469-403		
PYOLE HCMYT 630-550		PVOLF BVB	401-428		
PVOLE HEVEA 483-608		PVOLH KCMVA	674-508		
PVOLS MCMVS 550-580		PYOUR HCMYT	П		
PVOLC H8V11 487-480		PVOLM HBV11		003-827	
PVOLC HSVIK 487-480	Ц	PVOLH HSVIE		903-627	1
PVGLC H8V2 435-468	Ш	PVOLM BUNL?	31.56		
PVOLC M9V23 438-469	Ш	PVQLM BUNSH	99-10		1
PVGLM BUNL7 1387-1410	Ц	PVQLM HANTH	694.718		
PVOLM BUNSH 1387-1410	L	PVQLM RVFV	344.366		
Ť	┡	PVOLM RVFVZ	244-368		
PVOLY JUNIN 12:38		PVOLM UUK	601.696		
PVOLY LASSO 12-36	L	PVONM CPMV	311-336		
PVOLY LA85J 12:35	1	PVGP2 EBV	067-681		
	1_	V073 E8V	854-878		
		PVM1 REOVD	280-304		
	L	PVM1 REDVI	280-304		
		PVM21 REOVD	100-192		
PWRLY TACVE 12-36		PVM22 REOVO	100-192		
PVOLY TACY7 12:36		PVM2 REOVA	108-192		
PVOLY TACVT 12-38	Ц	PVM2 REOVE	166-162		1
	4	PVMAT MEASI	111.7		1
PVM1 REOVD 324-347	₹	484-477 PVMAT BEPVB	314-336		1
PVMI REOVL 464-477	Н	- PVME1 CVBM	137-161	-	
PVMAT MUMPS 227-260	H	PVINE! CVHOC	137-101		
PVMSA HPBDB 269-292	Н	PVME1 CVTKE	107-101		
PVM6A HPBDC 269-291	┝	PVME1 18V0	74.00		
	Н	PVME1 IBVB	74.00		
PVMSA MPBDW 269-292	H	PVME1 IBVB2	14.00		
	Н	PVME! IBVK	74-00		
	_	PVMBA HPBOB	271-206		
	L	PVMBA WHVI	200-203		
	<u>!</u> -	PVMEA WHV69	274-290		
	 	PVMSA WAV?	274-288		-
	+	BUMA ANNA	334.288		-
	4	BAUM YEWAL			
	_	PVMSA WHYBI	274-280		
	-	PVMSA WHYWB	126-149		
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014-030	807-828	188-180	743-768	130-182	420-410	427-448	426-447	057-070	884-878	414-430	21.28	304-328	106-217	132-164	196-217	106-217	166-217	132-164	131-162	203-216																									·
-					PYOLY LABO		1	l		ı	PVM1 REOV.																														-				

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TABLE XIII

SEARCH RESULTS SUMMARY FOR PIZLZIPC MOTIF

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	POLEMIIAL IN KD PADIEIN	100.00		I	ī			L				
AACCC	DRIA LIST	CHACLO PATTLE VIRIIS (STRAIN STM)		Ī	A-IDRIAL	VEC	A VIEW	ABEA			j	_
VIETE VACC	THE TANKS	VACCINA VINIS (SIPAIN CONTINUACION)		1	_		-		9	4	3	_
PHIS VARY	INCA-ISO	VACTURA VIRING (STRAINS W. R.)	2 :	2	_		_			İ		_
PATHI FOWING		VARRIL A VIRIL	\$	<u> </u>	_	:	· -	_				_
PATH VACCV	PARO A. TWO EAST COLUMN TO SERVICE TO SERVIC	TOWN TO WINDS HALL AND AND THE AMERICAN	j .		_							_
VAN TAN	ALL DE LA COLONIA DE LA COLONI	VACCORIA VIRING TO BASE TO BE	3.4	_	-	-	:	_				_
121111111111111111111111111111111111111	MILITARIA MILITA	VANIGLAVIRITA	20.4.0	<u> </u>	-					:	:	
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15	THE PARTY INCLUSION PROTECT	THE PERSON NAMED AND PARTIES.	143.22	_		•	_					
	ALPHA TRANS. INDUCING FACTOR 14 ED PROTEIN	THE PROPERTY OF THE PROPERTY O	:	<u> </u>	-	-	_					
A LID AACC	PUTATIVE A-TYPE INCTINENCE SECTION	TANKELLA ZOSIER VIRUS (STRAIN PINIAS)		<u> </u>	-	_		1	i	:		
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	LINAMSCHITTONAL REGULATORY PROTEST		1	1	:			!		i		
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	CELL SURFACE BINDING PROTEIN	CALCARIA CALLA CAL			3	į		İ	:	!	i	
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rEie Ablei	EARLY EIS 10 4 KD PHOTEIN PRECURSON	INDIAN ADENOVIBING TYPE?	E	İ	-				Ì	Ť	İ
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ŀ		BOVDE LEUKEADA VIRUS (IAPANESE ISOLATE BLV.)	<u> </u>	İ		Ī			İ	İ	!
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178.1		MALES VINCE (STRAIN PV)	244.286	1342.541			-			İ	
3	ANA POLTIMORASE DET	AABLES VIBUS (STANIN SAIDNIS)			1		_				
FRAT. BOV	AMA CHINECTED MAY PO	PARTY REPORT OF THE PARTY OF TH	ź	367.78	2	1	1003:131	1744.1761			
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THE PERSON	100	ATTECHNOLIC LEAD SPOT WRUS	121.249	1036.1054							
	TOTALINE SURPLINE CITED BYA POL	PERT WESTERN YELLOWS VIRUS (150LA SE FL.)	1								
MACO BYON	PUTATIVE MA-DORECTED FUA FOL	BARLEY YELLOW DONABE WANTE JIETH APP LIAN BELL									
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	PULL HAND COLLECTED AND POL	CUCLACREA GREEN MOTTLE ANSAIC VIRUS IWATERAISION STRAIN				-					
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2	PUTATIVE KINA DERE	IONACTO MINE CONTRACTOR	11.94	(X:5)		I					
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PARTO TAM	HITATIVE BUT KINE?	CHALLO MOSAR, VIRUS (SIRAIN KONEAN)	1	IX.	-					•	
PERMIT PAYA	LA PASPASA A	TOBACCO MOSAIC VIRUS (STRAIN TONIATOR)								Ī	Ī
	TAN-CHARC ED PAY	TOBACCO MECROSISTMENT (STRAIN A)	1	9	2	1317.1616			ŀ	Ì	1
3	ANA-DIRECTED BNA P	TOBACCO RECROSIC MAIN ASTRACTICAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TO		1					:		
AND ON	EMA POLYMERASE AL	Cliamina as Charles and Company			:	:	: :			=	_
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100		MUNUS VIRUS (STRAIN ENDERS)		-						İ	Ī
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2	100	PREWCASTLE DISEASE VIRUS (SPRAIM MEALUIC TILL TILL)			-	٠	-				
	MAN TOLINGTAN AL	HUMAN PARAING LIF NOT STUBBER				•		•	:		
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	WAY THE MASS ALTHA SUBLORY	MADILL MILLS ISTRAM SANATON		216-217		-			Ì	Ì	1
	PINA POL PARRASE AL	SAMILAN WASHER A 1878 THUTTER	77	216.317			İ	İ	İ	İ	
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	A CAUCALLE DISPAULA	VACCING VILLS ISTRAIN COSTMILACEM				-	İ	İ	Ì	İ	Ī
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ANY AND	SUPERDRIDE DISMUTAS	VARIOUS A VIBILIE	97		İ			Ì	1	1	1
THE ALEN	SPERODO	AURIA TIMORITE	07-61			Ī	İ	Ì			
THE CHO	SPIEADIDIN PRECURSOR	Charle Power Living Control (1)	26-30	973-679	T	†	İ	1	j	Ì	
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MAY AWKY	Switch Profession	HYXUMA VIRUS (STRAIN LAUSANNE)	84.9		1		j			-	<u> </u>
HALA MIN	A A GOOD TO A A SHOT OF CO.	SWINGFOR VIRUS (STRASH KASZA)			j				Ì		-
PIAL & BANK.	1000	BUDGENGAR REDGLING DISEASE VIRUS					-	-			Ī
	LANCE I ANTIKEN	POLYOMAYRUS BR (STRAIN AS)				-			l	İ	Ī
	LARGE I ANTIGEN		201:00	12.45			t	T		İ	Ĩ
2	LAFGET AMIGE		¥1:24	- TA-44					İ	1	1
YWO YY	= -	HAMSTER POR UNITED IN	387.460		-	İ	t	1	1		
TALA POYK	LAKOL I ANTICEN	PAC STATE COMPANY INCOM	97-50	30.55	İ	İ					
TALA MON.Y	LAKOK Y ANTICEN	Serious Augusta	18:18	177.00	Ť	1					
TYM YTYL	Wild Partices	THE MAN TO THE VINUS	17 (55.45	İ	1				L	1
TALA PONCA	LABCE FANKEL		194.46		j					-	Ī
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	CANCEL AND MAIN	STANK B NAM		7		-	İ	İ	<u> </u>	l	Ī
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Y	MIDOLE 1 ANTIODA	1116	200 223	411-441		l		1	Ì	1	1
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	I I WAS ALL I I A TONG THAN REG PROTEIN		1				ŀ	l		1	1
CIAIR PEVO	TRANS-ACTIVATING TRANS REG PROTEIN		27			\mid		t		1	-
_	TANKS ACTIVATORS TILANS REG PROTEIN		10414		l	1	1	\dagger	1	1	-
	TRANS ACTIVATING TRANS REG PROTEIN		15.39	İ		1		1			
PTAT WILLIA	TRANSLACTIVATING TRANSLED PLOTEIN	Γ	£.50			1	1	1			
	TRANS-ACTIVATING TRANS REG PROTEIN	HALLING STATE OF THE PRINCE (STRAIN ATK)	12.21		1	1	1	1			_
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TILL TABLE TIAN INVITED TO THE PROPERTY OF THE	VIBUS HIDAAN BEADMODEFICIENCY VIRUS TYPE (STANIN UGANDAN) ISO	0 0 1 2 3	17	7	1519	AREAJ	1210	ANIA	AREA	
TA ATT BECEBION DES										200
The second second	FELDRE LEUKEMIA VIRUS				1					
PTECP MAYED PROBABLE TECHNISH PROSPINAROTEIN	EQUINE HEADELYINGS TYPE I (STRAIN ABAP)	9 19 19								
TECHNERY PROTEIN	EQUINE HEAVE SYDAUS TYPE I (STRAIN RENTUCKY A)				L					
V CAUCE TECHNOTION	EPSTEIN BARR VIRUS (STRAIN BOLD)	101-166	767.789	114.415	1017:101	114.125	1	(¥ -149)	100	ALL OF
ATENDATION TO A PROBABLE LANGE TELEBOOKEN PROTEIN	INDICAM CYTOMEGOAL DVINUS (STRAIN AD 149)	142-156	M4468	10011001	107-1111	133.134	1016-1446	1304-1314	1937.1931	1141.111
VII LAUG TEUDAGNI PROTEIN	HERPES SOUTER WINS (TYPE I / STRADA 17)	13.21	977-(29	11111111						
THE WAY I LANGE TECHNORY PROTEIN	HERPES SWOLLX YIAUS (TYPE 4.1 STRABIGS)	131-152	345.345	917519	1037-1043	1301.1331	14.13H		Ī	
TIEGU IGWED LLAGG TECHNENT PROTEIN	EQUING HERPESYINUS TYPE I (STRAIN ARMY)	33.4%	200	20.00 100 100 100 100 100 100 100 100 100	-	1611.1440	700	3341.3544		
PTEGU HEVSA PROBABILI LANCE TEGIANENT PROTEIN	(HERVES VIBUS SALMIN (STRAIN 11)	167.491	16:31	1001	-	וונבוווו			14.0	1101 1001
		1431.1634			_					
PIECU VZVO LARCE TEOUNEMT PROTEIN	VANCELLA-205 FER VIRUS ISTRAIN DIGITALS	27.15	117.77	23.11	102	27, 17,	7177			
_			٠	÷						2
PTEAM ADEAD IDNA PELAMINAL PROTEIN	AN BLANK APPEARTURE TO BE A		Ŧ	Ť						
•	DOMINA ADELIA VIA US 11 F. 1	20	2		į					
TEACH AND DAY ILLUMING THE PROPERTY	MUMAN ADENOVIRUS 1 YPE 5	6)-00	101-616							
_	MUMAN ADENOYIRUS TYPE 1	99-(9	(09.90)		-					
_	MUNAN ADEMOVIRUS 1 YPE 12	19-18	174.350	3 3						
181 DHA TOPOISONERASE IS	APICAN SWING FEVER VIALUS ISTRAIN BATIO	101	(81.70)		ŀ					
PIOPI ALFINE I ISHA TOPOSONESASSI SI	APACAN SWING FEVER VISUS (ICCLATS MALAW) (1) 2011		100		1					
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The Supplement	A COST PACIFICACION CONTRACTOR A SINO									
	VAUCELLA-ZOSTER VIRUS (STRADA DUMAS)	¥-:								
PUINT, MAY NO PUSSIBLE DANCE CLOVIN RIPASE	PERPES SPOLEX VIRUS (TYPE 6/STRAIN LIGANDA-1102)	14004								
PROTEIN IL	HERPES SHOLEX VIRUS (TYPE 6/ STRAIN UDANDA-1192)	1			-					
	AUTOCAAPITA CALIFORMICA MUCLEAR POLYTICOROSIS VIRUS	411.471			1		Ī			
HAPOTHETICAL PROTEI	PANAM CTIONEGALOVIRUS ISTRAIN ADIAN	1					1		::	-
AVA HYPOTIETEAL PROFEIN IA.S	MANAM CYTHAPPAI AVIAGE 1818 AND ADDAS		1		+			!		
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Villa Pick Benefit Av I R A	TOTAL CITCHES CALLOT INCH ALTER	2								
Т	PLACES SPORES VINUS (TYPE I / SPACES !)	\$770								
T	EQUING MANUS TYPE I (STRAIN ABAP)	437-461			7.					
	DEDPENDENT SAMINI (STRAIN 11)	87-77								
PULCE ENV. HERUZ PROTEIN	EPSTERN-BALL VIRUS (STRACH RMS.0)	137-169	L							۱
	HUMAN CYTOMEGALOVIRUS (STRAIN AD189)	10.10	16.309							
1	HEAVES SOULEN VIRUS (TYPE I / STRAIN IT)	191.300								
	EQUING HEAVES WIRUS TYPE 1 (STRAIN ABAP)	6				Ī				
	HEADESVRUS EAGURI 18TEAN III					Ī	Ī			
PULLI YEND CEMESI MOTEIN	VARICELLA-EGSTER VINUS (STRADN DUNAS)	10.131	72.145							
_	HERBITE STATE LY VIRIOS IVAN I VETTANI IN						1			
•	WARITED A PRESED UND FOR A PARTIES.		ŝ							
-	TANCELLA COSTEN VIANO (STRAIN DOMAS)	511-512	393-616							
	MAJULIS SUPPLEX VIRUS (TYPE I / STRAIN IT)	564-584				Ī				ľ
	EQUIPE HEAVESYINGS TITIE (STILAIN ABAP)	161-161	613-420							
FULL VZ VD ORGEN OF MELICATION BINDING PROTEIN	VARICELLA-ECSTEA YTHUS (STRAIN DURAS)	16-03	168.190	406.900			Ī	I		
principal profes	HUMAN CYTOMEGALOVINIS (STRAIN ADIM)						Ī			
HINDREDICAL PROTEC	HUMAN CYTOLEGALOVIRUS (STRAIN ADIM)	646.443			Ī	Ī	Ī			
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PLALIA MEVILL PROPERTICAL LELIA PROTETIA	NEAPER LINGUE TO VINITARY 17 CONTINUE									
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17 64 15 14	EXCEPT REALISTINGS 11 FE. 1 (3.1 KAIT ABOT)	2								
т	HENTER SHOLLER VIRUS (TITTE I / STRAIM IT)	12-4								
POLICE RESIDENCE OF PROJECTS	EQUING HELPESYTAUS TYPE I (STRATH ABAP)	Î	111-161	34.33			Ī	I		Ī
7	PERPENTILS SAMINI (STRAIN II)	() ()	136.285			Ī	T	Ī	T	Ī
	VANCELLA ZOSTER VIRUS (\$1 RAIM DUNIAS)	100			Ī		Ī	Ī		
PROTEON BOLL!	REPSTEIN BALK VIRUS (STRAIN BOLL)						Ì			
PULIT HOMYA HYPOTHERICAL PROTEIN U.!	HERALD CYTOLECAL CONDING CONTACTOR AND					1				
PROTEIN 19	(Interest of the Control of the Cont	Ž								
T.	THE PERSON OF TH	-								Ī
Т	INDULATION SALKIN (STRAIN II)	1	141.370						Ī	I
INTROJUEJIRAL PRUTE	HUMAN CYTOMEGALOVIAUS (STRAIN AD189)	\$0-11			Ī		Ī	Ī		Ī

TENAME		An Visite (b. b.									
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PULJI MSVII	PROFFERENCE	PUNAN CYTONGOAL ONE IS ASSESSED.	391-234	L		1		-	Г	Т	1
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1000		TO STAND OF THE INSTITUTION OF THE					Ì	1			
	COM 18 PROTES	COURT MENUES VOLUE SYPE 1 (STRAIN ARCH		3		T	\dagger	1			
	MYNOTICAL PROPERTY.	SAN ELLA ZOSTERIYMUS (STRAIN DUNAS)	2	34.12	19.40	1	\dagger	1			Ī
	PROTEIN BLOK!	THE STATE OF DATE OF STRADY ADIAS		100.33		Ì	Ì	1			Ī
Š.		LYSTEIN-BARR WRUS (STRAIN ROLL)	1			1			-	Ė	Ī
TATA HEAVI	PROTECNIA	HUMAN CYTONE GAL OVINITY FRESH A	34.18		Ì	1		-		t	Ī
MAN TAN	Š	JOSEPH S SHOPLEY VIEW COME CONTRACTOR	104-111	Ī	Ī		L	l	İ	t	1
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	THOSE PROTECTION UL 15	THE STATE OF THE STRAIN ADION				ļ	1				Ī
	MINON PROTEINING 35	PROVES STAPLEX VIRUS (TYPE / STRABLE)	8	ĺ	İ	İ				-	Ī
_	WALCH CEAR 10 PROPERTY	EQUAL TRANSPORTED IN THE PROPERTY OF THE PROPE	0 4	İ	i		-		<u> </u>	İ	Ī
	A PROPERTY OF STREET	PERPER VINCE CALLED TO THE PARTY AND THE PERPENDING		-	_	~	: 	: :			-
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VALUE OF THE PARTY	MYPOTHETICAL MOTERATE 35	PUMAN CYTOMEGAL OVIRUS (STRAIN APIAN)	72.72	16.33	İ	1			L	<u> </u>	Ī
٤	WITOTAL MANAGEMENT	MONCH OF GAL DYBIR 1878 187	301.334	484.50	İ	1		L	-	1	Ī
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	L PROPERTY ULT	COLUMN VINUS (STRAIN LIO). B)				+	1	1		L	Ī
- 1		TOWARD LY TOMEGALOVIRUS ISTRAIN ABIAN	1		<u>:</u> 	-	:	1 : :			Ī
١.		MELDEL STRONG STATES TO SEE THE SEE		11403	İ				i	1	1
HISVEA	CENE A HENRY	EQUING NEW PETATOR TANK TO THE TANK THE	= 3		1	1		L	H	1	Ī
ı		PERPENDING CANADA CONTRACTOR ABOVE	I				L	-	1	1	7
T		AABICE STREET	7	S	L		-				
1	OLYCOPAGITERIA 13	THE THE PROS (STRAIN DURKS)	7	167-170	ŀ	-	1			_	
2	COPROTEIN UM	CANTOS SIDELEX VIRUS (TYPE 1/STRAIN)		317-516	ŀ		1			ŀ	Ī
CAZA ZONO	Ca Victoria	OUDAR HEAVESTANDS TYPE LATER IN THE CO.		1	\mid	1		L	-		1
TAN STAN	CAROTEO COUR IN SECTION 20	VAUCILIA-COSTER VIDE ACTES ALICE ACTES	20:00	1	1	-		L	1	+	7
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7			107	-	-	+				H	Ī
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THE HOW I			- A		1			L		1	1
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-	A ULA		T				L	1	$\ $	+	
			7	7	31.34	L	-				Γ
THE PERSON NAMED IN					L	-		1	1	L	Т
	CENT D MOTEON	STATES SOUTH WALLS (TYPE 1/STANK)			101.130 004.150	1				ŀ	T
1				113.50	445.463 6.44.45	7	7		L	ŀ	ī
2			ş	\$1.500	ī	7	23.4.5	1009-1021		H	ī
		VAUCELLA-ZUSTER VIRUS /STRAIN CHALLS	2			6				1	1
TO SOL			5.5	15.13		7	1	-	-	1	1
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اء	ALPILA FRANS-MOUCHIG FACTOR 91 8 KD PROTEIN		42.50	100	İ	Ī	Ī	Ì	T	Ì	Ī
	WOTHETICAL BIRDS PROTEIN	ENTERLAND VIAUS (STIANN BYS.9)	36.38	Ī	Ì	F	Ì	Ť		Ť	Ī
٠.	HYPOTHETICAL PROTEIN (ILA)	HEALAN CYTOMEGALOVIRUS (STRAIN ADIA)	12.15	12.15	İ	F	Ť	Ì	Ì	T.	ĺ
PULM HSVII	ECUMENT PROTEIN U.A.	HEADES SIACK EX VINUS (TYPE I / STRAIN IT)	236-353				Ì	T	İ	Ė	Ī
1	TPOTPATH AL GENE M FRUTEIN	PEARLS WINDS SAIMUU (STRAIN 11)	233-353								
A STATE OF THE STA	LUTEIN ULSO	PROMOM CYTOMEGALOVIRUS (STRAIN ADIEN)	94.119							Ī	
1 M	KOTKIN ULSI	IEWES SWOLEX VIAUS (TYPE I / STRAMI)	40.44				Ī	Ī	İ	Ī	Ī
	CHARLE FROITIN	COMMITTEE MESANTING A COMPINED TO THE PARTY	# T	:				•		_	
		PARAMINATION OF THE CAMPAN AND	1	-	-	.			_		
1		VAUCELLA-COSTER VIRUS (STRAIM DUNIAS)	30-48 0						<u> </u>		İ
- 1	OTEN BSLF	EPSTEIM-BAAR VIAUS (STRAIN BOLD)								T	
	STEW ULS	MENUES SIMPLEX VIAUS (TYPE 1/STRAM) 19)	,	19:50						İ	Ī
-1	OTEM ULS	EQUIPE HEAVESVIRUS TYPE 4 (STRAIN 1941)		7				Ī	İ	İ	Ī
_1		EQUINE HERPESYLLIS TYPE I (STRAIN ARCT)	Π	11.13	11111	-		İ	į	:	
1	AT MINI CENTE OF THE LESS	HERMINAMES SAMIRI (SIRAIM 11)	30,1	SE PER					_		_
	A REPLICATION CENS & PROTEIN	WARCELLA ZOSTER VIRUS (STRAIN DUMAS)	200	200	İ	1		Ì	İ	T	Ī
		PRINGAN CYTOMOGGALOVIEUS (STAAMS AD166)	1		ľ		I	T	İ	Ì	Ī
PIE I PSV6U	Log	PERPES SIMPLEX VIRUS (TYPS 4 / STRAIN UGANDA-1101)	5		İ	1		Ì	 	İ	Ī
	TEN CL &	HUMAN CYTOMEGALOYIRUS (STRAIN ADIES)				F	İ	İ	Ì	İ	
Y O	34.0	HUMAN CYTOMEGALOVIRUS (STRAIN ADISM)	Γ	12.03		Ī	Ī	Ì	İ		
WENT NOW		HUNGAN CYTONEDALOVIRUS (STRAIN ADIOS)	19:10	Ī	-	Ī	Ī	Ī	İ	Ť	Ī
MEN HOWA	CATION PACTED ULTO	HUNGAN CYTOMEDALOVIRUS (STRAIN AD166)	Г	88.438	11.00	1	18.83	Ì	Ì	T	
ا≥	IN UL1	INCHAM CYTOMEGALOVIRUS (STRABY ABIO)	Г		T	ŀ	T	T	İ	İ	Ī
	PROTEIN	EPSTEDLEARK VIRUS (STRAIN PPS.4)	1	T	İ	1	İ	Ì	T	İ	Ī
FLE TO HEIVEA HY	S) PROTEIN	PENESYRUS SAMMU (STRAIN 11)	1	Ť		İ	İ	İ	Ì	İ	Ī
PULM HOLYA HY	IN CE.14	HUMAN CYTONEGALOVIRUS (STILABI AD 14)	100	Ī	İ	F	Ì	Ì	Ì	İ	
PLET HON'A Y		HUMAN CPTOMEDALOVINUS (SPICATH ABINE)	L	103438	İ	1	Ì	İ	Ì	İ	Ī
MLN HOWA WY	MULN	PRINCING CALOVINUS (STRAIN AD169)	22:32	100.00	İ	ŀ	T	İ	Ì	İ	
PLE WANT H			200		İ		İ	İ	ļ	Ì	Ī
	CTURAL PROTEIN	HENDA CYTCHEGALOVIRUS (STRAIN ADISS)	111.00		İ	F	Ī	İ	ŀ	İ	Ī
ş١	CTURAL MOTEON	MUMAAN CYTOMEGALOVIRUS (STRADA TOWNE)	T		İ	-	T	İ		T	Ī
May Day	N PCON	EPSTED-BALK YRUS (STRADI 1995-3)	27 T	18535			İ	İ	İ	T	
Š	IN CA. BY	INMAN CYTOMEGALOVIRUS (STRAIN ABIO)	Г	Г	177		17.7	T	Ì	T	Ī
3	\$ 3	HEADER SHOLLS VINUS (TYPE 4 / STRAIN LICANDA-1102)	П	П			T	T	T	T	Ī
	ZAPROTEZN	REPRESENT STACK (STACK II)			116-363						I
		I DALAN CYTOMEGALOVEUS (STRATN ADIM)		151.179						l	
HI CANAL	THE PROPERTY OF THE PARTY OF TH	ALTER CONTROL (11TE 6 / STRAIN UCACOA-1101)	2	1	1						
HE OF MANUAL PARTY	17.	STEEDING COLOR BY CARING A VICE A THE LESS COLOR AND THE	2		1						
PULPS HENNY HY	FIG. 8	HELLAN CYTOMS GAL OVERUS (STRAIN ABLER)		İ	1		1	Ì		1	
7	L PROTEIN W	HEADES SAPLEX VIRUS (1971 6 / STEAN UCANDA- 1/0)	T	911.48	\dagger	Ì	1				Ī
ž		(ADIM)	T		T	T	1	T	1	İ	Ī
_	TEM BOLE)		111.101	T	t	T	T	T	Ì	İ	
Л	TEN ULOI		Г		T	T	T		t	t	Ī
THE PARTY OF	KITOTHETICAL PROTEIN IN	/ STRAIN UGANDA-I 102)	П	31.34		Ī		T		\dagger	Ī
Т	T ST PROTEIN								l	T	Ī
_	100	FILENCE CTION COLLECTION (STRAIN AD167)		195-191						İ	
-	Les Octos	FUNCTOR CT I UMBERALDY FEUR (STRAIN AD) 49	10.00								
	20,000									İ	
	TEN 12 100	HUMAN CYTUME GALDVINGS (STRAIN AD149)		87-130							
PLEASE HOLVA	0.12 (1)	THE MAN POTONE CALL CARRIES AND THE PARTY AN		j	1						
PULBI HOAVA HA	HYPOTHETICAL PROPENTAL!!		7	Ì	1	1					
PULBY JESTVA IN	MULIN	HIRAM CYTCHEGALOVRUS (STRATIS ADISM		İ	1	Ì	1	1	1	1	
ML MINING AN	WUL!!	MAKAN CYTOMEGAL BYRUS (STRAD) ADIEM	9170	T	t	Ť	†	1	1	1	
MUCE HOLIVA IN	MUCINI			T	\dagger	Ť	1	1	1	1	1
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THERM	PROTEIN	All Virginia (No Besterdephopos)	-								
	HYA HYPOINETICAL PROTEIN ULIS	HONE AND STATE OF THE PARTY OF	VIEW	1		Т	П	П		Ì	
	THE LIBRACEL DATA OF YCOSTILASE	FOUND AND COMPANY AND AND AND AND AND AND AND AND AND AND	2		7		3	AKEA	7	AREA	7.7.4.7
2	LUNACTUCKA OLYGOSYLASE	EOUNG VERSEALER STATE	12:00	I	1	7	1			Т	I
AACC	CC JURACE DHA GLYCOSYLASE	VAPPEND CONTENT OF STRAIN ABOVE	35.35	I	1	İ				l	T
	UNIVERSITY OF PEOPPLASE	VACTORIA METER SEE	19:10		Ì	1				T	Ī
	UNACEL DINA CL. PCOSTLASE	VALED A WALL	2	I	Ť	1				İ.	Ī
	MACEL DIA OLYCOS PLASE	VARKELLANGER	19:10		Ì	1				Ī	
	_ [COUNCE IN THE STATE OF THE PROPERTY	57.75		1	1	1				ŀ
NAME OF STREET		FOUND LEADER TO THE I (STRAIN ABAP)	199		1	1				F	Ī
SE PAN	PROTEIN UST HOUSE GO	AND THE PROPERTY TYPE I (STRAIM KINTIKKY A)			Ì				-	Ì	Ī
PUSED JICHYA	HOLD I PROTEIN	PSCUCCABIES VIAUS (STRAIN MA.))		İ				İ		-	:
VEN MEN	PUTATIVE OF VICES NEW TAIL	PROMO CYTOME CALOVINUS (STRAIN ADIES)					Ī	i	<u>:</u> 	1	j
TABLE 1852	MHAT WE GO WITH	MEMPES SHAPLEX WIRIS (1792 1.) CTB AND 11.	200			F	Ī	İ	1		
1	CANADA CA	MENDES SEATTLES WASHE / TOPE 1	11.70			1	1	1			
	ALC NO	HAMAN CVPOLARY DAILY	27.10		Ì	T	Ì				Γ
	HTPOTHETICAL PRO	HELLIN TYPOCHES (STANIN AD149)	20.61		İ	1	1			İ	
Y CO	HYPOTHETICAL PED	LEBELS OF STRUCK COVING (STRAIN AD 149)		Ì	Ì	1				Ì	Ī
2	HYPOTHETICAL PRO	CALLA COVINCE (STRAM ADIM)	9					-	-	İ	1
AVACH SISTA	WONETKAL PROFESSION CO.	AUTOM CTTOM COALOVINUS (STRAIN AD 169)		1	135-222	-			t	Ì	1
FURTHER HOLY	MYTOTAL PARTIES IN	MONAN CYTOMEGALOVIRUS (STRIABLANIA)		106-234			İ	Ì	1	1	
	TABLE TO SECURITION OF THE PARTY OF THE PART	MANAN CYTOMEGAL BYINGS (RTB AIN A TALLA)	2 2		İ		Ť	\dagger			_
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TO THE PERSON	THE PROPERTY OF	INDAM CHORECAL DURING STRATES TO	151-174	115.363	-	i	!	: :::	:	-	_
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	HYPOTHOTHCAL PROTEIN HWLF?	HALLING COLONIA STRAIN ADISS	28.60		1				-	-	Ī
LIZE HOWA	EALT MCLEAL PROFENINGS.	THE THE CALOVINUS (STRAIN ADIES)	1	7				-	-	t	Ī
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		85	HOPE JORGAN VILLE STRAND VATELL	40.59	ŀ	-	1	+	$\frac{1}{1}$	1		<u> </u>
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PVOL1 CYLLY	ES OL YCOPADITION PALCUNSON	BOVDER COROMAVIELE CETE AND 1 V. 144		T	7	╗	7	1235-1280		
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WOLS CALL	IN CHANGE AND BEEN BOOK	MUNICAL CORCINA VIRUS MOYY (STRADY WILD) TYPE 4)		\$201-646	1267-1290 [13	1317-1338	-		-	I
200	THE CANADA STATE OF THE PARTY AND THE PARTY	JACOUR CONCORAYTRUS MORY (STRAIN ASP)		_	11151301	1851286	ŀ	-		
200	TO SECURE AND ASSESSMENT OF THE PARTY OF THE	MUMUME CONCORDA VIRUS MONY (STRADH JAGAY / VARIANT CL.1)		\$501-464		1317-1334			-	I
	H A WASHINGTON MELLINGS	INCOMING CONCORAYING MAY (STRAIN MOX)		Г	1126-1149	1176-1197	l	-	-	
	IL OL TUPRO I INF PRECUESOR	MORCONE TRANSACSION & GASTROENTENTIS CONONAVIRUS (STRAI		18787	_	1	1374.1389			
	E C. TOMOTEN PRECISOR	PORCOR TRANSPOSSIBLE GASTROENTERITIS CORONA VIRUS (STRA)	Г	642.451	F	t	Т	1374-1307	-	I
	ALT COMPANY PRECUSOR	PORCINE TRANSMISSIBLE CASTROBYTERUTIS COROMA VIRUS (STRAL	Г	Т	T	T	7	19411161		I
	EL CLYCOPIONE PIECUSCO.	PORCHA! TRANSMISSIBLE GASTROENTENTIS CORGNAVIRUS (STRAI) (44.45	Γ	Г	Г	1	-	1777,1704	-	
	EZ GLY COMOTILIN PRECUISOR	PORCINE RESPIRATORY CORONAVIAUS (STRAIN MI) 1004 / BRITISH I		Т	7	1050,1601	-		$\left \right $	
	EZ CL. YCOPIOTEON PLECURSOR	PORCEME RESPUENTORY CORONAVENUS (STRAIN EMI)	L	34.591	T	1000.1071	\mid			
	ES CLYCUMINISM PLECUMISON	PORCINE TRANSHILE GASTROENTERITIS CORONAVIRUS (STRAJ	1	1	Т	+	1014-1042 137	1979, 1964	-	
	EL OL TOPROTEIN PRECUISOR	FELDE DEECTIOUS PEUTOMITIS VIX.US (STRAIN 79.1146)	614.16	t	t,	t	7			
- 1	E2 CL. YCOPHOTEIN PRECURSOR	AVIAN DEECTIOUS BRONCHITIS VIRUS (STRAIN 642)	Ē	÷	-	644-1661 116	111111111111111111111111111111111111111	+	1	
7	EZ CL. YCOPROTEIN PRECURSOR	ETTE	ı	Т	T	-				
	ED CL. YCOPROTEIN PRECURSOR.		Ĺ	100.00	1	100				
	EJ CR. YCCPROTECH PRECLASOR		1	Т	T		1		1	
Y C	EJ CL. YCOPROTEIN PRECURSOR		Γ	187.506	30.30	1001	\parallel			
	ES OL YCOPHOTEIN PRECURSOR		Т	f	Т		TAGE TAGE			
	E C. YOMOTEM		178.201	Т	Т	T			-	
1	EZ CLYCOPLOTEIN		178,201	T	l	\dagger	1			
	II C. TCM/IDTID		178-201	T	+	t	1			
b	CLYCOPROTEIN OF 18 PLECURSOR		132-752			t	\dagger			
V	ULYCOMOTER IN INSCINCE		Г	Г	136.737	1	+			
A COLOR	OLYCOTROPPE PERCUSOR	MUNICH CYTOMEGALOVICUS (STRAIN TOWNE)	35-336	107.133	31.3%	l	\dagger			
220	M. T. COTROLLER B. PRESCUEDOR		17:104		\mid		ł	-		
	A CAMERICAL IN LA CAMERICA		12-10)		ŀ	-	-			
	CLICOTACIENT PICE, URGO.		12-103	l	\mid	l	ł			
	CONTROLLING TRECORDS	toxy	P. 19		l	l	\mid			I
No.	CHICATACHEM BY ACCORDON	(TYPE 27 STRAIN 333)	39.90		-	t	-			
THE PERSON	OF UCCORDINGS BY FELLINGS	7)	36.96		-	l	-			
CASH TO	OLYCOPROTEIN B PLECUSOR	HEAPES SOULEX VIAUS (TYPE 2 / STRAIN SAE)	\$3.50	f	-	\dagger	1			
	CALYCOPROTEIN B (FRACMENT)	HERPES SINCE EX VIRUS (17PF. 67 STRAIN L'GANDA-1101)	T	13.144	\mid	\dagger	+	1	1	
TO STATE	CLYCOTROLLIN FRECURSOR	BOVINE HE BPESVING STYPE I	Γ.	104-999		\dagger	+		1	
2000	ALTOTROLEM BY PACCHESON	BOUNT IS AN SVINCE STATE AND BAND BOWINE MANNIELITIES	П	145.767	-	t		 -		
	CELECULARIES UNCON	INTERIOR OF A PAINT A TYPE, LASTRAIN COOPER)	016-269	9	-	ŀ	-			
								1		7

20044 20033	A COLUMN	Placentain	A Vinces (No Becterlophoges)					H			
EQUAR INDICATE WITH THE GENERAL MASSAGEMENT 131-151	CILL RANGE	PROTEIN		J.	1		Y V	7	Y WEE	7	2444
EQUAR REPUTANTS TYRE (\$170.00 km) PUTANTS TANKS THE (\$170.00 km) REPUTANTS TANKS THE (\$170.00 km) REPUTANTS TANKS THE (\$170.00 km) REPUTANTS	(ISOLATE HV\$25A) (EHV-I)		+			+					
EQUING REPARTANTS TITLE (STAND ALAD) 718-731 718-7	PVGCI HSVE	OLYCOPROTEIN B PRECURSOR		673-672	1	1		+			
EQUAR REALEMENT TITEL (FITAN MAN) EQUAR REALEMENT TITEL (FITAN MAN) EQUAR REALEMENT TITEL (FITAN MAN) REPETROIS LAWNOTH LOTTER (FITAN MAN) REPETROIS LAWNOTH LOTTER (FITAN MAN) REPETROIS LAWNOTH LOTTER (FITAN MAN) REPETROIS LAWNOTH LOTTER (FITAN MAN) REPETROIS LAWNOTH LOTTER (FITAN MAN) REPETROIS LAWNOTH LOTTER (FITAN MAN) REPETROIS LAWNOTH LOTTER (FITAN MAN) REPETROIS LAWNOTH LOTTER (FITAN MAN) REPETROIS LAWNOTH LOTTER (FITAN MAN) REPETROIS LAWNOTH LOTTER (FITAN MAN) REPETROIS LAWNOTH LOTTER (FITAN MAN) REPETROIS LAWNOTH LOTTER (FITAN MAN) REPETROIS LAWNOTH LOTTER (FITAN MAN) REPETROIS LAWNOTH LOTTER (FITAN MAN) REPETROIS LAWNOTH LOTTER (FITAN MAN) REPETROIS LAWNOTH REPETROIS (FITAN MAN) REPETROIS REPETROIS (FITEN			†		1	+		ŀ			
MAJER BEAR STREAM STREAM	2	CLYCOPROTEIN IN PLECIASOR				+	1	$\frac{1}{1}$	-		
WANGE FURNALE AND THE TOTAL TOTAL TOTAL TOTAL STATES 104-151	PYCLE HSVEL	CLYCOPROTEIN B PRECURSOR		117.00	t	-	+	+	-		
INSECTION LANGOTALCHERIT VAILS (STACK 613) 194-215 196-214	PVG B KING	CLYCOPROTEIN B PRECURSOR		Ť	Ť	31.7.1	-	+	1	ľ	
Intercretable Langeroff Activities with Stream Stales 184-181	100	TO UNION PRINTED PRINTED BY		٣	T	25	-	-			
International Control of the Contr	100	TALVAGENTERS NECT SOF		Т	L	6.766	 -	-	-		
MANDER CYTCHERADA OFFILES STATISTICS MANDER CYTCHERADA OFFILES STATISTICS MANDER CYTCHERADA OFFILES STATISTICS WALKELLA WALKELA OFFILES STATISTICS WALKELLA CYTCHERADA OFFILES STATISTICS WALKELLA CYTCHERADA OFFILES STATISTICS WALKELLA CYTCHERADA OFFILES STATISTICS WALKELLA WALKELD	L	Г		0.764	 -	-					
VALCELL COSTEE WILLS GTRAN INDUMAN VISION	WALL TOWN	AL VANDA OPENIA PREPARATOR	Γ	Г	Τ	1.765					
VARGELLA ZOSTEA VIRIGATES (198.4) 113 44.40) 14.20 1	1500	A WOMEN TO THE PRECISE	SKLITCHE ABITES VIEUE (STRAIN INDIANA FUNKLIAUSER PRICKIR)	L	Т	-	-				
INTERIOR SIDELEX VIRIS (TYPE 11 STRAIN US) 11:11 41:40 INTERIOR SIDELEX VIRIS (TYPE 12 STRAIN US) 41:41 INTERIOR SIDELEX VIRIS (TYPE 12 STRAIN US) 41:41 INTERIOR SIDELEX VIRIS (TYPE 12 STRAIN US) 41:41 INTERIOR SIDELEX VIRIS (TYPE 12 STRAIN US) 41:42 INTERIOR SIDELEX VIRIS (TYPE 12 STRAIN US) 41:42 INTERIOR SIDELEX VIRIS (TYPE 12 STRAIN US) 41:42 INTERIOR SIDELEX VIRIS (TYPE 12 STRAIN US) 41:42 INTERIOR SIDELEX SIDELEX SIDELEX VIRIS (TALAN US) 41:42 INTERIOR SIDELEX SIDELEX SIDELEX SIDELEX VIRIS (TALAN US) 41:42 INTERIOR SIDELEX VIRIS (TYPE 12 STRAIN US) 41:42 INTERIOR SIDELEX VIRIS (TYPE 12 STRAIN US) 41:42 INTERIOR SIDELEX VIRIS (TYPE 12 STRAIN US) 41:43	VALICALLA ZOSTER VIRUS (STRAIN DUMAS)	L	-	-	<u> </u>						
HEAPER SIGNETS WINLE (THE 1) HEAPER SIGNES WINLE (THE 1) HEA	1000	CU VANDA PETRON PREPAREDA	GENES SINCH BY WRITE CTYPE 1 / STRAIN (2)	Γ	(97-)	-	-	_			
HELDES EMPLEX WILLS (TYPE 7) 114-151 114		ON COMMENT SEEDINGS	GEPFS SINGLEY VIRILS CLYPE 1/STRAIN KOSI	Γ	1976	-		-			
HEAPES SENFLEX WILLS (TITLE 3'STRAIN 13); BOWING HEAPESVARIS TITRE ISTANICOWES) ECOUNG HEAPESVARIS TITRE ISTANICOWES) ECOUNG HEAPESVARIS TITRE ISTANICOWES) ECOUNG HEAPESVARIS TITRE ISTANICOWES) ECOUNG HEAPESVARIS TITRE ISTANICOWES) ECOUNG HEAPESVARIS TITRE ISTANICOWES) ECOUNG HEAPESVARIS TITRE ISTANICOWES) ECOUNG HEAPESVARIS TITRE ISTANICOWES) FELDERAL JOSTEM VIRUS (STRAIN MAY)	(TYPE 2)	100	l	L	-	-					
ECONOMIC REPRESENTS TITELS AND STREET 111-044 111-	1000	AL CONSECUTION OF MANAGEMENT		10.00	ŀ	-	<u> </u>	<u>:</u>			'
EGUING MEDICAL VALUE INTERNATIONAL STRAIN KENTICKA AT 1244 EGUING MARKES TREASTRUM TITLE INTERNATIONAL STRAIN KENTICKA AT 1244 EGUING MARKES TREASTRUM THE AT 11 TAKEN MEDICAL STRAIN ST		A VANDA CHEMINE AND THE WAR		2	<u>:</u>		<u>i</u>	:	<u>:</u> :-	:	:
ECUTION ACASES TEALEST REPRESENTED (STRAIN RES) ECUTION ACASES TEALEST REPRESENTED (STRAIN RES) FREDERS STRAIN STRAIN STREET (STRAIN RES) FREDERS SEPECAT VIRIA (TITAL NEW SITE)		444.459		l		-	 - -				
ECTING MARES STRUKER PERPENNIUS (STACKIN INC.) 194-21	1	CI VONDA OFTEN C PERCONADA	COURS MEANS VILLS TITLE LITTLES ARTHANDISTRAIN KENTING	429.442	l	-	-	<u> </u>			
ECTION WALETS DISLASS HEREFELVENUS (STACK)		WAS THE THE THE WORDS THE CASA SECURIOR		199-421		-	-				
FOR SOM WADEN'S DISAGE WEST-SWILLS (TRAIN CA) FOLDSOM WADEN'S DISAGE WEST-SWILLS (TRAIN CA) FOLDSOM SALES BEREAT WILLS (STRAIN CA) VARICELAL SOFTER VIRUS (TRAIN SOFT) VARICELAL SOFTER VIRUS (TRAIN SOFT) VARICELAL SOFTER VIRUS (TRAIN SOFT) VARICELAL SOFTER VIRUS (TRAIN SOFT) VARICELAL SOFTER VIRUS (TRAIN SOFT) VARICELAL SOFTER VIRUS (TRAIN SOFT) VARICELAL SOFTER VIRUS (TRAIN SOFT) VARICELAL SOFTER VIRUS (TRAIN SOFT) VARICELAL SOFTER VIRUS (TRAIN SOFT) VARICELAL SOFTER VIRUS (TRAIN SOFT) VARICELAL SOFTER VIRUS (TRAIN SOFT) VARICELAL SOFTER VIRUS (TRAIN SOFT) VARICELAL SOFTER VIRUS (TRAIN SOFTER VIRUS SOFTER VIRUS ENDANS ELEPATATON V STRCTTLAL VIRUS (STRAIN SOFT) MALAN RESPERATOR V STRCTTLAL VIRUS (STRAIN VALLE) COMPANY OF LAND COMPANY OF LA	LABER'S DISKASE PERPESVIRUS (STRAIN RD-19)	17746		-	-						
VALCELLA SOFTE VELUS (STRAIN MIN) 194-21 114-47 1		SECRETARY TO WANTE FOR TAKEN THE CHILDREN	AARPES INCLASE MERPES VIBILS (STRAIN CA)	146.420	l	-	-	l T	-		
VANCELLA 205TEN VIRLIS (TITALIN DIALAS) 11-44 11-45 11		SECRETARY OF TOTAL OF A DOLL OF A DOLL OF THE CONTROL	JAPER'S BASEA CO LEMBER CONTRACTOR AND LITTLE	100	l		ŀ	 			
VANCELL 108TES VILUI (ITANIN DURAS) VANCELL 108TES VILUI (ITANIN DURAS) WELLINI SARLEL VILUI (ITANIN DURAS) WELLINI SARLEL VILUI (ITANIN DURAS) WELLINI SARLEL VILUI (ITANIN DURAS) WELLINI SARLEL VILUI (ITANIN DURAS) WELLINI SARLEL VILUI (ITANIN DURAS) WELLINI WELLINI	THE PARTY OF THE CASE OF	Т			-	-	-				
VARCELL 2011B VINUS (TRAIN EXCIT) VARCELL 2011B VINUS (TRAIN 17 AND (TYPE 1.1 STAIN PLAN RELIES BEPELS VINUS (TRAIN 12 COLUMN 17 AND (TYPE 1.1 STAIN PLAN RELIES BEPELS VINUS (TRAIN EXCIT) VARCELL 2011B VERIA (TRAIN EXCIT) VARCELL 2011B VERIA (TRAIN EXCIT) VARCELL 2011B VERIA (TRAIN EXCIT) RELIES BEPELS VINUS	THE PARTY OF THE P	Т	†		+	+	ļ		1		
VALUES SEMELX VARIATION TOTAL AND (FAVE 1510.01) TOTAL SEMELX VARIATION TOTAL SEMELX VARIATION TOTAL SEMELX VARIATION TOTAL SEMELX VARIATION TOTAL SEMELX SEMEX	AZA Z	CLYCOPIOTUS OF	VACCELLA COSTEM VINOS (STRAIN DOMINA)		t	1	-	+	-		
REPUBLY VALUE (TYTE 1) 15-10 15-	70	OLYCOROTLA OV	VACACLES COMMENTED IN VIEWS (STEAMED SECTION)		T	+	-	+			
REALIST SEPLEX TOTAL TITLE IS STAIN 17 WALCELL - 2071B VEUL (TTAIN DUALS) 104-15 112-15 112-15 105-	-1	CLYCOTION OF BUILDING	MANAGED STREET, VINDA (STREET, STREET,		t		-	$\left {} \right $	-		
VALCEL LAGITA THAN IT AND THAN ATTEMS OF THE STATES OF THE	200	OLYCOPHOTISP D PURCUROR	MELTINE SECTION VINCE (1 FPS 2)	1			+	1	-		
### ### ### ### #### #################		OLICOPIOTER B PICCORDS	Т	1			-	-	-		
### ### ##############################	2	CLYCOTROLLER I PROCESSA	Т	T	T	39.5			-		
### ### ##############################	W PAN	PUSION OF TOPHOTEEN PLO	Т	T	7	3	1	╀			
CANNE DISTINCT VINUS (STAND ORDER STEPPORT) CANNE DISTINCT VINUS (STAND ORDER STEPPORT) HALAN RESPRANTORY STRUCTIAL VINUS (STAND AS) HALAN RESPRANTORY STRUCTIAL VINUS (STAND AS) HALAN RESPRANTORY STRUCTIAL VINUS (STAND AS) HALAN RESPRANTORY STRUCTIAL VINUS (STAND AS) HALAN RESPRANTORY STRUCTIAL VINUS (STAND AS) HALAN STRUCTIAL VINUS (STAND AS) HALAN STRUCTIAL VINUS (STAND HALLE) HALAN STRUCTIAL STAND AS A	ı	T	T	757		-					
High REPRATOR Y STACTTLE VIRIS (LUBGROUP B) STAIN 115 305-221 155-530 104-500 High REPRATOR Y STACTTLE VIRIS (STAIN A) STAIN 115 305-231 155-530 104-500 High REPRATOR Y STACTTLE VIRIS (STAIN A) STAIN 115 155-530 104-500 HIGH REPRATOR Y STACTTLE VIRIS (STAIN BELLE)	NS.	PUNCH CLTCOPULING THE LUCK		T	Т	1.446	+	-			
HALLAN REPRATORY SPRETIAL VIRUS STATUM A.2] 705-21 136-750 644-564 HALLAN REPRATORY SPRETIAL VIRUS STATUM A.2] 715-75 131-75 144-564 HALLAN REPRATORY SPRETIAL VIRUS STATUM A.2] 715-75 131-75 144-564 HALLAN REPRATORY SPRETIAL VIRUS STATUM A.2] 715-75 131-75 144-76 144-76 146-76		THE STATE OF COMMENDED IN PARTY OF STATE	GAZAN BESPRATORY SYNCYTIAL MALISTRIBOROUP BY STRAIN 185	361-23	Т	1,50			-		
HUMAN RESPONDED STREETILA VIRUS (STAAN RES.) 181-151 141-150		THE REPORT OF THE PARTY OF THE	HENDAN BREDINATORY SYNCYTIAL VIRIES ISTRADA AZI	L	Т	25.7	H	-		L	
MOLEAN RESPICATION STACKTION, VIRIAGISTAND 185.31 105.211 185.310 105.500	M. Com	THE SOUND IN THE PROPERTY PARTY.	HIMAN RESPERATORY STINCTIVE VIRUS (SUBGROUP A / STIKIN LO		Г	14-506					
DEALES VIRES (STAND ESPORATIONS—4 (STAND MALLE) 134-141 184-202 411-471	With Bay	ALSON OF YOOM BY THE	HIDGEN RESPIRATIONY SYNCYTIAL VIRUS (STICAIN 1855-3)			14-506					
PACALE VALUE (STAND VALGAYA.) 111-144 118-100 414-400 PACALE VALUE (STAND VALGAYA.) 130-140 131-140 AGAGE VALUE (STAND VALGAYA.) 130-140 131-140 AGAGE VALUE (STAND BLA) 130-140 131-140 AGAGE VALUE (STAND BLA) 130-140 131-140 AGAGE VALUE (STAND BLA) 130-140 131-140 AGAGE VALUE (STAND BLA) 131-140	AEASLES VIRUS (STRAIN EDMONSTON)AM (STRAIN HALLE)			11-433		Н					
MACKELS WILLS (FIALMY MAKAGATA.) 214.450 314.771 MACKET WILLS (FIALMY BLV) 124.450 134.771 MACKET WILLS (FIALMY BLV) 126.772 146.451 MACKET WILLS (FIALMY BLV) 126.772 146.451 MACKET WILLS (FIALMY BLV) 126.772 146.451 MACKET WILLS (FIALMY BLV) 126.772 146.451 MACKET WILLS (FIALMY BLV) 126.772 146.451 MACKET WILLS (FIALMY BLV) 126.772 146.451 MACKET BESELS WILLS (FIALMY BLV) 126.772 MACKET BESELS WILLS (FIALMY MAKELA) 126.773 MACKET BESELS WILLS (FIALMY MAKELA) 126.773 MACKET BESELS WILLS (FIALMY MAKELA) 126.773 MACKET BESELS WILLS (FIALMY MEENSLANDW)	MEASLES VIXUS (STLAIN IR-3-CA)			24.68			-				
MAMES VALUE (STALM BELL) 15-30 13-37 13-37 14-45 MAMES VALUE (STALM BELL) 15-37 14-45 MAMES VALUE (STALM BELL) 15-37 14-45 MAMES VALUE (STALM BELL) 13-37 14-45 MAMES VALUE (STALM BELL) 13-37 14-45 MAMES VALUE (STALM BELL) 13-37 13-37 MAMES VALUE (STALM BELL) 13-37 13-37 MAMES VALUE (STALM BELL) 13-37 13-37 MAMES VALUE (STALM BELL)	MEASLES VIILLS (STRAIN YAMAGATA:1)	П	┪			-	-				
MANDER WILKS (STANIN MAYANGA VACCINE) 131-577 144-461 MANDER WILKS (STANIN MAYANGA VACCINE) 131-577 144-461 MANDER WILKS (STANIN MAYSTRALLA-VICTORIAN) 131-379 144-461 MEWCATILE DESALE WILKS (STANIN MADERALI) 131-379 MEWCATILE DESALE WILKS (STANIN MADERALI) 131-379 MEWCATILE DESALE WILKS (STANIN MADERALI) 131-379 MEWCATILE DESALE WILKS (STANIN MADERALI) 131-379 MEWCATILE DESALE WILKS (STANIN MADERALI) 131-379 MEWCATILE DESALE WILKS (STANIN MADERALI) 131-379 MEWCATILE DESALE WILKS (STANIN MEXAS)	MONDES VILLES (STEADY SELLI)	Т	7	199	+	+	$\frac{1}{1}$				
MAGGY VALIG STRAIN NY MAGGY VALIG STRAIN NY MAGGY VALIG STRAIN NY MAGGY VALIG STRAIN SAY MAGGY VALIG STRAIN SAY MAGGY VALIG STRAIN SALLOSTTA. MAGGY VALIG STRAIN SALLOSTTA. MAGGY VALIG STRAIN SALLOSTTA. MAGGY VALIG STRAIN SALLOSTTA. MAGGY VALIG STRAIN SALLOSTTA. MAGGY VALIG STRAIN SALLOSTTA. MAGGY VALIG STRAIN SALLOSTTA. MAGGY VALIG STRAIN MAGGY VALIG STRAIN MAGGY VALIG STRAIN	MUMPE VIRUS (STRAIN MOTANCIAL VACCINE)	1	Ì	-	1	1					
MAGESTALM STALM SALES MAGESTALM SALES	PYOU MUSTON	FLEION CLYCOPROTED PRECURSOR	MAROS VOLIS (STRAIN RW)	Т	7			-			
HIGH CATOMEDIEN PLECIALOR WENCATLE DESAIS VALUE STAUM ASSIGLATOR COMPANY HIGH CATOMEDIEN PLECIALOR WENCATLE DESAIS VALUE STAUM REALDETTE COM HIGH CATOMEDIEN PLECIALOR WENCATLE DESAIS VALUE STAUM 111-189 HIGH CATOMEDIEN PLECIALOR WENCATLE DESAIS VALUE STAUM 111-189 HIGH CATOMEDIEN PLECIALOR WENCATLE DESAIS VALUE STAUM 111-189 HIGH CATOMEDIEN PLECIALOR WENCATLE DESAIS VALUE STAUM 111-189 HUBBOR	MAINERS VIRUS (STRAIN SIM.)	I	7	à	1	1	+				
HUSION CLYOPHOTEN PALCIAGON NEWCATTLE DESASS VALUE STAKEN ELOS 171-379 HUSION CLYOPHOTEN PALCIAGON NEWCATTLE DESASS VALUE STAKEN 171-379 HUSION CLYOPHOTEN PALCIAGON NEWCATTLE DESASS VALUE STAKEN 171-379 HUSION CLYOPHOTEN PALCIAGON NEWCATTLE DESASS VALUE STAKEN 171-379 HUSION CLYOPHOTEN PALCIAGON NEWCATTLE DESASS VALUE STAKEN VALUE STAKEN 171-379 HUSION CLYOPHOTEN PALCIAGON NEWCATTLE DESASS VALUE STAKEN TEXAS 171-379 HUSION CLYOPHOTEN PALCIAGON NEWCATTLE DESASS VALUE STAKEN TEXAS 171-379 HUSION CLYOPHOTEN PALCIAGON NEWCATTLE DESASS VALUE STAKEN TEXAS 171-379 HUSION CLYOPHOTEN PALCIAGON NEWCATTLE DESASS VALUE STAKEN TEXAS 171-379 HUSION CLYOPHOTEN PALCIAGON NEWCATTLE DESASS VALUE STAKEN TEXAS 171-379 HUSION CLYOPHOTEN PALCIAGON NEWCATTLE DESASS VALUE STAKEN TEXAS 171-379 HUSION CLYOPHOTEN PALCIAGON NEWCATTLE DESASS VALUE STAKEN TEXAS 171-379 HUSION CLYOPHOTEN PALCIAGON NEWCATTLE DESASS VALUE STAKEN TEXAS 171-379 HUSION CLYOPHOTEN PALCIAGON NEWCATTLE DESASS VALUE STAKEN TEXAS 171-379 HUSION CLYOPHOTEN PALCIAGON 171-371	NEWCASTLE DISEASE VIRUS (STIAIN AUSTRALIA-VICTORIAATZ)	217.72	1	+	1	+	+				
1930 OL VOORDITAL PIECUSOR PERCATILE DESAGE VOLG STAGEN 131-349 1930 OL VOORDITAL PIECUSOR PERCATILE DESAGE VOLG STAGEN 131-349 1931 OL VOORDITAL PIECUSOR PERCATILE DESAGE VOLG STAGEN 131-340 1931 OL VOORDITAL PIECUSOR PERCATILE DESAGE VOLG STAGEN 131-340 1931 OL VOORDITAL PIECUSOR PERCATILE DESAGE VOLG STAGEN 131-340 1931 OL VOORDITAL PIECUSOR PERCATILE DESAGE VOLG STAGEN 131-340 1931 OL VOORDITAL PIECUSOR PERCATILE DESAGE VOLG STAGEN 131-340 1931 OL VOORDITAL PIECUSOR PERCATILE DESAGE VOLG STAGEN 131-340 1931 OL VOORDITAL PIECUSOR PERCATILE DESAGE VOLG STAGEN 131-340 1931 OL VOORDITAL PIECUSOR PERCATILE DESAGE VOLG STAGEN 131-340 1931 OL VOORDITAL PIECUSOR PERCATILE DESAGE VOLG STAGEN 131-340 1931 OL VOORDITAL PIECUSOR	NEWCASTLE DISEASE VIRUS (STRAIN BEAUDETTE CAS)	A	1	1	1		1	1			
HISTOR OLYCOPOLISM PRECINESS	DIACK FROMO	FUSION OLYCOPROTEDI PRECURSOR	MEWCASTLE DISEASE VIKUS (STRAIN HER/J))	277-78	1		1	+	1		
HIGH OLY COPPOTENT PLECTALEON WEWCATTLE DESCRIE VALUE (STACH LADELAGE) 27-129	PWOLL HOWA	FUSION OLYCOPROTED/PRE	HEWCASTLE DISEASE VIRUS (STIVAIN B.I-HITCHMEUAT)	277:289	1	-	1	+	$\frac{1}{1}$		
FUSION CLYCOPHOLISM PRECUISOR FUSION CLYCOPHOLISM PRECUISO	PAGE 15W	PUSION OL YCOPROTEEN PL	NEWCASTLE DISEASE VIRUS (STRAIN LASVA)	£	1	1	+	+	4		
FUNCTOR OLY CORPOTED PECULAGO	PHOL HOW	FUSION OL VOOPLOTEDY PLA	NEWCASTLE DISEASE VIRUS (STRAIN MOYADERASI)	277-200	1	1	1	+			
FUSION OLYCOPROTED PECULSON. PREVIOUS ESTADAY TEXAS 0 M/S). FUSION OLYCOPROTED PECULSON. PREVIOUS (STALM TEXAS 0 M/S). FUSION OLYCOPROTED PECULSON. PREVIOUS PERMIS (STALM USTELMS). FUSION OLYCOPROTED PECULSON. FUSION OL	MOT TOW	FUSION CL. VICOPLOTEEN PR	PEWCASTLE DISEASE VIRUS (STRAIN QUEENSLANDAS)	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1	1	+	+	1		
PUSION CANOMEDITAL PLACUESTS. PREMOLE CANOMEDITAL PLACUESTS. PREMOLE CANOMEDITAL PLACUESTS. PREMOLE CANOMEDITAL PLACUESTS. PREMOLE CANOMEDITAL PLACUESTS. PROCEED PLA	WOLL DW	FUSION OL YCOPROTEDI PR	MEWCASTLE DISEASE VIRUS (STRAIN TEXAS)	42.172	1	+	+	+			
FUSION OF POSTBOLINA PERCURSON PROCEED BISTRICES VIRUS 187.311 187.311 187.311 187.311 187.311 187.311	TYCH NOVICE	PUSION OL MODPROTEDI PLE	NEWCASTLE DISEASE VIXUS (STRAIN TEXAS C B 745)	A	1	+	1	+			
PUSION CLYCOPROTEIN FIELDINGS JANUAR US LAUREN FIELDINGS JANUAR JAN	NO.	PUSION OF ICOPROTEDY FIL	TEWAS ILE INSENSE VIXUS (STRAIN ULSTERMY)	1	-	•		+	1		
1	TYCH HOOM		PHOCONE DISTEMPER VIRUS	1	-	1		$\left\{ \right.$			

TANK THE	PROTIEM	(1)									
		VIRO			1						
	I USION OF TOPROTERY PRECURSOR	MUMAN PARADALLENZA I VIRLIA SETRATIO PIA	4	4	7	AREA	148143	AREA	AREAS	V V V	100
	FUSION CLYCOPROTEIN PRECURSOR	MUNCAN PARADITLIENZA 9 CIRTIS 2812 31	436.431					г	L	7	
	FUSION OLYCOPROTEIN PRECURSOR	MOKAN PARAMETTEMPA SCIPLIS ASSESSED	426.43							Ī	
-1	PUSION OF YCOMO TEM PRECURSOR	MINAM PARAMILITARY STREET STREET	450-47:								
Way rus	FUSION CLYCOPROTTEN PRECURSOR	ROVING BABARATIESTS - THEIR (STRAIN TOSTINA)	430-431					I		1	
WCC PUH	FUSION OLYCOPROTEDI PRECURSOR	MOAN DASANCE TENSA STATES	405.436	483-484						Ī	
2	PUSION CLYCOPIO ITIN PLECUALOR	A PARCE MET VIGIT 12 11 11 12 12 13 14 15 15 15 15 15 15 15 15 15 15 15 15 15	2.7	213-310	45)-474				I	1	
OF REPORT	PUSION OF YOSPHOILERY PRECUREDA	PATIENTS OF CAPITAL CONTRACTOR (CAPITAL CONTRACTOR)	170-741	282-298	41.47					ľ	
Sapar Constant	PUSION OL YCOPROTEDN PRECURSON	(CADAL Walle general)	220-241	267.78	41.47						
MACE TENED	PUSION CLYCOPIOTEN PRECURSOR	SENDAL USAN (STACK Z / HOST MUTANTS)	460-481			ŀ					İ
PYGLI SENDH	FUSION CLYCOPIOTEM PRECURSOR	SENDAL Wells FIRE COMMIS	460-481			[1	1	
au seroi	PUSION OF PEOPLOTEIN P	SENTAL CASA (SINAIN MACCOS)	187-099			F				1	
-	PUSION CLYCOPROTEIN PRECURSOR	(SEPON VINCE (SEPON)	460-481								
	FUSION OL PCOPROTEIN PREPARECE	SHAVE COLORS	187-098							1	
	PUSION CLYCOPROTERI PRECY IN COR	SOUTH VIRUS 41	433-434							1	
WELL HER	PUSION GLYCOPAGITAN PARCY IN CO.	SIMILAN VIRUS S (STRAIN W))	401-425	46.46.9		F					
WOLD BOW	SPIKE OF WOODS OF THE PART IN THE	TURKEY KAMOTRACHEITIS VIRUS	-	27.25		I	I				
New Dir	SPILK (2. MODEOTEN PE	INTELTIOUS NEWATOPORETIC NECROSIS VIRUS (STRAIN ROUND BUT	BUT 17.99			I					
PVOLO BABWI	PIKE OF VICOMOTERN PAR	MADIES VIUS (STAIN ERA)	4,54.54			Ī					
CLO LUBVY	PIKE CL WOODSONE IN 10 EA	MADIES VIRUS (STRAIN MEP.FLURY)	372.381	24.474		Ŧ					
ALC LABOR	CHER OF WOMEN THE PARTY IN CALL	KABLES VIRUS (STRAIN PV)	434.434			Ŧ					
PWGLO EASY	SPIRE OF VOCABOTE SERVICES	KABIES VIRUS (STLAIN SAD BIP)	27.75	I		1					
ATH OT	MAINS STREAM OF THE WASHINGTON	INDIAN VIRUS (STAAM STREET)	27.25			T		1			
ASW OX	SPICE CLANDERSTEIN IN BUILDINGS	TUNCEY INDINOTACIDATE VIRUS	195.216			1			1		
NA HOW	CLYCOPLOTIFIED MARKET IN BOTH	VOCAL PERCONDIAGIC SEPTICEMIA VIRUS (STRAIN 07.71)	927-90¢	ľ		ŀ		1	1		
TO SAME	CL VOTBBOTTETA IN BESCH IN SOR	HUBICAL CTTOMEGALOVIRUS (STRAIN ADISS)	100	1	194.16						
	PVOLK NEVIL OLYCOPROTESTIVINE DA	HUMAN CYTOMOGOALOWINUS (STRAIN TOWNE)	ľ	Т	Т			1	1		
H KKVIS	OL WOODSONEN IN THE CHIEFLE	MEANES SEARCH X VIRUS (TYPE 1/8TRAIN 17)	Т	Γ	Т	ļ	I		1		
D RVID	OLVODROTEN HINECONDA	KEXTES SECTLEX VIRUS (TYPE I / STRAIN ISEM)	Г	T	103	1	Ī	1	1		
LH HEVE	OLYCOPROTERS N PREPING CO.	FEMALES SUPPLIES VINUS (TYPE 6 / STRAIN GS)	314-332	Т		I	1	1	1	1	
DAME I	OLVCOROTEN H PRECIMEN	EQUIPE REPORT TYPE 4 (STRAIN 1942)	304-323	107	T	I	1	1	1		
LI REVEA	PVOLA HSVSA OLVCOPROTION RESCUESS	DOUGHE PROPERTY IN THE 1 (STRAIN AB4) and (ISOLATE HVS)(A)	341.311	107-403	T	F	T	1		1	
NOW.	OLYCOPROTEIN H PRECIDEOR	MATERIAL STATES AND STRAIN II)		25.5	1	1		1	1		
THOM!	IS OLYCOPACITAL PLACIA LOS	M. LAND POR A MALL DATE OF THE SMITH IN	670-690		T	T		1	1	1	
HARI TON	GLYCOPROTEDA!	MERRY CARRY VIOLES (21 KAIR AD 169)	1186-180					1	1	1	Ī
WOLL HEWEL	CLYCOPROTESNI PAZEUREDA	FOLING URA SECURITY STATE IN STRAIN IN	4)-40						1	1	
WOLL VZVD	CAL POOPROTEIN I	VARIOTITAL POSTER VIBIR APPARATION	4443			T			T	1	I
PVOLLA BURGE	M POLYPROTEIN PREICINSOR	MCMYAVELY CERVISION	╗					† 	1	1	I
N MINE	IN FOLYMOTER PLECURIOR	MONYAVEDS LA CHOSES (COL A PET S.)		11.711				t		1	T
NEWS T	M POLYPROTEIN PRESURSOR	BUNYAVIOR CHOWCLES LAND		1 26-18	П	132-1345	387.1410		1	t	I
A BLANCE	M FOLYPROTEIN PLEISURSOR	BUNYALWERA VIRILE	٦		190-211	125-1341	1387-1410	1	1	1	T
A DOOR	M POLYPROTESH PRESINSOR	DUCAR VALLS	9776	1376-1404				1	1	\dagger	T
E T	M POLYPROYES PLEASES	HANTALM VIRILIE (1994 AND B. 1)							1	1	T
E E	M POLYPROTEDY PLECURSOR	NANTAAN VIDIN GERAPH MONON	7	٦	-	94-1019	-	T	1	\dagger	T
E S	M POLYPROYEM PRECINSOR	KANTAAN VIBLIS (STRAIN) PEN	П	П	0401-000I			T	1	\dagger	T
Š	M POLYPROTED PRECURSOR	MANTAAN VINLE LETTAIN SE 1161	٦	٦	1001-1031			\mathbf{I}		t	I
A DG A	M POLYPROTEEN PRECURSOR	De A TIENS MECHOTIC SPOT VARIE / NASA	_		1201-1001		l	t		1	Ī
È	M POLYPROTED PRECINEDR	PROSPECT NOT. VORUS	٦	36.76	148-167 51	1318-551	13.41		1	\dagger	T
¥ X	H POLYPROTEIN PLECURIOR	PUNTA TORO PIE PROVINCE	٦						t	\dagger	Ī
A PUSSO	M POLYPROTEIN PRECENSOR	PURDALA VIRINGETRAN UATTUACO	7	罛	1275-1302		 	T	1	1	Ī
N PUBES	M POLYPROTERN PRECURSOR:	PURMALA VIRUS (STRAIN COTE ALON	7		П			t	1	\dagger	Ī
À	M POLYPROTEIN PRECENSOR	ABT VALLEY PRIVER VIRUS	Ţ	П		1111-6401			\dagger	\dagger	I
Z X	M POL YPROTEDY PLECURSOR	ROT VALLEY PEVER VIRUS (STRAIN 21), (AB 1415)	I	7				H	+	\dagger	T
503	M POL YPROTEEN PRECURSOR	SECUL VINUS (STLAN) AS YOU	П	7	П	1154-1176		+		1	T
503	PYOLA SEOUR IN POLYMOTEDS PRECENSOR	SECUL VALIS (STRAIN 123)	Т	7	-	998. IDE6		\mid		1	T
	M POLYPROTEDI PRECURSOR	SECUL VIRUS (STRAIN SP. 11) (SAPPORO LAT VIBIR)	125.55		٦	9601-000					T
3	M POL T PROTEIN PRECONSON	UUKUMEMI VIKUS	L	Т		10			-	\mid	I
				•		ĺ					•

PCCAME	PINCHENE	All Virgen (No fine teriophoges)	1,444	Т		77447	2 7 7 2 7	7 7 4 4 7	6 7.84	77.87	12.84
DERAME	PROTEIN	VIRIUS (0.0 to the time			1006-1124	_	Т	1		L	L
NO.	PERCONDER OF TOWNS I EIN PA	EXAMPLE LEGISTRATION OF 1 / CTS ATM ABABI		Т		1		Γ		L	Ļ
2	GLYCOTION A PRECUNOR	COUNTY TO SERVICE THE LIGHT NOT THE AND A SECOND NOT THE PROPERTY OF THE PROPE				1				L	
¥	CLYCOMOTION OF PRECURSOR	EQUIPE PERCENTIAN TITE (STOCK AND UNITED AND AND AND AND AND AND AND AND AND AN						Ī			
VOX HEVE	CLYCOTABILITY OX	EQUIPE NECESTRATE 11 TE 1 (STACT) NECET OF 1 OF	¥.1.94			Ī				Ī	
WE YOU	SECRETED OF TOTAL DAY	Paradona Antonia Maria	1			Ī					L
Y 100	GL TCUTALI EN FOLTPROTEIN PARCUASON	LANGE CONTRACTOR AND	11.51	100	***	Ī	Ī				L
WG.V LA150	10 TOTAL SEPTEMBER OF THE SECOND	LAND AND TO THE LOCATION OF THE LAND AND THE LAND AND THE LOCATION OF THE LOCA		T	1	Ī	I				
3	GLYCOMOILE FOLYMOILE MINECUSOR	CONTRACTOR OF THE PROPERTY OF				T					L
XY LYCVA	OLYCOPROTEIN POLYPHOTEIN PRECURSOR	IL THUTHOLY IN CHANGOPENINGI IS VINOUS (SI RAIN AND SINONO)	۱	27. 99		ŀ	Ī				L
AY LYCW	CLYCOPROTEIN POLYPROTEIN PLECURSON	LETAPHOLYTIC CHOROCOMEPINGUITS VIRUS (STRAIN WE)	١		1	Ŧ					1
TAOM AT	CLYCOPADITA POLYMOTEM PRECURSOR	MOPELA VIRUS	ı		1	-					1
WOLY HARV	OLYCOPROTEIN POLYPROTEIN PRECURSOR	PICHENDE ARENA VIRUS	:	441.466							
VANT YE	GLYCOPROTEIN FOLYPROTEIN PAECUASOR	TACALDE VINUS	13:38			-					
1A-174 A E	CL VERHOPEN FOLVPROYEN PRECURSOR	TACALDE VINUS (STICALN VS)	11.31			7					
ATTA A RATE	AN WASHINGTON FOR YPROTEIN PARCURAGA	TACALDE VIRUS (STRAIN VT)	11:31			٠					
A PACKE	CLYCOPROTEIN FOLYPROT	TACALIBE WAUS (STRAIN TRYL (1996)	113.38			Į					
N. C.	CENTRAL BOX VOBOTERS B	COWPIA MOSAIC VALUE	101:101	25.72	197.783	1110-1135	1105-1164				
	AFCOLO DE CONTRES DA	COWSEA LANGAIC VIRING	507:115	74.74		-				L	L
١	CONCRETE TO STATE AND ADDRESS OF THE PARTY O	EDGESCHE BAND UNDER JETS ATM BOLDS AM BAND LIEBBERGWEINE AS	441.481			F					
ł	PLACE AND PARTICIPATE MAINTAIN	RESTRICTED TO THE CAPITY AND A PROSECULAR AND AND ASSESSION AS	184.479			ŀ				L	Ļ
	CAVELLITY OF TOWNS IN COMM	PROPERTY BASE CARING (STREET, BASE) CARING STREET,	19.69							L	L
ADA.	PROBABLE MEMBROATE AN INCH UP 5	STATEMENT AND CONTROL OF THE CONTROL		13. 13. 13.	76777	Ī	I				
ò	STRUCTURAL GLYCUPROTEIN PACEURSON	CONTRACTOR CONTRACTOR CANADA	171				I				
VCP MABWA	STRICTURAL CLYCOPROTE	MONGOUR CYLADS (STRAIN MUSCALE)	1		1	I	Ī				1
PVOP NAMV	STRUCTURAL CLYCOMOTEIN PRECURSOR	MAKEUNG YEUS (STRAM POPT)	700			1	T				1
DI VACCE	PROTEDLIYROSDIR PHOSPIL	VACCINIA VINUS (STILAIN COPENHAGEN)				1	I				1
PYHOL YACKY	PROTEIN TYROSING PHOSPIC	VACCINIA VIRUS (STRAIN WIL)		2		Ŧ					1
OL VARV		VALUE VIEWS		7		Ī					1
AACC		TALLING THE PARTY WAY									ļ
/AK	LATE PROTECT KY	TANCAL VACA POSITIO	30,50			1	I				ļ
AND THE		PARANTAMENT POPULATION	1			-			L		L
	+	WACCING WRUS (STRAIN COPENHAGEN)	180								
ATVA	T	WALIOLA VIRUS	120-135								
	Т	VACCINGA VIRUS (STRAIN COPENHACION)	194-230			-					Ц
A VACE	т	VACCEDIA VILLS (STRAIN WR)	194-170								
PUBLI VARV	PROTEIN IS	WALIOLA VIRUS	027 3								
VACCV	т	VACCINEA VIRLUS (STRAIN WR)	= 2	? ?		1					1
9 VAV	PROTEIN	VARIOLA VIRUS	2								1
PVIOT VACCE		VACCINIA VIXUI (ITTAIN COPENNAGEN)	2	2							1
OJ VACEV		VACCINIA VIRUS (STIVAIN WR)	2			T					1
FVIOL VARV		VALIGLA VRUS	Z I								1
WICE VACOC		VACCIPIA VULUS (STIVAIN CUPENTAUCEN)									1
VIGE VACEV	MINITIVE ENA PELICASE E	VACCINIA VIII (21 MAIN WIL)				I					
VICE VARV	PUIA IIVE UNA PELACASE II	IN BALLEN CHICKENET TOWN OF ACTUALITY AND	11.18	31.16							
VES RUMA	1	TANALAN POPULATION AT A CONTINUE ACTION AND A POPULATION	8	20							1
VIE HOW	7	IN BANK CONTRACTOR OF BANK ADIGM	1	300.404							ļ
	A LO CANADA VE BARI V BOTTEN 3	MARAN CYTOMEGAL DVIBUS STRAIN TOWNED	3	118-405			I			L	L
	DANKING TAKE O MOTERN 3	MUNDAR CYTCHEGAL OVRUS (STRAIN SMITH)	21:32								
A CONTRACTOR	SO P. D. S.	HUNLAN CYTOMEGALOVIRUS (STRAIN TOWNE)	3							L	L
ATMEN AND	DAKEDIA TE-BABLY MOTES	HERPESYRUS SABABU (STRAIN 11)	65.80								
VEN NOVAC	DOGEDATICALLY REG PRO	AUTOCILAMIA CALIFORNICA MUCLEAR POLYNEDROSIS VIRUS	100-116	273-290							
VBAD EBV	PROBINTECHAL MENDALANE	EPSTEDUBACK VIXUS (STRAIN 895-4)	2.18 8	135-153	203-212						
PVDA HONA	PROBABLE INTEGRAL MEM	HUMAN CYTOMEGAL OVIRUS (STRAIN AD169)	2				I				1
PVD-P HSVII	PROBABLE DITECTAL MEMBRANE PROTEIN	PREPARE MACLES VINUS (117E 131KAN 17)		101.10	131 271	175.17	161.191	111			1
PVD HSVED	PROBABLE DYTEORAL, NEW	EQUING PERCENTANCE (SINAIR ADAIR)			T	Т	T				1
VEV RSYSA	DATECRAL MEMORIAME PROT	NEVESTAVOS savientes (sination 11)									

PROTEIN II WOTER II WANTER FOTER	AB Warner (No. Berner)											
	TENANT	PROTEIN	YDRUS				П	П		ı		
		PROBABLE INTEGRAL MEN	VAUCELLAZOSTEA VIRUS (STRAIN DUMAS)			7	Т	1	ARIAA	H		NEA.
		-	VACCINIA VIRUS (STILAIN COPENHAGEN)	9			7					
	200	-	VACCINIA VIRUS (STRAIN WR)		1		1					
	ANY IN	~	VAUOLA VIRUS	9			1					
	10000	-	VACCINIA VIRUS (STRAIN COPENHACEN)		10.0			1				
MACHINE VACCOUNT WRITE (TAIL NO CORPORATE) 18-15	W	-1	VACCINIA VIRUS (STRAIN WR)					1				•
MATTER VACCOUNT WIRE STATE OF PROPERTY MATTER MAT	200		VACCINIA VIBUS (STILAIN COPENIAGEN)									
MATTER VOCACHA VIRGITALISM MATTER			VACCINIA VIRUS (STAAIN COPENHACEN)	1								
MARCHELL MARCHA	0 010			Ž	1	†	ŀ					
	W CITY	_		1	İ	-	1	į		:	•	
MOUNTAIL IN POTENT		TRUITING TO THE PROPERTY OF TH	VACCIDITÁ VIRUS (STRAIN COPENHAGEN)	71:17			-					
		PROTEIN LA	VACCINEA VIXUS (STRAIN WR)	17			1					
VANCOLA VOLLEGAM VANCOLA VOL	OKINO P	HAMMIN	VARIOLA VRUS	5	186.301	11, 104	1					
	1	TRUININ LS	VACCINIA VIRUS (STRAIN WR), AND (STRAIN COPEMIAGEN)				-					
March II Morth March Morth Mark March		rkutsin L3	VARIOLA VINUS	7	1	-	Ť		:	-		
		TRUBABLE LI PROTEIN	COTTOMIAL LABBIT (SHOPE) PAPILL DMAVIRUS (STRAIN KANSAS)	•	-	-	-					
MACAGE LEATTH MACAGE MATERIAN FOR ELL	170	PAUBABLE LI PROTEIN	HUMANA PAPELLONAVIRUS TYPE 16	т	1		-					
	S C		HUMAN PAPILLOMA VIRUS TYPE 41	19								
	1000		REOVINUS (TYPE 3 / STRAIN DEALING)	127	351.166	71.77	1					
ROOM ALE IS FROTEN RIGARY NATIOAN/WINS TYRE IS 13-15 1	11/04	PACRAMIE 1 1 PROTECT	HUMAN PAPEL CHAN VIRUS TYPE 8	24.17			†		Ī			
MORABLE INFORMATION MORAN PARLICAN/MINE TYPE II 11-14	2 10/13	PROBABLE L'S PROTEIN	HUMAN PARLICHAVIRUS TYPE 11				T				Ì	
HOGALE IS PROTEST HOGA	S PV S	PROBABLE LI PROPERI	HUMAN PAPELLONAVIRUS TYPE IS	33.59			T	1	Ī		1	1
FORGARD LIFEGUES FORGAR PART DATES 11-19	2 HFV18	PROBABLE LA PROTEIN	WOMAN PATILITIES TYPE 16	34-60			Ī	Ì	Ī		1	
MOGABEE IS PROFESS 111-121	VIA.	PROBABLE LE PROTEIN	MUNICAL PART CHANGE 177E II	33-39					Ī			
PROGAZE IJ PROTEST PROGRATI	MORAN SAMI TALAMA WATER TA	313-338			F		Ī		T	T		
The control of the	F	PROBABLE LA PROTEIN	MANAL PARM FALL COLUMN TO THE TA	=			-		Ī		Ť	Ī
PROBABLE I PROTEST PROBABLE I PROTEST	ARMAN PAPEL CALACIDIS PURE 13	99.7	665-462		-				İ	Ī		
NORMALL 12 PROTESS 18-34 14-410 14-35	ı	PROBABLE LI PROPIN	HUMAN PARILLOMAVIRUS TYPE 15		8						T	T
MOGNAL I PROTECT MOGNAL I PROTECT MOGNAL I PROTECT MOGNAL I PROTECT MOGNAL I PROTECT MOGNAL I PROTECT MOGNAL I I I PROTECT MOGNAL I I I PROTECT MOGNAL I I I I PROTECT MOGNAL I I I PROTECT MOGNAL I	HUMAN PAPILLOMAVIRUS TYPE 41	3			1							
MORAGE IS NOTED MORE IS NOTED MORAGE	HUMAN PAPILLOMAVIRUS TYPE 42	51	14.130		İ							
MOSTAL I I MOTER		PROBABILE 15 MOTERA	MUMAN PAPILLOMAVIRUS TYPE 47	256.263		-	+	T	1	İ	1	
PAGE AND EAST LEADTERN HALLOLANING 17 15 15 15 15 15 15 15	E S	PROBABLE LI PROFESS	HUMAN PARLICULARY (RUE)	13-38			l	Ť	T		1	1
HORAGEL IN PROTECT HORAGEL	10 Val	PROBABILE L2 PROTEIN	MAKAN PAPEL DAVING HERE AS	2.	96-114		•			T	\dagger	T
MODERN M	IAV.	PROBABLE L2 PROTEIN	EUROPEAN ELK PAPILLOMAVIEUS	\$.								T
MEGORA HOTEN LABOA MALAN MALLAN M		PROBABLE LS PROTEIN	MESUI PAPILIONAVIRUS TYPE I	į			1					
MACON COLF MOTER LANDA MACONALI (TYPE 1 STAND BUDGES) 114-115 111-11	Т	MONTH MONTH	MIMAN PAPELIONAVIRUS TYPE 38	2		1	†	1	1			
ACCORAGO PROTEIN LANGE A 111-1216 11	Т	MONOR CORE PROTECT ALMONA		114.117		\dagger	t	T	T		1	1
LW ROTEN 110-13	Т	ADVOR CORE PROTEDY LANGOA 1		114-739	1213-1236	\mid	T	T	1	1	†	1
100TEM H 196.181 196.	JAV1	LIN PROTEIN	П	114-111				T	T	T	1	T
MOTERN #1 17-119 111-120 111	NACC.	PROTEIN MI	EMIACENI	2		П	1961			T	T	I
MACON VALUE STRUCTERAL PROTER ALT: NALOA VALUE NALOA	2	PROTEIN MI	VACCINIA VIRUS (STRAIN WR)	1	Т	20(-101	1					
	1	- 4		8	T		1	1	1		Н	
MAJOR VENCH STRUCK POTTER MALIANLIC REDVELLS (TTPE 1/3 STAND BEALTH) 141-168 221-245 126-164 414-47				31.15	Т	Т	1	Т		1		
	NEOVO	MAJOR VILION STRUCTOROTE IN TALLANDA		141-168	Т	Т	1	Т			1	1
MACON VISION STRUC PROTEIN MALICALLIC REDVALUS (TYPE 21 STRAIN SUGGES) MACON VISION STRUC PROTEIN MALICALLIC REDVALUS (TYPE 21 STRAIN SUGGES) MACON VISION VISION STRUC PROTEIN MALICAL REPVENUS (TYPE 21 STRAIN SALVINO) MACON VISION PROTEIN MALICAL REPVENUS (TRAIN VISION STRAIN ASSOCIATION STRUCTURAL VISION STRAIN ASSOCIATION STRUCTURAL VISION STRAIN MACON PROTEIN MACON SERVINOS STRUCTURAL VISION STRAIN ASSOCIATION STRAIN ASSOCIATION STRAIN ASSOCIATION STRAIN ASSOCIATION STRAIN ASSOCIATION STRAIN	AEOVILLS (TYPE 1/ 878 AIM DEADAG)	164-192			П	T	T	T	1	T		
MAJOR VOLON STRUCTHOTEN MOLINALIC REOVENUE (TYPE 17 STRAIN LANG) 184-174 184-1		MAJOR VISION STRUC PROTEIN MJ. I MILIC	NEOVING CITYE 27 STRAIN DUIDARS	-6						T	\dagger	T
MAJOR MONTHLICTUALL PROTEIN MOLHS		MAJOR VOLON STRUC PROTEIN MULIANILIC	REOVINUS (TYPE 1/STRAIN LANG)								İ	Τ
MATAX MOTERN MOVTHE MESHALTORY STACKTIAL VIBUS (STRAIN ASSESS) 37-43		MAJOR HOHSTRUCTURAL PROTEIN MULHS		70.10	37.1	+						T
MATUR PODEDY MATUR PODEDY MATUR PODEDY MAKUR PROFEN MAKUR		MATRIX PROTEIN	(806)	17.63	*	1	1	1				
MARLY PROFEIN LA PERDALORY SYNCYTIAL VALUS (STRAIN A3) 4443 LA PERDAL-AGNOACAN-AGNICS TRUIS JII.338 MARLIE PROFEIN MARLES VRUS (STRAIN EDMONSTON) 215-309		MATIUX PROTEIN		Г	201.00	1	1	1			H	
MATRIX PROTEIN MEASURE VINUS (STRUNF EDMONSTOR)		MATINA PROFESS		Г	39.160	\dagger	t	1	1	1	+	
THE SEE A THOR EDWINDS TOWN	TALKET.	MATEUX PROTEIN	S	311-336		-	t	\dagger	1	1	1	7
				283-309		-	ŀ	t	1		1	I

				l						
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	VIKTURE SACTOR	All Viving (To Between project)		•			1		Т	
THE PERSON NAMED IN COLUMN	Mark Parket	LANGE AND LINE COLD AND TALL I BY	1				1			T S
PWAKE LEAST MAN	HATRIX MOTEN	NEAULT VIRUS (STIANN IP.) CA)		t	\mid	+	ł	-		
PYMAT MEASU MAN	MATEUX PROTEIN	MAKABLES YIRUS (STRADY HUS)		Т	-	 	-			
PYMAT MODEL MA	MATRIX PROTEIN	MUNES VIXUS (STILATIY SOL-1)	П		16.336					
PWAY MUNOS SAN	KATUK MOTEN	MARES VIXUS (STRAIN SEL.)	П		16.330	Н				
WAY BOYA	MATRIX PROFIEM	NEWCASTLE DISEASE, VIAUS (STRAIN AUSTRALIA-VICTORIA/13)	1	╗	206-378	1				
TANK TON	LANGE TO STATE OF THE STATE OF	NEWCASTLE DISEASE VIRUS (STILATE BEAUDETTE CAS)	200	8	F. 186	\dagger	\dagger	$\frac{1}{1}$		
	MATHER PROTEIN	HERAAN PARAMPLIENZA 3 VIRUS (STRAIN TOSIIDA) (1973)	T	18,265	100.13	\dagger	$\frac{1}{1}$	+	1	
PWAY HAM	NATELY PROTEIN	HUMAN PARADIFLUENZA 4A VIRUS (STRAIN TOSHIBA) (MV.4A)	T	T		 	1	-	-	I
•	MATRIX PROTEIN	HUNGAN PARADISLUENZA 48 VIRUS (STRATIV 6E-331) (NV-48)		t	\mid	ļ	-		-	
•	MATNUX PROTEIN	RINDERPEST VIRUS (STRAIN KADETE D)	L	235.846	367:30	-	\mid	-	ŀ	
-	MATRIX PROTEIN	SENDAI VIILUS (STRAIN FUSHIMI)			\mid		+	-	-	
	MATRIX PROTEIN	SENDAL VIRUS (STRAIN HARASS)	195.27		-	-	-			
PYMAT EDITIC MAT	MATRIX PROTSIN	SENDAI VIRUS (STRAIN Z)	13.21		<u> </u> 	<u> </u>	 :			
	MATRIX PROTEIN	AOSINO PANENCEPITALITIS VIKUS (STRAIN BIKIEN)	161.00	314.338	L	-	<u> </u>	-	-	
PYMAT SV41 MAT	MATRIX PROTEIN	SHALAN VARUS 45	133.194	186.205 30	826-90	- :		-	-	
	MATRIX PROTRIM	BINING VIRUS S (STRAIM W2)	П	131-141 30	301.335		<u>. </u>			
SVCV	MATALK PROTEIN	SPILING VIRESHEA OF CALIF VIRUS (RHABDOVIRUS CARPIA)	141-167			-				
	AATILX PROTEIN	TRICKY IMPORTACIONS VIAUS	3	П		·				
1	EI GLYCOMOTEIN	BOVINE CORCHAVIRUS (STRAIN MEBUS)	П	133-161	11.140					
CMOS	EI CL.YCOPŁÓTED	INDALAH CORONAVIRUS (STICATA 200)	135					_	-	
PYARI CYNOC RIG	LYCOPACTEIN			[1]	137-161	H	-	-	_	
PWAII CWAN IEI O	EI OLYCOMOTEIN	IMURUNE CORONAVIRUS MITY (STICATN ASP)	16.39					_		
		INCIDENTE CORCONA VIREUS MENY (STRAIM HOA)	10-37			-			L	
	I I OLYCOMOTED PRECUESOR	PORCINE TRANSMISSIBLE CASTROENTENTIS CORONAVIRUS (STRAI				<u> </u>	H	L	-	
		PORCHE TRANSMISSIBLE GASTROENTEATES CORONAVIRUS (STRAI	(61-69)	161-761		-				
	RI OL PCOPROTEDI PRECURIOR	PORCINE RESPIRATORY CONONAVIRUS (STRAIN BAN)	1)	П		H	H		-	
	(i ol ycoprotiem	TURKEY ENTERIC CORONAVIRUS	П	191761	0)16		Н			
	LYCOPIOTEN	AVIAN INFECTIOUS BRONCHITIS VILUS (STRAIN 642)	74.91							
٦	II OL YCOPIOTEIN	AVIAN DEFECTIOUS BLONCHTIE VALUS (STLAIN BEALDETTE)	2 2			-				
╗	LYCOPLOTEIN	ETTEAM	<u>5</u>					1		
7		TRUS (STRAIN RBISZI)	7		1	1				
-	MONABLE MEMBERSHE PROTEIN	ENTERNMENT (STIAM B994)	7	┪		-				
_	MOVEMENT PROTEIN	CAULD LOWER MOSAIC VIRUS (STRAIN CM-1M1)	7	7	107-101	1				
_	MOVEMBER PROTECT	CAULPLUMER MUSAC VIRUS (311AIPT LPR)	7	1	107-101	-	1			
_	MUVEMENT PROTEIN	CALLE LOWER MUSAIC VIRUS (31 MAIN 60C.)	7	7	107:101	+	1	-	_	
-	LANGENT MOTERA	CALLE BY AMERICAN AND AND AND AND AND AND AND AND AND A			R S	\dagger	1	1		
7	MOVEMENT PROTECT	CANA BE CARE LOSA IC WILLS (STRAIN WAS)	Т	T	5.5	+	$\frac{1}{1}$			
PAGE CEAV	MOVEMENT PROTECT		T	T	+	\dagger	+		1	
+	MOVEMENT PROTEIN	(DXS)	Т	2		\dagger	+		-	
•		Г	Т	23.5.1	ł	\parallel	+	-	\mid	
	-	DUCK HEPATITIS B VIRUS (BROWN SHANGHAI DUCK ISOLATE SS)	127-EX	王美		-	ł	ŀ		
	-		in i	266-794			ŀ	-		
ì	_	DUCK HEPATITIS & VIRUS	157.114	231-237	ŀ	ŀ	-		L	
	MAJOR SURFACE ANTIGEN PRECURSOR	ANOHAI DUCK ISBLATE SJI)	П	164.285	-	-	-			
PYMEA HEROS JAKA	MAJOR SURPACE ANTICEM PRECINSOR	TIS VIRUS	П	21.77	100-395	H		-	-	
PWEA HERE MA	OR SURFACE ANTIQUE PRECURSOR	B VIRUS	~	M)-320		H	H			
PWGA Jenso MAZ	CR SURFACE ANTIGEN			20.00			L			
PWGA MENY MAN	OR SURFACE ANTIGEN PRECURSOR	HEDATITIS B VIRUS (SUBTYPE ADW2)	П	144.270			Н	_		
PWISA HOBY	OR SULVACE ANTIGEN PRECURSOR		╗	144.270		H	Н	-		
PWGA 19879 MA	MAJOR BURNACE ANTRORN PRECURSOR	NEPATITIS B VIRUS (SUBTYPE ADW / STRAIN 991)	J		+	+	+			
WEY NOW	OR SURFACE ANTINOM TRECUNOR	MEANING VILLS (STRUM ALPHAI)	Ţ		1	1	+			
TAKE PER USE	AL THE LITE TURNES IN CHINCLE	т		2	1	1	+	1		
TALL THE PARTY	OR RUNA ACT ANTIONNI PRECIDENCE	MEDA TITLES CONTINUED THE ANALYSISMAN LABORATION	1	213.515	\dagger	+	+	+		I
		7	ı		1	$\frac{1}{1}$	-]

	Pichal	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1									
THE NAME	PROTEIN	(Applications of the precision of the control of th		L							
PVASA HOBVI.	MANOR SUPPACE AMPROEM PRECURSOR	MEDATOR S VIDE IN THE STATE OF	AREAL	AREA 1	AKEAJ	AREA A	A SEA	747	ABEA 3		1
PWKA HOBYN	ANOR SULLYACE ANTHORN	WEST STORY OF THE	134-191	13)-159		Ŀ			ı	Т	1
PMAA MOBVO	MAJOR SIRPACE ANTICEN PRECISED	TECHNICO VINUS (SUBTYPE ADR / STAAIN NC-1)	H*11	Z,							1
PVACA LORVA	A WAS BOILD A CHILD AND A CHILD BANK	METATITIS II VIRUI (SUBTYPE ADW / STRAIN OKINAWAPODW282)	174.191	23.750		1					
WAY LAND	THE WALL AND INCH	HEPATITIS B VIRUS (SUBTITIE ADW / STRAIN PHILIPPINOPFOWIN)	(00, 70)	344.310							
2004	PANCE SURFICE ANTICOM PRECURSOR	HEPATITIS D VIRUS (SUBTYPE ADR)	200						-		
	WOLK BUILDING ANTICEN	HEPATITIS B VIRUS (SUBTYPE AR)									
A COLUMN	MANOR SURPACE ANTIGEN PRECURSOR	HEPATITIS & VIRUS ((COTYPE ADW)									
	ANDRE BURNACH ANTROEM	HEPATITIS & VIRUS (SUDTYPE AYW)								-	
WAT HENY	MAJOR SURFACE ANTIGEN !	MEDATTHE BUSING TO 18 TO SELECTION AND SELECTION OF SELEC	1654	103-259							
WASA WHY	WORK SUBJACE ANTIGEN	A LOW COLOR OF THE PARTY OF THE	174-191	133-239	•	ŀ				Ī	
PARCEA WHYS	ALION STATES AND	TOOLANDER METALLIS VIRUS I	207-234	165-793	171.30		ŀ				
DAYS TRANS	A ACT OF STREET	WULCHUCK HEPATITIS VIRUS 39	312.316	314.34	101						
A.K.	A STATE OF THE STA	WOODCHUCK HEPATITIS VIRUS 1	913.916			1					
	ALON SUIVACE ANTICEN	WOODONCK HEYATTHS VIRING			783-378						
PANCIA WHY!	PROB IMAJOR SUNSACE ANTIDEM PREZ	WANTED THE A TITLE WILLIAM TO THE	677.212	1 × 20	363.398						I
PUNCA WHYWE	15	MANAGER AND A STREET ST	112-239	174.298	F		1		:		
WALL FAM	: 1	WULLANDER HELATITES VIRUS WAS (ISOLATE PWS2))	100	334.340		1					
27	NAME OF TAXABLE PARTY.	BPLUENCA A VIRUS (STRAIN ANNIN ALBORANO)	3			1					
	THE WAY IN INCHES	INFLUENZA A WILUS (STRAIN ARANCK CKII PH				-					
4	MATRIX (ALT) PROTEDI	DOLUMBA A VIRUS (STRANK ARTRET WARRELLING)									
TATA CAPA	MATRIX (AC) PROTEIN	DOLLENZA A VIBIR (STRANA A ARMAN DA ANTINA DE LA PROPENSION DE LA PROPENSI	į			1					I
	MATRUX ACS PROTESI	MATTER A CONTRACTOR OF THE PLACE VIRUSACSTOCKOW)	23-46			•		I		Ì	1
	MATRIX GOT PROFES	THE THE PROPERTY OF THE PROPER	37-56			F				1	
	MAN WANTED	INTELLINGA A VIRUS (STRAIN ALENDAGRADY) 14/51)	97.2			·					
	Mallor (ma) moltan	l	74.44			I					
	MAINLY (ME) PROTEIN	TO P. R. S. Co. Co.									
A TANK	MATRIX (ACT) PROTEIN	1	8							İ	I
WITH LABY	HATTER GALL PROTEIN		34			-				1	I
PWITT INITIO	MATRIX GAS PROTEIN		23-46			F			İ	1	
WATE LAWE	MA TRIE ACT PROTEIN		87 FE			Ī		I			
AND STANK	7.5.7.6.7.8.5.7	M-SMITH/33)	7		Ì	ł	1	Ī	1		
CANAL PARTY	A STATE OF THE STA		234.341	\prod	1	1					
	POWS I NUCLUIOUS PROTEIN INSIA	N SHINTOKU	1114.161		1	1					
7	10 7 KD PROTEIN									l	
7	NO CLYCOPROTEIN									l	
	NS OLICOPROTEIN		4			•		Ī		t	
PVN BOLL	INB OLYCOPADITAIN	THE PART IN COLUMN THE PRINCIPLE OF THE PART IN COLUMN THE PART IN COL	1.19			F		Ī		t	Ī
_	MB CL YOOPROTEDY		13.39				İ	I		t	I
7	No. of Victors are all	-	841			Ī	Ì	ı		1	
PVA PALA	ALL AND		*		Ì	Ī	1				
200	Na Constitution		95.50		Ì	Ī		1			
THE PERSON NAMED IN	Na GL TOURNI EIN		97.3		1						
7	MANAGEM RE-	ALEUTIAN MONE DISEASE PAR VOVINCE (STRAIN C)		8	1	1					
	TOTAL PROTEIN MS.	DOLAFOR DENE							_		
	NUMCAPIED PROTEIN NS.	HUMAN PARVOVIRUS BIO	3		1						
HILL STATE	NONCAPED PROTEIN NE.	Т		1	1				-		
NEW YORK	POPS TRUCTURAL PROTEIN INSI	A 4 / STRAIN VACABLES							ŀ	1	Ī
1	MONSTRUCTURAL PROTEDY NS:	Т	1	7						l	Ī
	NONSTRUCTURAL PROTEIN IS		X	1	167-192					l	Ī
NOW I	MOMETIC LEGAL, PROTEIN INST	1587	1		107.192					l	T
	NONSTRUCTURAL PROTEDNINS		1	7						l	T
_	MONSTRUCTURAL PROTEIN INSI	FRANKAINE	1	٦	167.192			ľ		l	T
	HONSTRUCTURAL PROTEDN YS!	1		22				r		\dagger	T
PWISI LADAS	NONSTRUCTURAL PROTEIN NSI		28-47	641791		l	l	1		1	7
TANSI LADE	NONSTRUCTURAL PROTEIN HS!			761-491		T	T	T	1	1	7
	NOWSTRUCTURAL PROTEIN MS!		11-17	<u>\$</u>		Ì	1	T	1	1	
L	HONSTRUCTURAL PROTEIN KS!		21-17	2 - E		T	T	1	1	1	1
Ī	MONETHER PROPERTY ME		8-10	Г	167.192	T	T	1		1	
7	MONTH CTIMAL PROTEST AND	┖		Т	69:193	1	1	1	1		
Т	NONSTRUCTURAL PROTERVING	COLUMENCA A VIKUS (STRAIN AFOWL PLACUE VIRUSACOSTOCICAL)	Γ	t		T	1	1	1	1	
L	HONSTRUCTURAL PROTEIN HS!			Ε	100	İ	1	1	1	1	7
П	HONSTRUCTURAL PROTEIN NS!	METERNAL VINIS (STRAIN ALEMINGRADIANI)	97:15	П	167.192	t	\dagger	\dagger	\dagger	+	7
1			11-50	Т		t	t	t	1	1	7
						1		1		-	

1435A	PIXCTURE	All Virgins (No Bacterles) servi			-		-			
	PROTEIN	Vaus	ARTAI	ARCA! AR	AREA AREA	A AREAS	AS AREAS	V AREA!	AREAS	AREA
PYNGI IMAUN	HOMSTRLICTURAL PROTEDI HSI	INFLUENCA A VIRUS (STRAIN AMALLANDANEW YORKA) SOTI	9F-16	167-192	L	П	П			
	MONSTRUCTURAL PROTEIN HS!	INFLLIENCA A VIRUS (STRAIM AMALLARDANEW YORKKATATI)	31-30	167-192			L			
Į.	MONSTRUCTURAL PROTEIN NS!	INFLLENZA A YIRUS (STRAÍN AMYNAMAKANEDA-TKALTA)	26-47	164-119	L	L	\vdash		L	
7	HONSTRUCTURAL PROTEIN NS	INTLUENCA A VIRUS (STRAIN APPRTAIL/ALBEATA/11979)	<u>=</u>							
	HONDING TOUCH PROTEIN INST	INTLUENCA A VIXUS (STIVAIN APPORTABL/ALBERTAVIZION)	8	163-153			\parallel			
1	MONSTRUCTURAL PROTEIN POS	DYFLLEDGA A VIXUS (STRAIN APPRIAD/ALBERTAGALTS)	2	167.193						-
	NORTHUGIUM, PROTEIN ISI	DPILUDIZA A VIXUS (STRAIN APPRITAL/ALBERTANSUP)	2	T		+				
Т	POPELIA DE LA PROFESIO POR	INTLUENCA A VIKUS (STRAIN APPLEATO RICCANDA)	2	ᅥ	67:192	+				
N CHA	MONSTRUCTURAL PROTEIN ISS	INPLUENZA A VIKUS (STRAIN ATURKBY METHLEHEM-CULITY) 492-4-7		163-193						
Т	MONTH I MUCH UNIVERSITY IN THE STATE OF THE	INTLUENCA A VIRUS (STRAIN ATURKEY/CANADARS)	2	167-192		-	_			
T	ACRESTALIC TURAL PROTEIN PS	PITLERGA A VIRUS (STRAIN ATURKE Y/ORECON7))	*							
1	CONSTRUCTURAL PROTEIN INSI	INTLIERCA A VIRUS (STRAIN ATERNSOUTH AFRICANI)	11-17	144-119		Н				
7	NONSTRUCTURAL PROTESK KSI	INTELLEDZA A YTRUS (STRAIN ATEXNTUREXAGNIA/1972)	31-50	167-193	L	L	L	L		L
_	HONSTRUCTURAL PROTEIN HS!	PAFLUENCA A VIRUS (STRAIN A/LOORUNJOITZ)	31-50	Г	167.192	L	-	-		
_	HONSTRUCTURAL PROTESK MS!	DNFLUENZA A VIAUS (STRAIN AUSSANDIT)	8-1	114-133 163	167.192	F	-		L	
PWG: WE!	HOMETRUCTURAL PROTEIN INSI	DIFLUENCA A VIALIS (STRAIN ASWINGNOWALISTO)	31.30	167-193			F			L
PWSI NCA	CONSTRUCTURAL PROTEIN HS!	DIFELLENCEA C VIRUS (STRAIN CANN ARBONUSO)	112.24		-	<u> </u>	L			
YOU IN	MONSTRUCTURAL PROTEIN MS!	INFLUENCA C VIRUS (STRAIN O'CALIFORNIA/NS)	112-340		-	 -			_	
PVNID BTVIG	MONETRUCTURAL PROTEIN MES	۶.	191-101	120100	-	L	L	-	-	
7	NONSTRUCTURAL PROTEIN HS:	BLUSTONOUS VIXUS (SEROTYPE 17/150CATE USA)	145-161	201-213	H	 -	-			
WED BINES	MONSTRUCTURAL PROTECN INSI	RELIETONGUE VIRUS (SEROTYPE I / ISOLATE SOUTH AFRICA)	145-161		L	L	-	-		
With BTVIX	KONSTRUCTIONAL PROTEIN NS1	SLUETOWOUT VIRUS (SEROTTPE 16)	145-161	L	Н	H	H			
PWED DOWN	KONSTRUCTURAL PROTEIN YES	EPIZOCTIC IEDIORANACIC DIBRASE VIRUS (SEROTYPE \$ / STRAIN AL 145-161	192-191		Ц	Н				
Ŧ	NONSTRUCTURAL PROTEIN NS3	INFLUENCA A VIDLUS (STRAZM APVIENTO RUCOMOA)	97.58							
1	MOMESTRUCTURAL PROTEIN NS2	INTLUENZA A VIRUS (STRAIN APERNSOUTH AFRICAS)	24.00			-	Н			
LANCE LANCE	OPSTRUCTURAL PROTEIN 2	PREUMORIA VILLE OF MICE								
	MOMENTURAL PROTEIN 3-1	PORCEME TRANSMESSILE GASTROENTERETS COROMAVIRUS (STRAI	10741							
CALLS CALLS	MOMESTALIC TURKET PROTEIN 2-1	PORCINE TRANSMESSING GASTROENTEATHS COLONA VIRUS (STRAL)				Н				
WAS CARR	NOVEMBER OF TRUITED AS	FORCING MESPERATORY CONORANTEDS (STICAIN RM)	2				\mid		Ц	
_	MONETINGE PROTEIN MY	ALCE STREET VALUE	3			-				
	MONSTRUCTURAL PROTEIN &	HUMAN CONCONAVILUS (STRAIN 229E)	8 2				Н	-		
-	MUTE LINUX I DRAW PROTEIN 4		2	1	-					
	ACCOMPANY OF A PROPERTY	CARCING LIAMBERSHIP GASTRICENTED IS CORUMNING (STRAL	2		-	+				
	CONTRACTOR IN THE SAME IN A	MACLINE BEFORE A TOTAL & PARTIES CHANGE CONTINUES (STRAIN			1	-	-			
2	INDESTRUCTIONS PROTEST NAME	MARKET STREET WAS CONCINCTED AND CON	2		1	+	1			
1	MONETRIX TURAL PROTECTION INST	RICH PRIDE VIEW	R	1. X. X.	- 1	+	+			
PWS COND	NONSTRUCTURAL PROTEIN ?	FELING ENTEUC CORONAVALIS (STRAIN 78, 1681)		T		+	+	-		
Ť	HONSTRUCTURAL PROTECT ?	FELLING DESCRIDUS PENTOWITIS VIRUS (STRAIN 74-1146)	3	-	-	+	+	1		
	NOWSTRUCTURAL PROTEIN C	HUMAN PALATYTE UENZA I VIRUS (STRAIN COS)	ž			+	+			
PVICE NINC	HONSTRUCTURAL PROTEIN C	HUMAN PARADITURNEA I VIRUS (STRAIN CP)	r.		-	-	-			
	KONSTRUCTURAL PROTEDI C	HUMAN PARADITLUENZA I VIRUS (STRAIN CI-5/1)	76-93	175-197	-	-	-			
M 128		HOMEN PARADIGLUENZA I VIRUS (STRAIN CL.1463)	1		-	-	-			
7	13 KD NONSTRUCTURAL PROTEIN	BOYDA CORONAVIRUS (STRAIN QUEBEC)	901-109							
_	NONSTRUCTURAL PROTEINS INSTANS	DATUEDCA C VINUS (STRAIN CKREAT LAKESHI14794)	223-340			L				
PWST BCH	MONSTRUCTURAL PROTECTS NSI-NS2		¥22			Н	H			
7	PURST BLACK LINAL PROTEINS INSTITUTE		Z.			Н				
7	MONSTRUCTURED TROJECTO IN THE PARTY OF THE P	N CTAMAGATA/IGISI)	27.72							
7	MANUAL DRAW TROITED TOS	FORTA TORO PRESIONIUS	Ş							
TOTAL STATE	NOWSTRUCTURAL PROTEIN MS-3	MATTER FIRE SCULAN VINUS	3		$\frac{1}{1}$	Н	Ц			
7	MONSTRUCTURAL PROTEIN MS-5	CURCOMISM VIRUS	33.73	19:10×						
-4-	PROBABLE MULLEAR ANTIGEN		75.77	1563-1583	1	H	H	Ц		
A CONTRACTOR	ACTUAL PROPERTY	EROL A VIRIA	121-134	757-324	+	+	-			
-	And Post Office	INTELLIGINAL A VIREIR (CTR A DA A A MANAGA A PER A ARBITANDE BALLER PACE		212.723		+	+	-		
-	NICE FOROTON	INCLUENCE A VIRUS (STRAIN A/ANN ABBORNAM)		117007		+	+	-		
1	NUCLEOPADTEIN	T	194.101			+	$\frac{1}{1}$			
1						$\left\{ \right.$	-	$\frac{1}{1}$		1

1	PINCTIZIP	All Virges (No Betterisabages)							1
	ROTER	YORKS	, , , , , , , , , , , , , ,	1	7	7	- 1		
PANCE MAIG	NUCLEOPROTEIN	INTLUDICA A VIRUS (STILAIN ABUTICISEIDABAINER AIRANG)	4	4	1737 PART	7	7	AREAI	ARIAS
PWICE LICK	UCLIONOFIEN	DAT UDIZA A VISUS (STRAIN ANTA) ISOBRAMANA	181.71						
PVNC MOKO IN	NUCLEOROTEIN	Brei Feren China Service March 1970	173-197				L		
•	Mind Evenores	BY LUBICA A VIRUS (STRAIN ACHICKENCERMIANY)	1152-197		-	-		Ì	Ī
-	COCCUPACION IN	INTLUENCA. A YIRUS (STRAIN ACHICKENPENNSYLVANIA) A					-	1	
	MUCLEUMOTER	INFLUENCA A VIRUS (STRAIN ADUCKAUSTRALIA/149/10	131.101	\dagger	1				
A MAC MORE	UCLEOPROTEIN	DATLUENZA A VIRUS (STRAIN ANDUCIC/BELLINGLINE)		1				-	
WALK MOC	UCLEOPROTED	BOLLENZA A VIRCIS ATTRAIN AND PRACTICAL AND PRACTICAL							
PVNUC LADE! IN	MUCLEOPROFEIN	INCLUENZA A URBIE 1445 ANI AMERICA CALLA LA	173-687	1				·	
WALK INDE	JOHO BOTEON	AND THE STATE (STRAIN AUGUSTICATION)	173-197			L	L		Ī
THE PARTY	VI IN COMPANY	INTLUENCE A VIRUS (STRAIN ADUCINENCIANDINS)	143-187	-					Ī
Т	ADDRESS THE BAN	INTLUDICA A VIRUS (STRAIN ADUCKMONG RONGIA)	19:10	\mid	-				Ī
7	CECANOTEIN	POLLENCA A VIRUS (STRAIN ADUCKMENTHISM2874)	1	\dagger	-				
_	M.C. EOPROTEIN	DOTUESCA A VIRUS (STRAIN ACHICECMANITORALIAN)		1	1				
	MACLEOPROTEIN	INPLIENCE A VIBILE SETT AND ARMICHANISM SEAL AND CO.	141-141						Ī
PANC INDU	ICLEONOTEIN	AM 1919 A MAIN ASSESSMENT A CEALAND 170	197-197		-	-	-		T
	PY BASEA SEA	INTELLEGIZA A VIAUS (STRAIN ADUCKURRAINE 2/60)	141-411	ŀ	-	ŀ	-		Ī
2	ACCUPACION BAN	IMPLUENCE A VIRUS (STRAIN AENGLAND/1993)	197:161	ł	-		1		1
MON NA	CLEOPTOTED	INTLUENZA A VIRUS (STIAIN AFORT LACHOACH THUM?)	101 101	1					
	MACLEOMOTERI	DATE DO A VISIT AFTER AND A MARK WAS BELLINES.			-				Γ
	CEOMOREA	And the Court of t	173-197		:		L		
WALL LAND	T CAMPATEN	WITH THE WAY A WIND IS INVIN A FOWL PLAGUE VIRUS DODS ON DUTY (17)	133-197	ŀ	•				Ī
	TO THE PERSON	INCLUENCA A VIRUS (STRAIN AFOWL PLAGUE VIRUSROSTOCICAS)	187:61						
	ALEUTROI EIN	INPLIENCA A VIXUS (STRAIN AKGREY TRAL/AUSTRALIA/2/79)	10.10	\dagger	+				
	MUCLEOPROTEIN	INTLIENCA A VIRUS (STRAIN AKRILLALARY) ANDVOT		1					
PVNUC INGUD IN	CLEOPROTEIN	OFT UPAZA A VIRUS SCENA IN AAKIN I ALANO ALICONALIA							Γ
	MICLEGREOTEN	MAN THAT IS A STANDARD OF THE	172-197		L		L		I
NAME AND PARTY.	W BALLANDE	MATERIAL A VINUS (STRAIN ACKILLACARYLAND) 112471)	117-197		L		-		
	ALEXA ROLL	INPLUENZA A VIKUS (SITIAIN AKKILLAKAKYLANDVISISM)	192.197		-				
AND TO A	CLEOPROTEIN	INPLIFIE A VIBLIS (STRAIN ANDULLAS PILAKILANDIPAS	1		1				
WALC DAGUE IN	CLEOPLOTEIN	DOLLIERZA A VINIS (STRATH AVER) ALAREA CUI ICCOTOMACA				·			
PANCE LAGEN IN	M.Ka. bornottibl	TANK THE STATE OF THE ANALYSIS OF THE STATE	163-161		,				
PANCE LABOR INC.	M. COT DOMESTIC	THE PROPERTY OF THE PROPERTY O	12:10		Ļ				Ī
PARIC LAKE	N ICI BORROLL	INTELEMENT A VIXUS (STITALIY AMERICACIONA)	175-197	-	-				T
TO A PARTY OF	N. WALKERSON	INTLINES A VIXUS (STRAIN ARQUINESIGLINGIAS)	183-181	-	-				
	ALEGORIAN ILLON	BOTUERCA A VIRUS (STRAIN ARQUINEALDHOON(1416/1))	13:18	-					1
A TANK	MULEUROTEDA	INTLUENZA A VIRUS (STRAIN AEQUINENDAMULAS)	100						1
VALC AND	CLEOPROTEON	DATLIENZA A VIBIUS (STRAIN AMONG KONG/IMA)	100	1					
TYPE TANKS IN	CEDFICHED	DOLLEDCA A VIRLIS (STRAD) AAONO KONDONIS		1					
	NUCLEONADED.	INTLUENZA A VIRLIS (STRAIN ARCHINE PRACTIFICAL)	161071						
PARK MITTER	CLEOPAOTEIN	TAKE I BOOK A VINE IN CITE AND A SECOND COMMENTS OF THE COMMEN	187-187					L	Γ
PWALE LAKE	NEIO ROPROTEIN	DAY 1838 1 (MILE 1888)	175-197			_			Ī
WATER AT	A PART ACTION	INCLUENCE A VIKUS (STRAIN AKIEY/S979)	601761	-	ŀ	ŀ			Ī
	CLEOT NO I BUT	DIFLUENCA A VIXUS (STRAIN ALENINGRADISA!)	19:197		-				1
WALK AND	MCLEOFIGHED!	BOTLLENZA A VINUS (STRAIN AMALL ARD/ASTRAINLAND/24402)	7.0	1	1				1
WHILE LANGER THE	MUCLEOPROTEIN	DAPLINENZA A VIRLIS (STRAID AMALL ANDARSW VOREAS) (OTEN)		1					
WALK LANDY	CLOPROTEON	DOLLIERZA A VIRLIS ISTRAIN AAGNERAWEDENAAN						-	l
PWALC LANTS NO.	CLEOTAGTEON		, Ala.,					-	
PWACE LACKE NO.	MUCLEOPEDFEIN		/41-7/1		_	_		ŀ	Ī
•	CHOPLOTEN		73-107		L	L			Ī
PWALE LAMIR NO.	A ICH ROPE CHAIN	ANTICOMEN A VIEWS (STINGTH APPARACIONAL STERM)	133-197		-				Ī
MAN TANK	A NAME AND ASSESSED.		133-197	-	L			1	I
-	A IN MANAGED	LSEY/A1/	141.641	-	-				1
7	CLEOTING ILM		19:10	\mid	-				
7	RUCLEOFTOTEIN	٥	191.161	1	-	$\frac{1}{1}$			
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_	HUGLIOHOTEN	1144.401.							
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-	MUCLEOPROTEIN	٥	17)-187			L		\mid	T
Т	NUCLEOPEN	ANTI-COLLAR A VIRUS (STRAIN A/TERNSOUTH AFRICAS!)	13)-16)	ļ.	-	\mid		\dagger	T
T	NA PARAMETER		191-161				1	1	T
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7	CLEOTROTEIR	INFLUENZA A VIRUS (STRAIN AVICTORIA/SM)	19:101	-					
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141-159 141-15	PCCENE	Prichale	All Virgins (No Besteriophoges)	П	П	П	П	П	П	• 7.48	0.4964			
	PILENAME	PROTEIN	VIRUS	Į.	Т	TOTAL PORT		4	4	1				
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	AME AZCA	MOLEGRICIES	INTELLEGIZA A VIAUS (BIRAIN ASWING A LINGUAGE)		T									
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CALLEMANDER INT.UBELIA A WILLS (TALM ASSUREDALIVE) 17-19		NOCESCATION OF THE PROPERTY	131.167	l			-							
CALLEMANTER FINELISTA A VIRIUS (STALIN ASWINGANETICALANISTINS) 13-191 ACALEMANTER FINELISTA A VIRIUS (STALIN ASWINGANETICALANISTINS) 13-191 ACALEMANTER FINELISTA A VIRIUS (STALIN ASWINGANETICALANISTINS) 13-191 ACALEMANTER FINELISTA A VIRIUS (STALIN ASWINGANETICALANISTINS) 13-131 ACALEMANTER FINELISTA A VIRIUS (STALIN ASWINGANETICALANISTINS) 13-131 ACALEMANTER FINELISTA A VIRIUS (STALIN ASWINGANETICALANISTINS) 13-131 ACALEMANTER FINELISTA A VIRIUS (STALIN ASWINGANETICALANISTINS) 13-131 ACALEMANTER FINELISTA A VIRIUS (STALIN ASWINGANETICALANISTINS) 13-131 ACALEMANTER FINELISTA A VIRIUS (STALIN ASWINGANETICALANISTINS) 13-131 ACALEMANTER FINELISTA A VIRIUS (STALIN ASWINGANETICALANISTINS) 13-131 ACALEMANTER FINELISTA A VIRIUS (STALIN ASWINGANETICALANISTINS) 13-131 ACALEMANTER FINELISTA A VIRIUS (STALIN ASWINGANETICALANISTINS) 13-131 ACALEMANTER FINELISTA A VIRIUS (STALIN ASWINGANETICALANISTINS) 13-131 ACALEMANTER FINELISTA A VIRIUS (STALIN ASWINGANETICALANISTINS) 13-131 ACALEMANTER FINELISTA A VIRIUS (STALIN ASWINGANETICALANISTINS) 13-131 ACALEMANTER FINELISTA A VIRIUS (STALIN ASWINGANETICALANISTINS) 13-131 ACALEMANTER FINELISTA A VIRIUS (STALIN ASWINGANETICALANISTINS) 13-131 ACALEMANTER FINELIS A VIRIUS (A VIRIUS (STALIN ASWINGANETICALANISTINS) 13-131 ACALEMANTER FINELIS A VIRIUS (A VIRIUS (STALIN ASWINGANETICALANISTINS) 13-131 ACALEMANTER FINELIS A VIRIUS (A VIRIUS (STALIN ASWINGANETICALANISTINS) 13-131 ACALEMANTER FINELIS A VIRIUS (A VIRIUS (STALIN ASWINGANETICALANIS	VIII VIII VIII VIII VIII VIII VIII VII		THE LEASE A VIEW COME AND MENTAL AND THE PARTY OF THE PROPERTY	1	T		<u> </u>	<u> </u>		:	! :			
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ACCEPTATION PREVIOUS PREVIOUS PREVIOUS		MAC ENGAGE	INFLUENZA A VIRUS (STRAIN ASWINE/OHIO?)///	133.197										
ACCEPTORIES WATELERS A VARIE STRAIN GANING 19-11	STATE AND A	March English	INFLUENCA A VIRUS (STRAIN ASWINGANISCONSINUIS)	133-149			-							
COLEMBRICATION PRILICIPATA VALIA (STACKE MARCHING CO-DANATOR) 19-218	PVAILE LATERS	MUCI EDMINITION	HALLENZA A VIXUS (STRAIN ASWINEN ISCONSIMIN)	173-187										
PACE DEPOPTER PACE OF THE GENAL OF MALE STATES 19-211	PVALC INDIA	NUCLIONOTEIN	INFLUENCA & WAUS (STILAIN BLANC ARBORUMS (COLD-ADAPTED))	1334-258										
CALESTONION CALEST	PVACE NAME	MUCLEOMOTEIN	INFLUENZA & VILLE (STRATH BANN AUDONING WILD-TYPE))	1334-258				_						
ACCESSION ACCE	PARC DEL	NOLLONGIEN	BAPLUEICZA B VIRUS (STRAIN BALEBAO)	1334.250				4						
ACTECHOTHS	PWALC DOM	PUCLEOMOTER	DAYLUENCA & VILUS (STRAIN BASINGAPORE/12/74)	24.35										
11 12 13 14 15 15 15 15 15 15 15	WALL JUNY	MICLEOPROTEIN	INVANCED VALUE (STRADE MUSCICE)	7	=		-	-						
11	PWICE KASVI	NOLOMOTEN	KANDUNG YINUS (STRAM POPP)	1	7				1					
HOUTER OIL VARIOLA VALUE HOUTER OIL HOUTER OIL	PYCOI VACCC	PROTUBLOI	VACCIPITA VIRLUS (STRAIN COPERNAGEN)	7	╗	200	-	1						
ILST DE PACTEM	PWOSI VALIV	PROTEING	VALICILA VIRUS	٦	7	<u>.</u>	-	1						
115 DE PROTEST 115	PYOR! FIDAY	ISS ES PROTES	POXTAL MOSAIC VIRUS	Т	400	-	+	\downarrow	1					
13	MON! NEV	166 KD PROTEDN	INACOSOUS MOSAC VICUS	T	T	111.11.11.11.11.11.11.11.11.11.11.11.11	-8	+	Ţ					
151 D PROTEST 152 D PROTEST 153 D PROTEST 154 D PROTEST 154 D PROTEST 154 D PROTEST 155 D PROTES	PWCK! JWA	11) KD PROFILM	POTATO VILLO M (STRAIN ROSSIAN)	Т	Т			-	-	T				
151 D ROTES 151 D ROTES	PVOLI MS	ID KD MOTUR	POLATO VIDE BEING TANK THAT	Т	Т	104-122 1010-1030	80							
131 ED PROTEIN 19 CALTO VELUE X (STALME ED) 131-141 131-15	PVORI PYX	16) KD PROTECT	MONTH OF THE ACT AND CP.	Т	Т	f	K010101	-						
19 ED ROTEIN 19 ED ROTEIN 19 ED ROTEIN 10 TO ROTEIN 19 ED ROTEIN 10 TO ROTEIN 10 T	NA MAIN	TO TO THE PARTY	POLATO VIEUS X (STRAIN X)	Г	1	Т	-	L						
		TO THE PROPERTY	OS STRAWNELLY MELD YELLOW EDGE-ASSOCIATED VIRUS	Г	195-175	-								
INTERPROTECT INTERPROTECT INTERPRETATION INTERPRE		143 KB PROPEN	WHOTE CLOWER MOSAIC VIRUS (STRAIN M)	П			Н							
PROGNALE PRINCENS PROPERTY PROPERTY PROGNALE PROGNALE PRINCENS PROGNALE PRINCENS	WON I WOW	147 KD PROTEDA	WIGTE CLOVER MOSAIC VIRUS (STRAIN O)	П	П	П	Ħ	_						
PIO PROTEIN	WAS HIVE	SILVE ANT	HERMETARUS SADARU (STILADA III)	П	Т	11.575	1051-1072							
PIP PLOTEIN	PVPH JevAC		AUTOCRAPHA CALIFORNICA NUCLIAR POLYNEDROSIS VIRUS		5	1		1						
POP HOUSE	PVP16 NEVOP	PIO PROTEIN	OKOYIA PSEUDOTSUGATA MULTICARID POLYMEDRUSIS VIKUS		1	+	$\frac{1}{1}$	1						
WOURTH WILE HOTEEN FROM WAS STATES DATE OF TAXON 1974 131-31 WOURD THANK THE WOURTH WAS STATES AND WOURTH WENT 1974 131-31 WOURD THANK T	TRAM MAAR	Pis PROTEIN	STUDITED EXIGIA MULLEAR FALTHELMOSIS VIKUS (STICKIN US)		1	212.121	19 Yes	33						
MOSTALL LECORAL MATERIAL STREET LOOK WILE (STALE 191-9) MOSTALL MATERIAL MATERIAL	VOIS BESTON		MULE BLACK STRAKED DWANG VIKUS	I	1	†	Т	T						
PROSE CLATED ASSESSMENT AND DATA LATUR NOTE BETTER DATA VELIS (\$17.04 FOR 12.04) 170.04 170.04 PROSE CLATED ASSESSMENT AND DATA LATUR NOTE HINDAY CYTOMEGOLOWING (\$17.04 IN.) 170.04 PROSE CLATED ASSESSMENT AND DATA LATUR NOTE HINDAY CYTOMEGOLOWING (\$17.04 IN.) 120.04 PROSE CLATED ASSESSMENT AND DATA LATUR PROTEIN 150.04 PROSE CLATED ASSESSMENT AND DATA LATUR PROTEIN 150.04 STRUCTHALL MOTERN YOU PROTEIN CONTRACTOR SAVING STATES 170.04 CONTRIBUTION OF A STATES	2 2 2 2 2	MONSTRUCTURAL PROTEIN PRISTS	SECTION OF THE CASE OF A SECTION	T	t	1134.1141	-	ļ						
PLOS CAPED ASSESSED, VAND DAY, MATUR, PROTES REALCHWIRDS (STRAIN AD189) 171-181	Welt 53V	PROBABLE MENGRAPHS AND INCOME TO SECOND	EPERAL SAME UP 15 (STEAM)	Τ	T		-							
MOR CASE AND SHA MATTAN PROTEST READ (STALM II) 194.85 CAYED ASSESSAY AND SHA MATTAN PACTEM VALCELAL STATEM DAACE) 15.11 CAYED ASSESSAY AND SHA MATTAN PACTEM VALLE PARTICLE SAY! 1.51 CAYED ASSESSAY AND SHA MATTAN PACTEM VALLE PARTICLE SAY! 1.51 CAYED ASSESSAY AND SHA MATTAN PACTEM VALLE PARTICLE SAY! 1.51 COME PROTEST 71 CAYED SHA MATTAN VALLE STALM CHEMAN 1.64 COME PROTEST 71 CAYED SHA MATTAN VALLE STALM CHEMAN 1.64 COME PROTEST 71 CAYED SHA MATTAN VALLE STALM CHEMAN 1.64 COME PROTEST 71 CAYED SHA MATTAN VALLE STALM VALLE STALM VALLE CAYED PROTEST 71 CANADO SHA STALM VALLE STALM VALLE CAYED PROTEST 71 CANADO SHA STALM VALLE CAYED PROTEST 71 CANADO SHA STALM VALLE STALM VALLE CAYED SHA MATTAN VALLE STALM VALLE STALM VALLE CAYED PROTEST VALLE CAYED SHA MATTAN VALLE STALM VALLE STALM VALLE CAYED SHA MATTAN VALLE STALM VALLE STALM VALLE CAYED SHA MATTAN VALLE STALM VALLE CAYED STALM VALLE CAYED SHA MATTAN	rvrii) Erv	THE CAND ALKANDLY A	MINIST CYTTAFTAL OVINTS (STRAIN AD169)	Τ	Т	90.00	-	-						
CAFED ASSESSIOLY AND ENG MATUR PROTEIN VARIED LABOR STRUCTURAL PROTEIN 1-31	A MANAGEMENT	MAN CANTO AKSTORY A	HEAVESVIRUS SAINITU (STRAIN !!)	Г	Г		-							
STRUCTURAL PROTEST VP PRECISSOR SULFOCORIN POUGLIES PARTICLE SAVI 14-15	1000	PAPER ASSESSED VAND DHA MATUR PROTEIN	VANCELLA ZOSTEA VIRUS (STILAIN DUNAS)	153			L							
COMETINE FILE CATACHORE MOTITED CURRELL WILLS 1344	POST SEVE	7 I	BULDOLOGIN VOIUS-LIKE PARTICLE SSVI	ŝ			Н	H						
CONTEMPTOR CUCLOMBES VERTICAL STATES CONTEMPTOR	A PART		AXTICHOUS MOTTLED CRUNKLE VIRUS	37-43			Ц							
CONE PROTEST FILE CONE PROTEST	100	CORE PROTEIN 711	CUCUMBER RECROSIS VALUS	10-65										
COLL PROTEIN FIT PROALE CASE MOTEN VII.1 (1704ATO BUSHY STUAN VII.1 (171AN CHELAN) PROGALE CASE MOTEN VII.1 (171AN CTOMEQUADVILOY (171AN CHELAN) [ALYEO ROCHEN VII.1 (171AN CTOMEQUADVILOY (171AN VII.1	VAN OLV	COLL PROTEST PAI	CYMBIDAUM NINGSPOT VIRUS	70										
PROGABLE CAPED MOTERN V733 HOLAND CHOMEGULOVRUS STRAIN AD189 111-115 117-201 CAPED MOTERN V73 HERBEI BENELEN KNUS (TYPE 15 TRAIN 17 117-210 SECOLUS FROM MOTERN V73 HORANS SECOLUS VIRIAS (TYPE 4 5 STACK UGAPOA-1167) 706-231	WPI TROVE		TOWATO BUSHY STUNT VIRUS (STILAIN CHEILLY)	П	П									
CAND MOTEN WITH 17	WATE HOW		HUNCH CYTOMEGALOVIAUS (STRAIN AD169)	7	П	261-212	-	1						
THE CALL IN TABLES PROFER VP.1	WAS LEVIL		HERPES SEGLEX VIRUS (TYPS I / STRAIN I?)	197-220	1									
PROBABLE CAND TABLE VIEW	PVPUS HSVRU		HERPES STAPLEX VIRUS (TYPE & / STRAIN UGANDA-1102)	206-232				-						

KCINI	16137-41 216										
FILERAME	PROTEIN	(Viete	П	П					₣	Ì	ſ
נישה מצים	PROBABLE CAPSID PROTEIN VP23	VARICELLA POSTER VISITE AREASTE PARTIES.	7	3	33	ARCAN	ALKAS	16.16	AREA?	AREA	AREA 9
h.	PM PROTEIN	AUTOCIA ANIA CALIFORNICA MINISTERA CARGAGOS CITATION	_			+	П		П	1	I
L	OUTEL CAPED HIGHEN WY	ABBITAN MORER CITINGES MORE ACCOUNTS ASSESSED	15.22	1	=	·					
	OUTER CAPIED PROPERTY VP2	ALTERACEPIE CONTROL SECTION OF THE S	168	7	П						Γ
INT CAN	OUTEL CAPED PLOTED VP2	BLIETONIE VERNINGER IN LOCK IN THE INC.	1	7	٦	27.5				•	Γ
1	DUTEA CAPED PLOTEIN VP2	BLIEFONGUR VIEW (SEPONGE 13 1904 15 15	1	╗	П					Ī	T
1 1	OUTER CAPED PROTEIN YPS	BLUETOWOUE VALCACEROTYPE 17 1501 A 75 18 A1	717.70		200	657-476					
	OUTER CAPSID PROTEIN VP2	BLUSTONCIUS VINUS (SEADOTYPE I / ISOLATE ALIETEALIA)		1977	1					4	
1	OUTER CAPSED PROTEIN VP2	BLUETOWCZE VRUS (SEROTYPE 1/1501.ATE SOUTH AFRICA)	Т	Т	1						
	OUTEX CAPSID PROPERTY VP.	EPIZODITIC MEMORANAGIC DISEASE VIRUS (SEROTYPE I)	Ī,	Т	Т						
	KNA-BINDOND PROTIEDA VP2	BOVINE ROTAVIRUS (STRADA R.)	Т	Т	17		700,770		-		7
	RULA DIDDING PROTECN VP2	BOVING ROTAVIRUS ISTRADA UK.)	T	Т	-						
LI	AMA-BONDING PROTEIN VP2	HUNCAN ROTA VIRLIS PERCETYPE 1/ STRAM WAY	I	Т	-1	2					
L.	ANA-BINDOND PROTECN VP2	PORCONE BOTAVERIX (CARGES P. 7. PER A NO. CHUNCHE)	Т	Т	- 1	7					
PWN LOTH	AMA-BENESHAD PROTECH VP3	STACKA II BOYAVBIIC APPARACATION	T	7	î î	1	7				
PVP30 LAABVP	KINGK NUCLEOMOTEIN VP36	MARBURO VIBILIS (STRAND ANICONE)	I	27.2	┪	Ž	22.34	67-70	163.790		
PVP31 ADTS	PHOSPHOPROTEZN P72	AFRICAN SWINE PEVER VIETS CONTINUES IN	2		1						
VOID LITTLE	×	EDOLA WAUS			1						
-	POLYNEMAZII COMPLEX PROTEIN VP35	MARBURG VIRUS (STRAIN MUSOKE)	T	72	1	1		1			
	POLYMENASK CONDILEX PROTEIN VP35	MARBURG VILLE GITAAN POPPI	T		1	1					
	DANDHOODAMANT BAYSLOFE PROTEDI PS	VACCINIA VILUS (STRAIN CONEMIAGEN)	Ī,		Ī	·			1		
•	DOMUNICOMONANT INVISIONE PROTEIN P13	VACCIDAL VIXUS (STRAIN WR.)	100	T	1					1	
	BOACHOCOMENANT IDAYSLOPE PROTEIN P15	VARIOLA VIRUS	200.00	Ì	1	Ī		1		1	1
PVP38 HEWARD	14 KD PHOSPHOPAGTEDE	HALLEK'S DISEASE HELPES WILLIS (STRAIN GA)	246.38	T	İ	F				1	1
	A KD PHOSPHOPLOTEIN	MANEK'S DISEASS HELDESVINUS (STRAIN NO 1/1/1/0/1/1	8638	†	T	1			1		1
	MAJOR CAPIE MOTEIN	AUTOGRAPHA CALIFORNICA MUCLEAR POLYHEDROSIS VIRUS	1100	T	T	Ī		1		1	1
_	MUOR CAPED MOTEIN	OROTA PEDIDOTSUBATA MALTICAPSID FOLTHEDROSIS VIRUS	t	214.340	364.3114	7		1	1		1
MA ANGVA	VPI CORE PROTEIN	APRICAN HORSE MICKNESS VINUS (SENOTYPE ASTRAIN VACCINE)	Ť	۲	f		Ī		1	1	T
TALL CALL	V7) COUL PROTEIN	BLUETONGUE VIRUS (SEROTYPE 16/15 OLATE USA)	131-141	213.237	1	Ī	T	T	T	\dagger	T
PWZ BTV!	V7) COLL PLOTEIN	BLURTONCUE VIRUS (SEROTYPE 17/15OLATE USA)	Г	113.117	T	Ī	T		T	1	T
AINT CAN	IV73 CORE PROTEIN	BLUETONCUE VIRUS (SEKOTYPE I / ISOLATE AUSTRALIA)	121-144	111:111	T	-	T	Ī		1	T
TOTAL STORY	VP) COULT PROTEIN	EPIZOOTIC HEMORILIAGIC DISEASE VIRUS (SEROTYPE 1)	121-142	63 69 5		Ī		T	T	\dagger	T
VACATION 1871	VALUE IN PROPERTY BAXES.	EPECOTIC MEMORINACIC DISEASE VIAUS (SEROTYPE 2/STRAIN AUS	121-142	Г	i			T	T	†	I
TANK THE		MULE DWALD VIKUS (RDV)		340-340	9 (66-196	640-919	347.74	10 M	1100	t	Ī
	DATE COST IN CHEST US	FUNCTIVE RUTA VICEOUP C / STRAIN COWDEN)									T
PWW CONV	CAPIED PECHTINA	SOURCE INDICATION SAID	7	2014	6 955-715	771-94				l	Ī
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PVP-0 HSVEI	CASO PROTEIN PA	FOUNDE NEW PERVICE TYPE I VETTA AN A BARD.	Т	7							
PYPE HIVIA	CASE HOTEW N	HERDESYBLIS SABAIN (STRAIN (1))	Ţ,			1		1			
PVP40 LTVT		INTECTIOUS LANTHOOTIACHEITTS VIRUS (STRAIN THORNE VILL)	100	T	T	Ī		1		1	
PYPO MABYA		HANDURG VIRUS (STILAD) MUSOKE)	62-110	T	t	T	T	T	1	1	
	MATHER PROTECTIVATE	MARKING YIRUS (STILAN POPP)	95-110	l	T	Ī	T	I	T	1	I
200	STRUCTURAL CLYCOPROTEIN PO	DOMBYX MONU MUCLEAR POLYMEDROSIS VIRUS	_	234-272			T	T	T	\dagger	T
	CHILDRING OF CHILDREN AND	WALLELLA-203 TER VIXIOS (STRAIN DUMAS)	П						l		Ī
WALL ROTE	OUTER CAPSID PROTEIN VIN	CENTAL II BAT LOWING AND AND AND AND AND AND AND AND AND AND		242.278						f	Γ
PAPAS ROTSI	OUTEX CAPED PROTEIN VIN	SECAN II BUT AVRIE (STRAD CALL)	T		1						Γ
PVN1 NVAC	VIDAL TRANSCILLTION RECUELATOR NO	AUTOGRAPHA CALIFORNICA NUCLEAR POLYGENEGRIE URTIE	10.00	Į.	1						
PVINE NEVOF	Na Montain	ORBITA PRUDOTSUCATA MULTICAPSID POLYIEDROSIS VIRUS		1	1	1	1	1			
PVF4A VARV		VAUGILA VIRUS	273-211	\dagger	t	Ť	T	1			1
MINI VACCE		VACCOMA VIRUS (STRAIN COPENNAGEN)	31.33	\dagger	t	Ť		1	1	1	T
WIND WACK	MAJON CONE PROTEST FIS PRECURSOR	VACCIMIA VIRUS (STRAIN WR)	31:33		\dagger	Ť		T	†	\dagger	T
WIND WAR	MAJOR CORRESPONDED FAR PARCUASOR			П		T	T			1	T
TVA BTVI	VA CORR PLOTEDA	BLUE TOWOUR VINUS (SEROTYPE IG/150LATE USA)		П	18:50 28:50					t	T
PVP4 BTV13	VA CORE PROTEIN	ALLIE FOWER VIRES (SERVITE 11/150LATE USA)	1	П	135-551						Ι
		PECELONOS (SEASITIFE IS/190LATE USA)	174-193	113-249 (5)	135-551						
											1

PCCEME	Princhizie	AN Viruse (No Baterriophages)		7	П	t	7	-1	1	-
INVESTIG	ROTT	WRIS		J	AREA AREAS	AN AREA	7	TO TO	4	3
PVN BTYZA	VP4 CORE PROTEIN	BEUERGORGA'S VINITE (VERGITTE 27 ISOLATE USA)	7	4.7-412	165411	+	\dagger	+	-	-
A PARTIES	COURT CAND PROTEIN WAS	BICE DWARF WEIK		493.514	636.448	+	+	+	+	-
100	- 1-	Boothe Bott A Visit CASE OF VER A VISITALIA BAATI	101.101	Т		+	ŀ		ļ. -	Į,
Table Por	COURT CARGO PROTEIN VA	BOVINE ROTAVIRUS (STRAIN CARA)	<u>8</u>		-		H	-	-	
	CALTER CAPSED PROTEDS VP4	DOVING ROTAVIRUS (STRAIN UK)	447.50		_	-	-		-	L
1	DUTER CANED HOUSE VIN	EQUING ROTAVIRUS (STRAIN H.3)		П				_		
1	DUTEL EASED PROTEIN VIN	HIBAAN ROTA VIRUS (SEROTYPE I / STRAIN 1076)		П	183.503					
PVM ROTHS	OUTEA CASED HOTEIN WY	HUNAAN KOTAYRUS (SERÖTYPE 27STAAIN RV-1)	П	134.240	105-201		+			
	OUTER CANTO PROTEIN VPA	HUMAN KOTAVÍRUS (SEROTYPE I / STRAIN 691)	٦	7	-	-	+		$\frac{1}{1}$	
	OUTEA CAPSID PROTEDI VPA	HIBITAN ROTAVIRUS (SEROTYPE 3 / STRAIN DS!)	7	_	482-507		-	-	$\frac{1}{1}$	
PWH LOTHU	OUTLA CAPAD PROTEIN WA	HUNGAH BOTA VIRUS (STACIN KS)	461-508	П	7	-	$\frac{1}{1}$			4
PWH KOTIKE	OUTER EASID MOTEIN WA	HEMAN ROTA WALUS (STRAIN KU)	П		314.340 412.941	į	-		_	
PVM ROTHE	OUTER CAPITS PROTEIN VA	HEMAN ROTAVIRUS (STRAIN L26)		234.249	483.507	•	-			
TOHOUS NAME	OUTEA CAPSID PROTEIN YN	HAMAN ROTAVIRUS (SENOTYPE 1/STRAIN M37)			495-181					
WK ROTON	OCHEL CARSO PROTEIN WA	HUMAN ROTA VIRUS (SEXOTYPE 37 STRAIN MCN:3)	161-204	068-667	107-117	•				
WK TOTO	CUTES CAPAD PROTEDI VPA	HEDIAN ROTAVIRUS (SEROTYPE 3 / STRAIN P)	Г	234.369	411.507	-	\vdash	-	-	L
WW BOTTO	OUTER CANID MOTION WA	HENCHAN ROTAVIRUS (SEROTPPE 4/8 TRAIN ST THOMAS 3)	Γ	\$4.36	413.507	-	-		L	
PWN LOTHV	OUTER CAME PROTEIN VP	HUDGAN ROTAVIRUS (SEROTYPE 4/STRAIN VAYO)		497-70			Н		4	
1	OUTER CANID MOTERN WA	MUMAN ROTAWAUS (SEROTYTE I / STRAIN WA)	(02-18)	106-549			Н	-		Ц
	OUTLA CLYB FROTEIN VY	POACHAE KOTAVIALUS (SEROTYPE 37 STRAIN OSU)	135-256	805-[89						
FUN LOTTC	OUTER CANSID PROTEIN VP4	PORCEME ROTAVIRUS (GROUP C / STRAIN COWDEN)					Н		-	
	OUTER CASE MOTER VA	POACDAE ROTAVIRUS (STRAIN OOTTF NED)	134.249	105-589						
WAY TOTAL	OUTSA CARID MOTEIN VP4	PORCINE ROTAVIRUS (STIJAIN YM)	133.236	105-530						
	DUTER CANSID PROTEIN VIN	ING BUS ROTA VIRUS	483-306			÷	Н			
WA LOTS	OUTEA CAPED PROTEIN WA	SPEAN II ROTAVIRUS (STIAIN SAIL-PEM)	483.508							
	DUTER CAPIED PROTEIN VPA	SBEAN IT ROTAVIAUS (STRAIN SA II-SEM)	116541	105-C11						
PVN EBAV		SOUTHERN BEAN MOSAUC VIRUE			П					
ALA RAI	NONSTRUCTURAL PROTEIN PHSA	WOUND TURKER YIRUS	П	7	\$ 15 S	<u></u>	-		1	4
PVPS LTV16	OUTER CARID PROTEIN VPS	INLUSTONOUS VIRUS (SENOTYPE 10 / ISOLATE USA)	7	7	55.5	+	1		+	
PVPS BTVII	OUTER CAPED PROTEIN VP.I	INCLUSTONGUE VIRUS (SEROTYPS 117 ISOLATE USA)	1	Т		-	1			1
SIAM FIAE	OUTER CAPAD PROTEIN VPS	INLUNTONCIUE VIRUS (SEROTYPE D.) / ISOLATE USA)	12.		$\frac{1}{1}$	+	+	1	$\frac{1}{1}$	1
AVE BIVIA	OUTER CASED PROTEIN V?)	ELUCTOROUGH VIRUS (SCRO) TTG 1785CA18 AUSTRALIA)	7777		Ì	+	\dagger	+		1
IVE BIVIS	COTTEN CAPAD PROTEIN VIS	TALLIER CONTRACTOR CANDERS OF A STACK A TRACTOR OF THE STACK A TRACT	115.7			$\frac{1}{1}$	\dagger	\downarrow	+	-
A 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	COURT ONLY BUTTER BY	BICE DWARF VILLS	765-254	65.53	20.73	ŀ	ł	-	-	-
TOTAL PROPERTY.	_	INITIATORICIE VIRUS (SEROTYPE 107 ISOLATE USA)	17	Г	261.276	\vdash	\mid	-	ŀ	L
PWKI NPVAC	+	AUTIOGRAPHA CALIFORNICA MUCLEAR POLYHEDROSIS VIRUS	321-333	П	Н	H	H			Ц
PATE BIVIE	VIA PROTECT	BLUETONGUE VIAUS (SEROTYPE 10 / ISOLATE USA)	5.13	157.272					4	
PART SOBY	PROB MONSTRUCTURAL 34 3 KD PROTEIN	MALIZE ROUCH DWARF YRUS	130-146					-		
PVP64 NOVOP	MAJOR ENV OLYCOPROTEIN	ORGINA PSEUDOTSUGATA MULTICAPSID POLYFEDROSIS VIRUS	6		206-313	$\frac{1}{1}$			-	
PVP67 NPVAC	NAJOR IDAY OLYCOPROTED	AUTOCHAPHA CALIFORNICA NUCLEAR POLYNEDROSIS VIRUS	100	28.23		+	+	1	+	4
PVPC) NEVON	_	GALLERA MELLORELLA MUCLEAR POLYREDROSIS VIRUS	21.4	,,,,	-	1	\dagger	+	$\frac{1}{1}$	1
	VIN PROTEIN	BLUE CONCUE VIROS (SERO) 17E 117 SOCATE VIA)	25	Т	117.11	+	t	+	-	\downarrow
	VIEW PATER	ALTERTONICA VIEWS (SEROTYPE 17/150LATE USA)	2	Т	187.171	+	\dagger	l	1	1
	VAL PROTEIN	BLUETOWATE VIRUS (SEROTYPE I 7 ISOLATE SOUTH AFRICA)	2	Т	9(2:192	l	ŀ	-	-	
1	101 POT 101 POT	BLUSTONGUE WRUS GEROTYPE 1/150LATE USA)	104.20	Т		-	ŀ	-	-	L
	STRICTURAL PROTEIN PA	WOUND TUNDA VIXUS	334.39			\vdash	\vdash		-	L
NAME OF STREET	STRUCTURAL PROTEIN PO	WOUND TUMOR VIRUS (STRAIN NI)	34.30				-	-		L
PUPIL NEVAC		AUTOGRAPHA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS	254.275				H			
WHI BYLL	PROBLEG MEXIGANE ANTICEN 75	HEBSTERVIRUS SABARA (STRAIN 11)	П	П		H	H			
PVP BAVAC	19 KD PAOTEIN	AUTOGRAPHA CALIFORNICA NUCLEAR POLYHEDRÓSIS VIRUS		027500	678-304	Н	H	H	H	Ц
PVPI BITVIS	VP1 CONE PROTEDA	BLUETONGUE VICUS (SEROTYPE 1) / (SOLATE USA)	10,23			$\frac{1}{1}$	+		$\frac{1}{1}$	1
WP7 EXDV1	VP) COAL PROTEIN	EPIZOOTIC HENDRINAGIC DISEASE VIRUS (SEROTYTE 1)	707-707	66:100		+	+	1	+	1
441	NONSTRUCTURAL PROTECT PAST	INCEDIMON VINOS	18.5%			+	$\frac{1}{1}$	+	+	
A	HONSTRUCTURAL PROTECT PRES	WOUND LOWOR TIRUS	707:107			$\left \right $	$\ $			

PCCEME	Michiga	AB Virgini (% Barteria)								
V.7.2	ZAOTEN	Traus	П		-	-				
AND LAUNA	Costo Professor Pro	AUTOCIACHI CALIFORNICA MICTIEVE BOX SAGREGAS	4		AREAJ AREAS	AREAG	77747	T.		
PAN BANIE	CANAD MOTEON PET	OROVIA PSEUDOTSUDATA ACIL TICABITI POL VIENEZATE TERES		938-460	1	ı			A A A	3
WI PROIL	MONETURE TRUTTER PE	BLUETONGUE VIRUS (SEKOTYPE 16/1901 A PE 1164)	27.72						1	
101	MONSTRUCTURAL PROTEIN PR	BLUSTOWOUR VINUS (SEACHYPR II / 1501 A TE 115.	20						1	7
	MONSTELLER PROTEIN PR	BULETONGUE VIAUS (SEROTYPE 31/1501 A 78 184)	81.8						1	T
	POST FOURTH PROTEIN PR	BLUETONGUE VIRUS (SEACTIVE 197 ISOLATE 194)	R							T
PVN BTV1	MONTH CHIEF A MARKET IN	BLUETOWCKE VIAUS, SEROTYPE I / ISOLATE AUSTRALIAN	2 2	1				ľ	1	
1	MONSTRUCTURAL PROPERTY	BLUETONOUE VIRUS (SEROTTYRE 1/150LATE SOUTH AFRICA)	2 2	†					ľ	1
	OUTEX CAPSID PROTEIN PE	BLUE TOPOUR VENUS (SEROTYPE 1/150LATE USA)	104.1%	\dagger	1				-	Ī
PVPI RODV	OUTER CAPED PROTEIN PA	ACC DWALL VIOLE	7K-48	t						
	STRUCTURAL PROTEIN VM PRECINEDS	WAS COLL DWAY VIII'S	Τ	216-242 10		\parallel				Γ
	STRUCTURAL PROTEIN VYS PREPLIATIVE	CONTRACTOR (STRAIN COPENHAGEN)	Т	Т						Γ
	STRUCTURAL PROTEIN VPS PRECINGOS	VACUATA VIRUS (STRAIN WR)	2330	\dagger	1					
VIII WIL	OUTER CAPITO PROTEIN PA	VACOLA VIRUS	135.36	t						
VP LOV	MONSTRUCTURAL PROTEIN PAGE	TOWNS TOWNS AND	Т	214.941	101 101					T
VPS RCDV	NOMSTRUCTURAL PLOTEIN SO	INC. DWALP VIRUS	Т	Т	T					Ī
VHIE NEVAC	29 KD POLYHEDRAL BAYET OPP PROTEIN	MACH LALLE DWARF VIRUS	X	1					\mid	T
PVPIR NEVOF	32 KD POLYREDIAL ENVELOPE PROTEIN	AUTOMORPHA CALIFORNICA MUCLEAR POLYHEDROSIS VIRUS	Τ	316.346						Ī
VIRT ADEIS	ENDOPROTEASE	CALCULATION TO STUDIES AND THE ANSIED FOLY PREDICTS VIRUS	Т	+				-	l	Ī
WART MAKETYIB	PROTEASE	MUMAN ADENOVIRUS TYPE 12	181-191	1						T
	PROTECUE	PRODUCE MANDENANT TUMOR VIRUS (STRAIN BRS)	19:00	+					-	I
PVPRT SACKVH	PROTEASE	PARTY PASCING A VIRUS	8.2	1						Ī
PVPRT SAVI	ROTEASE	SQUIMEL MORKEY RETROVIRUS	14.67	1						Γ
١, :	A MOTEN	SIMILATE RETROVICES SAV.	2.0	1					-	1
	N Moreiza	PARAMETER PROPERTY VIRUS TYPE I (BHIG ISOLATE HXII)	1	\dagger					\vdash	Τ
• 1	VPU PROTEIN	THUMAN DOMINOCOFFICENCY VIRUS TYPE I (BITE ISOLATE)	100	+						Τ
	PUROTEIN	IN BALL ROLL BELLENCE VIRUS TYPE, I (DRAIN SOLATE)	1	1	1	1				Γ
	VPU PROTEIN	HANAN HANDONE FICE MEY VIRUS TYPE I (URI) ISOLATE)	100	+	1		1			
	VPU PROTEIN	HINAN HANDER FRANCE VIRUS TYPE I (ELLISOLATE)	2	ľ		1	Ì	-		
PWC WIR	VPU PROFESS	HOMEAN MAN MAN MAN MAN MAN MAN MAN MAN MAN M		T	T	1	+	1		
	VPU PROTEIN	HUMLAN BOACHOOFFICERY VIRES FOR	3.28	-				1		
ŧ	PU PROTEIN	MANAN BOADNOOF CENTY VALUE TO BE AND SELECTED	12.1	H	1		T	1	1	7
7	VPU PROTEIN	HUMAN BOADHOOF KIENCY VIRIN TYPE I ANN 1451	2					1	+	7
7	70 PROTEIN	HAMAN BOADNOOFFCENCY VIBILS TYPE (ALC)	17.				l		1	1
7	VPU PROTEDI	HUMAN BERCHODERCIENCY VIEW TYPE 1 (48) 1 1821	1						1	1
.l.	N AUTO	HUNKIN DERCHOOFFICENCY VIRIAS TYPE I COTTEN ATTE	B2-7				T		1	T
	VPU PRUITED	HUNAN DARMODEPRIBACY VIRUS TYPE I 123/CTC - 34 HG/ 4-5	R.	+				\parallel	+	T
VPX HVIBE		Ŀ		1					\dagger	T
ı				1			ŀ	-	+	Τ
ı	Vex Page 1	HARAN BOADNOOLPICIENCY VALUE TYPE 2 (1801, ATE CAM2)		+				-	ł	T
L		MANAN DAMINODEFICIENCY VIRUS TYPE 2 (150LATE DIM)		+				-	\parallel	T
ı	VPX PAGTLES	T	1 7	+					-	Τ
ı		3	16.32	+	+				-	Τ
			113	1			1			Γ
			17.0	┞	-		1	-		
		HINAM BARBONE INTERNATIONAL TYPE 2 (ISOLATE SBLISY)	633	-			1			Π
			16.32	-	-		1			
7			145-165	\vdash			1			П
7		SOUTH BOUNDEFICIENCY VIBIG DALLY STORY CLONE GILLI) (SI	45		-		1	1	1	7
NEW SIVING		ICIENCY VIRUS (KAN PON ATENCE) (SIV. MAC)	10.33	Н		T	\dagger	\dagger	+	7
T			200						1	7
7			200	Ц			1	1	+	7
WINT BELOW		MC 11 ICH ATEL/COUTY M	200				1		+	T
Т	NOWSTRUCTURAL PROPERTY LEVEL	SMV)	20,110				-	+	+	T
1			Т	-	7		Н		H	Т
	•		1							Γ
•										1

17100	Tolisceri 316	All Virgen (Ng Bertsetaphages)	П	П		7	- 1		1 101 1 101 1	
1011		IVIRIS	173V	Ţ	¥	3	4			1
even kom	NONSTRUCTURAL PROTEIN INCVP2	HOMAN ROTAVIRUS (STRAIN IOV-10-1)	آ۔	2	-	į				
VISITORY	MONITALICATIONAL PROTEIN MS33	POACING ROTAVIALS (CACKIP C./ STRAIN COWIDIN)	11.112	:	:	:		:	;	:
1101 101		SIMIAM II ROTAVIKUS (STRAIM SAII)	346.4				1		†	T
PACA EARER		BOVINE ROTAVIAUS (STRAIM RF)	221.123	1				1	ļ	T
PVIOR ROTES	VYS PROPED	BOVING ROTAVIRUS (CROUP C./STRAIN SHINTOKU)	S 2 3	1	-		1	\dagger	+	T
UMOR BOTTE	UNA PROPILIN	BOVING ROTAVIRUS (STRAIN UK)	227 707				†	T	1	Ī
West LOTED	т	EQUINE AOTAVIAUS (STRAIN FLIA)					-	-		1
HELDE PONE	т	EQUING KOTAVIRUS (STRAIM II-2)	203-229				1		t	
10,00	+	ROTAVIRUS (CROCUP B / STRAIN ADRY) (ADULT DIABULEA ROTAVIRU							1	
	_	ROTAVILUS (CROUP B / STLAIN IDIR)	23-40				1		1	I
	7	HERLAN BOTAVIBUS (SELOTVPE I / STEALN 1076)	111-101							
NION BEAL	7	LEALAND BANK CORP. C. STRAIN BRISTOL	2		L					
PYSON BOTHC	7	THE PETER WAY A LINE OF THE PARK A LINE AND A PARK AND	200.235		ŀ					
PVSOR BOTHS		MUMAN KUTATAUS (SEKULTICE ET STEAMER SE)		-				-		Γ
PVED LOTTE	VA)10155	HUMAN KOTAVIRUS (SEROTYPE I / STIMIN WA)	1		+			\dagger	1	Ī
PART BULB	Т	PORCEME ROTAVERUS (CROUP C./ STRAIN COWDEN)	٦	314.340				1	t	T
	Use 18 APRIL	HORCEACE BOTA VIRUS (STRAIN COTTY NED)	102-215		-			1	1	T
2	The state of the s	BOADS BOTAWILK (CHAN KNA)	101-135		:					
PVSM ROTE	OLYCOPROTEIN V7	AND THE PARTY COLUMN TO SEE AND TOWNERS	×11.6	-	•					
PVDM ROTTIC	CLYCOPHOTEDI VP7 PRECURSOR	TOTAL MAINTENANCE OF STREET	114.304						-	
PVSM ROTS!	NONSTRUCTURAL PROTEIN NEVPA	SECAN II KUTAYAUS (SIRAM SAII)			†				l	
PYSOF ROTTA	GLYCOPROTECN VP1	BOYING ROTAVIRUS (SEROTYPE 6/ STRAIN 61A)			1				t	
1944	Т	BOVING ROTAVIRUS (STRAM A44)	131-155					t	Ì	
	т	INCOME BOTAVIRUS (SEROTYPE 10 / STRAIN B221)	131-155						1	
	7	BANANC BATAMBER (STRAMBER)	881-181						1	
PVSON NOTOK	_	TATALAN A AND UNION DEPO AND A 1 APP A 14 TANK	131-131		-					
PVSOF LOTTE		BOYING KULAVING (SCHOOL VIE 17 STROKE 1777)			-			l		
PVSO ROTO		COCKEN ROLAYBUS A (SEKULTER // STRAIN CH.)			1			l	l	
PVSG LOTEL	QUYEOMOTEDI VA	EQUING ROTAVIOUS (STRAIM L.) 18)			ŀ					
DLC POLCE	CALVOORIGITATIVITY PLECUASOR	NOTAWALS (GROUP B / STRAIN IDIR)	Ť					\dagger	t	
THE PARTY		HEMAN ROTAVISUS (SEROTYPE 4 / STRAIN RV-4)	7	21246				l	t	I
ALTA PARTY	•	HUNDAN ROTAWAUS (SEROTYPE 27 STRAIN NUS)	212:26					\dagger	t	l
Carried Marie	•	HOMAN ROTAVIRUS (SEROTYPE 2/STRAIN DSI)	22.52					1	†	
TANK MAN	CE VOYAROTERA VP)	HOMAN ROTAVIRUS (SEROTYPE 27 STRAIN HOUZE)	7		1				t	
	Ca VOSEGNEDI VP7	HUMAN ROTAVIRUS (STRAIN L'24)	7	1111				1	1	
TO THE PARTY OF		HENKAN ROTA VIRUS (SEROTYPE 17 STRADY MJ?)	7	217.16				1	T	١
No.		HUNGAN BOTAVBUS (SEROTYPE I / STRAIN MO AND STRAIN D)		197-212				1	1	
	Т	HIDAAN BOTAVRUS (SEROTYPE 3 / STRAIN P)	131-155				1		1	Į
2	т	MINAM BOPAVIETS (SEROTYPE) / STRAIN RRV)	131-138							
PVSO ROTIO	7	LA MAN BOTA VIBIR PEROTYPE 27 STRAIN \$1)	197.213	-						
WO TOTAL	7	MARAN BOTAVBIR (SEBOTVE 4) STRAIN VATO	197.213	_						
PYSOF ROTHY		ANALIZE AND COMPROSE OF COMPANY OF A CENT AND WAY	Γ	197.212	_					
PVEDE ROTHW		MUNICIPAL PART ALIGNIA OF BOATON OF STREET	Т	117.10	-					
PVSD# NOTPS		FORCING ROLAVIROS (SCHOLLTES A STRUCTUS)	t		-					
PV506 ROTH		FUNCTION NOT A VALUE OF THE STATE OF THE STA	818.84		-	ļ				
PVED KOTPS		MULTER MULTER WORK (1977)			-			l	T	
PVSOS ROTPIA	OLYCOPROTEIN VP7	PORCINE HOTAVIRUS (SEROTYPE 47 MINAIN BAILT)			\downarrow			T	T	
PASS ROTTE	г	RHESUS KOTAVIKUS							T	
PATES LOTTE	Г	SDIGAM II ROTAVBUS (STRABA SATI)	60-101	1				t	Ì	l
1000	MONSTRUCTURAL MOTE	RETAVIBLE (CROUP BYSTRAIN ADRY) (ADULT DIABUREA ROTAVIRU						1	T	l
100	Т	HUMAN RESPONTORY SYNCYTIAL VIRUS (STICALN AZ)	1						1	
	CALAST BYTH CONCORD PO	MORES VILUS (STRAIN SAL-I), AND MURITS VIRUS (STRAIN SAL)	3.5						1	
	ALC: 1 LONG CAMPAINT	MACHINE VIELUS (STEATH EDINGBURGH 1 & 4)	1.29					1	1	۱
	A PARTY OF THE PAR	INTERS VILLE (STRAIN EDINGBURGH 4)	677					1	1	
	STATE OF THE PARTY	MORAN VILLE GERADI MATSUTAMA)	8401							
ANSWERS AND A	SALL MTDROTTORY A	LANGES VIREN SERVINE AND	87	-						
PVSM MURON	SAAL HTDROTTORY, TRUILIN	LA LAGO COSTA (STA ANI ENDREY)	\$.7°		-					
PVSH KULOT	SAAL MORDHOOK 7	LA L'AR CARLA CATA ATRIA	27							
PVXH MCMO	SMALL HTDROPHCBIL TR	LA CARL CASTA - 25% A TAILT	**						Ī	
PVSH MUNK	SHALL HYDROPHORIC PROJECT	MUMBER VISION AND RESERVED. 11	5.3			-				
FVEH MUNT	SALALE HYDROPHOBIC PR	AND THE COLUMN THE PROPERTY OF CAPACITY OF	5.0		-					
PVSH MUMON	M SAZALL KYDROPHOBIC PROTEIN	MUMP'S VIRUS (STRAIN PRITAIN TRAINING								

		ĺ						
MANUAL PROPERTION PROPERTY MANUAL PROPERTY	And Virginia (To Dethyrlopha prz)		-					
W. IDALI, PROPRIETE PRINTING	V1.05	Г	1	11111	Т	7	П	L
THE CONTRICTORY THE CONTRI	MUMOR VIRUS (STRAIN RW)	ī	т	7	4	ONTA SANA	SALEN CA	7
	MUMPS VIRUS (STRAIN TAKAJIASIE)		1	1				
	MOROS VAUS (STRAIN IMARE VACCINE ALM)	67-03					<u> </u>	
	NEOVELIS (TVPS T) THE ALL SAME	67.61			L			
W. HOLD, HATTER	CANAL PROPERTY OF THE PROPERTY	10-136						
Machine Mach	THE TANK OF THE STRAIN DEALING)	152-170		-				
	ALOVATUS (TYPE 2/ STRAIN DAJONES)	4 65	1					
	REDVINUS (TYPE 1/STRAIN LAND)	27.75						
NATIONAL MOTIONAL NATIONAL PROCESSION 19-21		132-120						
A. STREETOLA, PROFESS FREEZINGS SECURITY BY UNLIGHT BY UNLIGH BY UNLIGHT	75.10							
No. Interfector, No. Inter		303.311	-					_
STATE COLOL. BOTTON PROCESSION SEAS	MENATITIS & WINUS (STRAIN MEXICO)						L	
MACHINAL MORTER	MEPATITIS & MIRLIS (STRAIN LAVAINATAR)	III CATA	_	•		L		
Wester W	CANADA STATE OF THE STATE OF TH	392.311		-				
TOWARD WESTSHIP ACTION TO BE STATEMENT OF THE WILLIAM MENTS WILLIAM MENTS	THE VIEW OF VIEW PARISTAN	1392.311		1				
TOWOR VERGINGS PATRICK TO BE CEPTOR REC. PATRONA VIRIGE STRAIN LAUGACE		1						
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PCT/US95/16733

TABLE XIV

SEARCH RESULTS SUMMARY

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_	RNA POL YMERASE BEIA STRIBATE	SI KDAI VINIS (SIBAR 2 LIDST KLITAMIS)			!		1618.001	<u> </u>	1
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THE BENNY	UTATIVE RMA DIRE	ATD CLOVER MICROFIC MISSAC VIRISS (NCINIS)	178.314	130.353	Τ	-		-	
TAKED REDVI	MA-DIRECTED RNA	REQVIRUS (TYPE 27.5TRACH DYKONES)	314-315					 	
NAME OF STREET	RIVA-DEBECTED RIVA POLYNIERASE SUBLINIT VP.	NOVINE ROTAVIALIS (STRAIN AS)	3.66	100.001	347.316			-	ĺ
2000	AA-OIRECTED BYA	HOVING ROLAVIATION (IR.)	2	341.376					
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	BAS BOX VAICE ARE	SIMIAM II NOIAVIRUS (SIRAIM SAII)	9	٦	247-276				
PATEN TRUE		TACAMILE VINOS	₹	3	2076-2112				
71,011	PROMA REPLANA. DIRE	PERSONAL STORY THROUGH CHERKY (TEST)	Š.						
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	LARGE TEGUARENT P	PSTEIN-BARK CIRCS (STRAIN 1995-b) CEINIAN ITRIPISCIRITA	2	144-150	1	103:111			
	PROBAMLE LANGE, TI	HEBIAN CYTONII GALOVINUS (STRAIN ADISO)	161.141	696.736	11.040	11111			
PTECU JISMO	LARCE TECLARENT P	HERPES SHAPLEX VIRUS (TYPE &) STRAIN GS)	111.19	¥6.40!	┍	100-1466	101.101	İ	
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PILLA AVISA	TRANSFORMEND PROTEIN MA?	ANTAM MUSCULO (POMITMOTIC FINA OSANCONIA VIRUS ASA)	10 163			İ	İ	İ	
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PVIII ALME		ALFALFA MOSAIC VIRUS (STRAIN 47) / ISOLATE LEIDEN	363.363		Г		ľ	ł	Ī
PVIIK TRVP		TOBACCO RATTLE MAUS (STRAIN PLN)	14-41					ľ	Ī
PVI45 MPVAC		AUTOGRAPHA CALIFORNICA KUCLEJAR POL MICOROSIS VIRUS						T	Ī
PATING BSMV		PART EY STRIPE MOSAIC VIRUS (BSNIV)	25.45					†	
PLIA CAIVIN		CHE LAINTA MOSAIC VINUS (STRAIN INVIICINS)	24.70					İ	Ī
P1 270 ASJ B1		ATRICAN SWINE PLVER VIRUS (STRAIN BATIVILASEV)	10:00						
PV3A BRMV		NACAD DE AMANDITLE VIRUS	616-67					İ	
PVIA CCAIV	N POLCE	COWPLA CHI OROTIF AND TILE VIRIES (CANY)	3 3	631.61)	10.19			Ì	Ī
PLIA CLIVEN	_	CIA (MMI) A BRITANE VIRIS (STRAIN INVITEDAY)	(F)	21:00				Ì	Ī
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		POBACCO BATTLE VIRUS (STRAIN TCXI)	100.00					l	
		BROAD BEAN MOTILE VIRIS							
		PROME MOSAIC VIRUS (BMV)	39.18					İ	Ī
		COWPLA CIR DADITE ADDITE VIRUS (CCAIV)	9						Ī
		AVIAN INCRETIOUS INCONCIUTS VIRIUS (STRAIN BEATING TELLINY)				I		Ì	İ
		AVIAN INSTITUTES BEONCHES VISUS A BANKET TRAV						1	İ
FVIA MVP3	N. W.	AVIAN IN COMON RECORDERS VIEWS						Ì	Ī
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PVA21 VARV	FROIEN ASI	VARIOLA VIRUS		ig.	T	Ì	Ť	l	1
7	PROJECT ASI	VACCINIA VIRUS (STRAIN COPENIAGEN)	Ī	İ	İ	Ī	İ	1	Ī
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	PROJECT A 40	VACCINIA VIRUS (STRAIN COPENIAGEN)	 				Ī	ľ	Ī
	PROTEIN A41		2			Ī			
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PVA41 VARV	PROTEIN A41		97.130					f	ĺ
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FILE NAME.	PROTEIN	Visit	Τ				11461		
L	ALS PROTEIN	BEET CURLY TOP WAUS (BCTV)		Т	Г	1	I	Ī	Ī
PVALJ CLVK	ALI PROTEIN	CASSAVA LATENT VIRUS (STRAIN WEST LENYAN 844)	25.11				-	\downarrow	T
PVAL) CLVN	ALI MOIEN	CASSAVA LATENT VIRUS (STRAIN INCERIAN)	1					ł	Ī
PVAL) TYLCH	ALI PROTEIN	TORIATO YELLOW LEAJ CURL VIRUS (STRAIN MAINIANDE) (TYLCV)	1				-	ł	Ī
אין געני	ALJ PROTEIN	TOKIATO YELLOW LEAF CURL VIRUS IT MCV	11:11				-	l	Ī
×1	APHID TRANSMISSION PROTEIN	CALILIT LOWER MOSAIC VIRUS (STRAIN CIM-1641) (CAMV)	18:33	911:10				-	ĺ
WY C75	APHID TRANSASSION PROTEIN	CALLIFLOWER MOSAIC VIRUS (STRAIN DAI) (CAMY	Ş	01.501					
200	ACHID HANDARDSKIN FROIEIN	CAIR IF LOWER MOSAIC VIRUS (STRAIN BBC) (CAMV)	ŝ	=					
200	APIRE SEAMANCE AND SECTION	CALLIFORNIA MOSAN VIAUS (STRAIN NITHES) (CAMY)		2			-	+	1
VAT CANN	APRILI TEAMSON PROTEIN	CALL RELOWER MODAL VINUS (STRAIN PRESENTED IN CALL)						1	Ī
PVB04 VACC	PROFFINE	VACCINIA VIBILITATION CONTINUES	Į,	240.10				1	Ī
L	MOTENT	VACCINIA VIRUS (STRAIN WR)	Т				1	+	T
PVB04 VARV	MOTEIN	VARIACA VIRUS	Т					1	Ī
×	•	(694)	97.138					+	
	INTERLEUKIN.) BIN		2				 	H	Ī
	SURFACE AMINCEN	VACCIMA VIRUS ISTRAIN COPENIACEN)	₩. ::: :::				 	ŀ	Ī
AMIS VACCO	SURFACE ANTICEN S PRECURSOR	VACCIMIA VIRUS (STRAIN DAIMEN !)	311-343						Ī
AVCCA	SURFACE ANTIGEM 5 PRECURSOR	VACCINIA VIRUS (STRAIN WR.)	21.30						
PAGIO VARV	SURFACE ANTIGEM S PRECURSOR	VARIOCA VIRUS	211-343						Ī
PVBR BONV	- 1:	DEAM COLDEN MOSAIC VIAUS	104-191				-		_
PWC0 SFWCA	C-PROTEIN COUPLIN RECEPTOR MOMOLOGICS	SHOPE FIDEONIA VIRUS (STRAIN KASZA) (SEV)	٦					-	Ī
אנפי אינננ	PROJETHICA	VACCINIA VINUS (STRAIN COPEMIACI N)	٦	32.0					Ī
	MOJEINCA	VACCINIA VINIS (STAALS W.R.)	100	10.211					<u> </u>
	PROTEINCE	VARIOLA VIRUS	9:10					L	_
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PYCO VANV	PROTEIN CO.		3						_
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•	PROTEIN C21/629			Ī				1	Ī
PVCAP 68V	MAJOR CAPSID PROTEIN	NIAM HERPESVIRUS 41		2		Ť	1	+	ī
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200	El Moltin		107:19					
.	E. PROICEM	1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2						L
	EI PROTEIN	•				I		
ZVAV	EARLY 33.9 KO PROTEIN	ALITICALAMIA CALIFORNICA MUCLEAR POLYMEDROSIS VIRUS (ACHINEV)	2			1		
	32 COL COL	_	21.6		Ì			
•			117.147					
1	ILS PAULEIN	THE PROPERTY OF PARTY AND THE PARTY OF THE PROPERTY OF THE PARTY OF TH	1					
١.,	EARLY 40 9 KD PROTEIN	-						L
	PROBABLE ELA PROTEIN		2					ļ
	AND AND REAL PROJECTS		2					
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	PRODALLE USA PROJECT	The second secon	١					
	PROBABLE ES PROTEIN			Ī				
			=					ļ
		TYPE	11-36					
1			104.140					إ
L KELL	TROBABLE CO TRUITING		91.02					
	NOTICE AND DESCRIPTION OF THE PROPERTY OF THE		R	İ			<u> </u>	
Š	Million Co.		1					L
	UF PROTEIN							
ı	ET PROTEIN				<u>.</u>	_		_
1.					_		_	
			2.4					
21.1		A THE PARTY OF A VERY STATE OF THE PROPERTY OF	1					
PVE J INVI	I'V PROTEIN		41.61			L		
I (Ad) (Md)	E) PROTEIN				İ			
PVET 18V3	ET PROTEIN							
10041	E) PROTEIN							
5 CO 2 1 1 10 VA 3	CT PECTEIN	HINIAN PAPIL LONIA VIRING TYPE 47	8					ļ
1000	M1112764 E11		A.4		_		_	
			11.11		_			
			9.5					
A A	ET PROTEIN							
DAY 13V4	EJ PKOTEIN							\mid
PVET PAPVO	I PROTEST		3					
200	E S BB O F ED.		60-03			_		
		M YHEDROSIS VINUS (ACKINPV)	133-157	229-059				
PVEM MVAC	EARL WAD INCIDEN	ī	2			-	L	L
PVEF CVTN	VIRAL EMILANCING FACTOR		,	11111		-		ļ
WHY IEV	HAVE COPE PROTEIN					+		1
12 22 23	FEMURITAR CLYCOPROTEUN PRECUASOR	-	21.15			-		
	LA NOT PAYOU OPE PROTEIN	E I (MCVI)	105-116				-	
	TOTAL PARTY		20,216				L	L
PVENV MC)	MAJOR ENVELOPE P						-	ļ
WHY VIEC	MAJOR ENVELOPE P	MAGEN						
TOWN OVER	LAIDE ENVELOPE	1000	Ž					
277	MAIDE KNYFLOPK		<u> </u>					
7.00	LIAME ELVE ON: PROTEIN	S (STRAIN WR)	106.341					
PVIN VALL	MARK ENVISOR		135-167	104.34		L	Ц	Ц
PVENV VARV	MAJOR EPATILIONE							

	AREAI	AREAI	AREAJ	AREA	ANEAS	ACA C	AREA
NIAGEN)	240	61.93					
	8	62-93			1		1
	297-130			1	1	1	†
	227-267			1	1		1
	19.118						1
IIIAGEN)	23.61						1
	28-61					1	1
	ž						1
NNEL CATFISH VIRUS) (CCV)	317.36						
RAIN ADAP) (EHV-I)	163-196						1
(STRAIN CUPENHAGE	92.120					Ì	1
	92-120						
NNEL CATFISH VIRUS) (CCV)	101-136						
MNEL CATFISH VIRUS) (CCV)	34.83				j		1
HAGEN)	99-136						
	961-66						
HAGEN)	111.165						
	113-145						
HAGEN)	161-101						
	101-992						
	1 CC-10C						
	150-183						
NNEL CATFISH VIRUS) (CCV)	(142-902						
	901-19						
	254-292	101-111	414-452				
	300-337	647-678					
CATFISH VIRUS) (CCV)	70-101						
NEL CATFISH VIRUS) (CCV)	94-125			,			
-	36-74						
VIRUS) (CCV)	491-521						
VIRUS (AMEPY)	180-217						
	207-244						
NNEL CATFISH VIKUS) (CCV)	15-46	190-216					1

		7 Y AMPI				, .	
	ANIA.		7 VIIV	14.Ks.4.	1015.52	A REA 9	15MG
ANNEL CATFISH VIRUS) (CCV)	187-231					-	
8~	97-81						
S VIRUS (STRATH BEAUDETTE) (1817)	1719-1747	1836-1891	2109.2146	3601-3633			
TRAIN AD169)	80-115	153.183					
1815)	1259-1794						
11.9)	119-159						
11.Y-138)	139.1391						
I NEBUS)	1259.1294						
(QUEBEC)	1259-1294						
I VACCINE)	1339-1394						
1 229E)	1053-1088						
TRAIN WILD TYPE 4) (AIIIV.4)	1267.1304						
IRAIN AS9	1215-1352						
TRAIN MINIV / VARIANT CL-3)	1267-1304						
TRAIN JILI)	1126-1163						
ROENTERITIS CORONAVIRUS	632-665	116.764	1328-1363				
ROENI ERI TIS CORONA VIRUS	632-665	136.764	1328-1363				
ROENIERITIS CORONAVIRUS	630-663	114.762	1326-1361				
ROENTERITIS CORONAVIRUS	199-019	314.762	1326-1361				
AVIRUS	112.540	1104-1139					
AVIRUS (STRAIN RNA) (PRCV)	108-441	312.540	1104-1139				
ROENTERITIS CORONAVIRUS (STRAIN NET	6)0.66	134.761	1326-1361				
15 VIRUS (STRAIN 19-1145) (FIFV)	615-668	139.767	1331-1366				
S VIRUS (STRAIN BEAUDETTE) (IIIV)	53.18						
TRAIN AD169)	116-147	106-743					
TRAIN TOWNE)	116.14.7	701.144					
I STRAIN UGANDA-1102)	72-110	,					
	254-288						
TRAIN IINIVI (IIOVINE MANIMILLI IIIS VIRUS	745.774						
TEAN COURT	1351.247						

	AREA I	ABEAL	AREA?	AREA	AREAS	AREA	AREA!
	337-336	434-487					
ATA-1)	224-156	481-484					
	3.31	446-474					
רא גאכננואבן	446-474						
	446-474						
	5.38	146471					
RAIN ITALIENAS) (NDV)	133.165						
WIN LASHO (MOV)	133-165						
	531.565					, ,	
S (STRAIN C19)	456-484						
	45)481	·					
S (STRAIN NIH 47885	187 (50						
ETE 0) (NDV)	220-152	447-480					
(AC	220-352	447-480					
NUTAHISI	460-488						
	460-488						
	460-488						
	460.488						a.
	160.411			,			
	446-474						
S(TRIV)	457-481						
RAIN AB4P) (EHV-I)	327-364						
YNV)	\$14-553						
YPE INDIANA / STRAI	450-488						
CROTYPE NEW JERSEY / STRAIN OCDEN)	457.492						
STRAIN SAN JUAN)	430-488						
MAIN AD169)	681-119						
RAIN TOWNE)	690.718						
SIRAIN GS)	215-147	640.677					
	114.150						
	103-143						

	AREA	AREAS	ARCA A	AREA S	AREAS	AREA ?
12.50						
12.50						
12.50	89-124					
12:50	89.124					
12-50	89.124					
1527-1555						
209-242	141-771					
50-86	479-515					
766-799						
78-111						
20-111						
34.19						
54.19						
115-149						
115-149						
133-167	`					
107.143						
\$4.12						
34-12						
55-88						
55-11						
391-624						
591.624						
591-624						
243-271						
243-271						
42.78						
142.70						
	12-50 12-50 12-50 12-50 12-50 1527-1555 209-242 209-24		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	1	15% 124 15% 15% 17% 17% 17% 17% 17% 17% 17% 17% 17% 17	1595 124 1595 24 1595

	AREAI	AREAL	AREA 3	AREA 4	ARFA S	AREA 6	AREA 7
	19.59	265-313					
2	344.379						
	16-57						
	19-59						
	17.57						
IE160	29.59						
VIRUS TYPE I	19-59						
MSI:CT INIDESCENT VIRUS 1 YPE 1)	144-177	616-718					
DNI	280-318	124.361					
	200-318						
NG)	168-199						
ING)	161-199						
4ES)	168-199						
	168-199						
NG)	133-364						
	308-342						
(TRIV)	122-150						
IEBUS)	64-102						
C4J)	201-19						
AIN AS9)	65-103						
AIN HUI)	65-103						
TCV)	64-102						
	73.101						
IRUS (STRAIN BEAUDETTE NI42) (IBV)	73-101						
-8) (HUNIAN HERPESVIRUS 4)	178-213						
(CERV)	93-126						
	86-99	173-103					
ISHANGHAI DUCK ISOLATE SSI (DHINV)		169.101					
CHINA) (DHBV)		364-301					
	157.190	131.264					
SHANGHAI DUCK ISOLATE STITHINY		169.301					
IUS (GSHV)		171.307					
1	159.195	136.269					

	1071		1	13067	7 7 8 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	ABFA A	
XR)	<u> </u>	Ē-120					_
XE)	246-282						
AGEN	16-16	-					
	1610						
	35-68						
TRAIN CONDEN)	336-366						
(3)	163:196	101-59(
	180-217	146.377	139-071				·
SEROTYPE 47 STRAIN VACCINE)	251.310				.,		
ASKAW11)	114-144			,			
IN ARDON/6/60)	114-144						
ILE/M)	114-144						
HCKENKHRAIANY/N/19)	107-144						
IICKEN/JAPAN/24)	104-141						
JCN/ALBERTA/60/76)	107-144						
JCK/ENGLAND/1/56)	104-141						
CK/UKRAINE//61)	104-141						
AT MONHOUTHIND)	114-144						
PT VARREWISO)	114-144						
MT PLAGUE VIRUS/ROSTOCK/34)	107-144						
NINGRADITUST)	114-144						
NINGRADISMI)	114-144					-	
ALLARD/ALBERTAIN'S)	107-144						
ALLARIANEW YORK/6750/74)	107-144						
ALLARIYNEW YORK/637478)	107-144						-
YNAIMIANEDA-TILAUTÓ)	104-141						
NTAIL/ALDERTA/119/79)	107-144						
NTAIUALDERT N121/79)	107-144						T
NTAIL/ALBERTA/264/18)	107-144						
	107.144				_		

	AREAL	AFEA ?	AREA?	AREA 4	AREA 5	AREA 6	AREA 1
ICKEN/FENNSYLVANIA/IA))	354-3B1						
UNELCHDOW(41673)	154-301						
JINEPRAGUE/1/56)	134-38						
UINE/TENNESSEE/S/A6)	354.308						
	97.9						
	97-02						
ICEN	511-539	530-581					
	511-539						
	21:120	541-671					
)(PVh()	1667.1703						
ASSOCIATED VIRUS (SAIYEAV)	131-153						
	462-493						
CAR POLYHEDROSIS VIRUS (ACKINPV)							
LESID POLYHEDROSIS VIRUS (OPKINPV)							
IUS (RDSDV)	162-992						
IN AB4P) (Eirv.i)	239-368	217.325					
IN AD169)	141-172						
RAIN UGANDA-1101)	46.79	206-238					
(IN AB4P) (EHV-I)	11-48						
	124-853						
SEROTYPE 4/SIRAIN VACCINE)	198-809						
/ ISOLATE USA)	649.683						
/ ISOLATE USA)	558-586	649-683					
/ISOLATE USA)	191-424	564-59]					
ISOLATE AUSTRALIA)	654-681						
ISOLATE SOUTH AFRICA)	654-688						
VIRUS (SEROTYPE I) (ENDV-1)	178-915						
	114-167	522-557					
	114.367	333-558					
	142.377	195-215					
RAIN COWDEN)	\$14.549	\$19-685	13.E				
		123-558					
.CEN)	378-311						

	> =		AREA 3	AREAS	AREAL	AREAS	AREAS	AREA
NIMPY) 283-313 INPY) 281-316 198-233 155-183			210-245					
NNPV) 283-313 198-233 198-233 189-183 180-209		٥	222-257					
NPV) 281-316 198-233 155-183 155-183 159-187 130-209 180-209 180-209 180-209 180-209 180-209 180-139	SID POLYHEDROSIS VIRUS (OPHINTY)	2.2						
135-181 155-181 155-181 159-187 131-159 180-209 180-209 180-209 180-209 104-139 104-139 104-139 104-139 104-139 104-139 104-139 104-139 104-139 104-139 104-139 104-139	LEAR POLYHEDROSIS VIRUS (ACHINPY) 281	910-						
155-181 159-187 180-209 180-20		1-233						
155-183 139-187 131-159 180-209 180-209 180-209 180-209 104-139 104-139 104-139 104-139 104-139 104-139 104-139 104-139 104-139 104-139 104-139 104-139 104-139 104-139		5-13						
131-159 180-209 180-209 180-209 180-209 180-209 180-209 104-139 104-139 104-139 104-139 104-139 104-139 104-139 104-139 104-139 104-139 104-139 104-139 104-139		5-183						
NPV) 104-139 104-139 104-139 104-139 104-139 104-139 104-139 104-139 104-139 104-139 104-139 104-139 104-139 104-139 104-139 104-139 104-139 104-139	+AFNCA))-[1]						
NINPY) 100-209 180-209 180-209 104-139 104-139 104-139 104-139 104-139 104-139 104-139 104-139 104-139 104-139 104-139 104-139 104-139 104-139 104-139 104-139		1.159						
NIPY) 454-490 NINPY) 77-112 104-139		0-209						
NINPV) 403-442 454-490 104-139 104-139 104-139 104-139 104-139 104-139 104-139 104-139 104-139 104-139 104-139 104-139 104-139 104-139 104-139 104-139 104-139		109				÷		
NINPV) 77-112 104-139 104-139 104-139 104-139 104-139 104-139 104-139 104-139 104-139 104-139 17-74 11-73 41-73	LYHEDROSIS VIRUS (ACMNPY)	201.						
NINPY) 77-112 104-139 104-139 104-139 104-139 104-139 104-139 104-139 104-139 104-139 104-139 104-139 104-139 104-139 104-139 104-139 104-139		0611						
104-139 104-139 104-139 104-139 104-139 104-139 104-139 104-139 104-139 104-139 104-139 104-139 104-139 104-139	CAPSID POLYHEDROSIS VIRUS (OFNINPY) 77-	112						
104-139 104-139 104-139 104-139 104-139 104-139 104-139 104-139 104-139 1-74 41-73	_	(-1)9						
104-139 104-13		1.139						
104-139 104-139 104-139 104-139 164-198 172-131 V-1) 172-131 V-1) 172-131 V-1) 172-131 V-1) 172-131 V-1) 172-131		1.139						
104-139 104-139 104-139 374-412 164-193 118PV) 145-173 11-74 11-73 41-73		1-139						
104-139 104-139 174-412 164-195 1MNFV) 145-173 V-1) 37-74 41-73 41-73)	1.139						
104-139 374-412 164-195 1164-195 145-121 17-74 11-71 41-71		1-139						
164-195 164-195 18PV) 145-173 145-171 17-74 11-73 41-71		1.[]9						
MNFV) 145.173 WNFV) 122.151 V-1) 37-74 41-73 41-73	776	1-012						
MNPV)	164	1.195	211-62(
V-I)	_	1.173						
(1.v		1-151						
		74						
	TYPE 2 (ISOLATE HEN) (HIV-2)	23						
:		71						
		13						

			_				
	AREAI	AREA 1	AREAJ	AREA 4	AREAS	AREA	AREA 1
	15-92						
	29-55						
STRAIN 1076)	53.91						*
RAIN BRISTOL)	64.93	312-340					
STRAIN S2)	55-92					-	
STRAIN WA)	\$5.91	313-349					
TRAIN COWDEN	26-63						
TFAED)	55.92	311.349					
113)	55.93	311.349					
11)	274-392						
STRAIN ST. THOMAS 1)	131-159						
I STRAIN BEN-144)	131-159					8.1	
\$	\$2-09						
	52.09						,
	52.09						
CLONE 2)	52.89						
CLONE 6	52.89						*
STRAINWAI	52-89						
(1)	52.10						
I STRAIN WA)	99.130						
4ES)	146-384						. `
	110.147						
(SFV)	147-182						
NE)	261.290						-
A52A) (SFV)	210-249						
	116-130						
-8) (HUNIAN HERPESVIRUS 4)	166-199	\$65-505					
AIN ADI69)	176-209						
MEL CATFISH VIRUS) (CCV)	756-788			*			
	57.93						
	55.83						
UCAN ISOLATE) (MSV)	24.54						
	12-59						
	22.59						
							•

	·						7.5.7.5
	REAL	AREAL	AREAL	ABLA	20103	COLO	
	P6-13						
	84.73					1	
	117-271				1		1
	3-J4.						
	2))-263						
	91-134						T
(STRAIN KRAI) (TIVI)		3					
		20.10					
L			1				
NAL.	3		+	1			
	017-011						
HERPESVIRUS 4)	17.2				+	+	
	92-120		-	-	+	1	1
	306-336				+	1	
	21-53					1	1
STACENTA VIBILS ISTRAIN COPENHAGE 11-49	611				1	1	1
	22-53					+	1
NA COMIA VIRUS (STRAIN COPENHAGE) 1-44	14.IE			+		+	1
	273					+	1
	1-35				+	+	
STAGEN)	23-57			+	+	+	+
TIE VIEUS (STRAIN PASTEUR)	1-32	-					

TABLE XV RESPIRATORY SYNCYTIAL VIRUS DP1 CARBOXY TRUNCAT

- X-YTS-Z
- X-YTSV-Z
- 5 X-YTSVI-Z
 - X-YTSVIT-Z
 - X-YTSVITI-Z
 - X-YTSVITIE-Z
 - X-YTSVITIEL-Z
 - X-YTSVITIELS-Z
 - X-YTSVITIELSN-Z
 - X-YTSVITIELSNI-Z
- 10 X-YTSVITIELSNIK-Z
 - X-YTSVITIELSNIKE-Z
 - X-YTSVITIELSNIKEN-Z
 - X-YTSVITIELSNIKENK-Z
 - X-YTSVITIELSNIKENKC-Z
 - X-YTSVITIELSNIKENKCN-Z
 - X-YTSVITIELSNIKENKCNG-Z
- 15 X-YTSVITIELSNIKENKCNGT-Z
 - X-YTSVITIELSNIKENKCNGTD-2
 - X-YTSVITIELSNIKENKCNGTDA-Z
 - X-YTSVITIELSNIKENKCNGTDAK-Z
 - X-YTSVITIELSNIKENKCNGTDAKV-Z
 - X-YTSVITIELSNIKENKCNGTDAKVK-Z

\$67~1/96 OM

Additionally,

polyethylene glycol, or carbo including but not limited to carbonyl (FMOC) group; an acetyl g macr butyloxycarbonyl; an acetyl g macr limited to butyloxycarbonyl; an acetyl g macr limited to butyloxycarbonyl; an acetyl g macr limited to butyloxycarbonyl; an acetyl g may represent an amino gr

polyethylene glycol, or carbo including but not limited to T-butyloxycarbonyl group; a m T-butyloxycarbonyl group; a m OT

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TABLE XV RESPIRATORY SYNCYTIAL VIRUS F2 I AMINO TRUNCA

5

10

15

X-LIKQELI X-KLIKQELI X-KLIKQELI X-KQELI X-KLIKQELI X-KLIKQELI

OT

"Z" may represent a carboxyl qroup; a may represent not limite group; a may conjugates, polyethylene glyck conjugates, polyethylene glyck

"X" may represent an amino gre including but not limited to c T-butyloxycarbonyl; an acetyl fluorenylmethoxy-carbonyl (FMC macromolecular carrier group i to lipid-fatty acid conjugates or carbohydrates.

WO-96/19495

TABLE XVII RESPIRATORY SYNCYTIAL VIRUS F1 CARBOXY TRUNCAT:

X-FYD-Z

X-FYDP-Z

X-FYDPL-Z

5 X-FYDPLV-Z

X-FYDPLVF-Z

X-FYDPLVFP-Z

X-FYDPLVFPS-Z

X-FYDPLVFPSD-Z

X-FYDPLVFPSDE-Z

X-FYDPLVFPSDEF-Z

10 X-FYDPLVFPSDEFD-Z

X-FYDPLVFPSDEFDA-Z

X-FYDPLVFPSDEFDAS-Z

X-FYDPLVFPSDEFDASI-Z

X-FYDPLVFPSDEFDASIS-Z

X-FYDPLVFPSDEFDASISO-Z

X-FYDPLVFPSDEFDASISOV-Z

X-FYDPLVFPSDEFDASISQVN-Z

15 X-FYDPLVFPSDEFDASISOVNE-Z

X-FYDPLVFPSDEFDASISOVNEK-Z

X-FYDPLVFPSDEFDASISQVNEKI-Z

X-FYDPLVFPSDEFDASISQVNEKIN-Z

X-FYDPLVFPSDEFDASISQVNEKINQ-Z

X-FYDPLVFPSDEFDASISQVNEKINQS-Z

ST

OT

C

group including but not limit conjugates, polyethylene glyc

S6761/96 OM

WO 96/19495

TABLE XVIII RESPIRATORY SYNCYTIAL VIRUS F1 AMINO TRUNCATIO

	X·
_	X-1
5	X-KS
	X-RK:
	X-IRK:
	X-FIRK:
	X-AFIRK:
	X-LAFIRKS
	X-SLAFIRKS
10	X-QSLAFIRKS
10	X-NQSLAFIRKS
	X-INQSLAFIRKS
	X-KINQSLAFIRKS
	X-EKINQSLAFIRKS
	X-NEKINOSLAFIRKS
	X-VNEKINQSLAFIRKS
	X-QVNEKINQSLAFIRKS
15	X-SQVNEKINQSLAFIRKS
	X-ISQVNEKINQSLAFIRKS
	X-SISQVNEKINQSLAFIRKS
	X-ASISQVNEKINQSLAFIRKS
	Y-DASTSOVNEKTNOSTARTOV

S6761/96 OM

HUMAN PARAINFLUENZA VIRUS 3 CARBOXY TRUI

```
X-ILTUNGAYTDSIDIGIETUKYKZDTE-
X-ILTMM2AYTDBIDI2IETMKYK2DT-S
X-ILTUNRAYTDBIDIZIETNKYKZD-Z
  X-ILTUNRAYTDBIDIRIETNKYKR-Z
   X-ILTUNRAYDDIDIRITUKYK-Z
    X-ILTUNRANTDBIBIETUKY-Z
                                SI
     X-ILTUNRAYFDBIDIRIETUK-Z
      X-ILTMNSAYPDBIDISIEFN-Z
       X-ILLUNSVALDPIDISIEL-Z
        X-ILTUNRAYTDBIDIRIE-Z
         X-ITINIAAVIDDIBIEL-X
          X-ILLUNSVALDPIDIS-Z
           X-ITLNNSVALDFIDI-Z
                                OT
            X-IITMRAYFDFID-Z
             X-I4GJAVSNNJTI-X
              X-ILINNSVALDP-Z
               Z-CTYVSNWITI-X
                Z-ITVNSNNITI-X
                 Z-AVZNWITI-X
                  Z-ASNNTLI-X
                   Z-SNNTLI-X
                    Z-NNTLI-X
                     Z-N'ILI-X
                      Z-TLI-X
```

S6761/96 OM

HUMAN PARAINFLUENZA VIRUS 3 F1 AMINO TRUNCATIC

X-bidizietnkykzdreezkemii X-IDIZIETNKYKZDFEEZKEMIŁ X-DIZIETNKYKZDTEEZKEMIL X-ISIETNKYKSDFEESKEMIE X-SIEPNKYKSDFEESKEMIE X-IEPNKYKEDPEESKEMIL SI X-EPHKYKEDPEERKEMIE X-PAKYRDTEERKEMIL X-NKYKZDIEEZKEMIE X-KYREDIEESKEMIE X-YKZDTEEZKEMIŁ X-KEDTEERKEMIE X-SDFEESKEMIE OT X-DIEESKEMIE X-reerkemie X-EERKEMIE X-E2KEMII X-SKEMII X-KEMII X-EMII IIM-X 5 II-X I-X

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TABLE HUMAN PARAINFLUENZA VIRUS : CARBOXY TRU

X-ALG-Z

X-ALGV-Z

X-ALGVA-Z

5 X-ALGVAT-Z

X-ALGVATS-Z

X-ALGVATSA-Z

X-ALGVATSAQ-Z

X-ALGVATSAQI-Z

X-ALGVATSAQIT-Z

X-ALGVATSAQITA-Z

X-ALGVATSAQITAA-Z

X-ALGVATSAQITAAV-Z

X-ALGVATSAQITAAVA-Z

X-ALGVATSAQITAAVAL-Z

X-ALGVATSAQITAAVALV-Z

X-ALGVATSAQITAAVALVE-Z

X-ALGVATSAQITAAVALVEA-Z

X-ALGVATSAQITAAVALVEAK-Z

15 X-ALGVATSAQITAAVALVEAKQ-Z

X-ALGVATSAQITAAVALVEAKQA-Z

X-ALGVATSAQITAAVALVEAKQAR-Z

X-ALGVATSAQITAAVALVEAKQARS-Z

X-ALGVATSAQITAAVALVEAKQARSD-

X-ALGVATSAQITAAVALVEAKQARSDI

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HUMAN PARAINFLUENZA VIRUS 3 FL AMINO TRUNCATI

X-TAAVALVEAKQARSDIEKLKE! X-AAVLVEAKQARSDIEKLKER X-AVALVEAKQARSDIEKLKE! X-AYPAEYKŐYBEDIEKPKEY X-YFAEYKÖYK2DIEKFKE X-LVEAKQARSDIEKLKE SI X-VEAKQARSDIEKLKE! X-EYKÖYKZDIEKIKEI X-YKŐYKZDIEKIKEI X-KOYKEDIEKIKEI X-ÖYKZDIEKIKEI X-YESDIEKIKE X-BEDIEKIKE OT X-SDIEKPKE X-DIEKIKES X-IEKIKE' X-EKPKE X-KPKE X-TKE X-KE X-EI I-X ·X

TABLE X REPRESENTATIVE DP107/DP178 A

Anti-Respiratory syncytial vi

- X-TSVITIELSNIKENKCNGTDAKVKLIK X-SVITIELSNIKENKCNGTDAKVKLIKQ 5 X-VITIELSNIKENKCNGTDAKVKLIKQE X-VAVSKVLHLEGEVNKIALLSTNKAVVS
 - X-AVSKVLHLEGEVNKIALLSTNKAVVSL X-VSKVLHLEGEVNKIALLSTNKAVVSLS
 - X-SKVLHLEGEVNKIALLSTNKAVVSLSN
 - X-KVLHLEGEVNKIALLSTNKAVVSLSNG
 - X-LEGEVNKIALLSTNKAVVSLSNGVSVI
- X-GEVNKIALLSTNKAVVSLSNGVSVLTSK
 - X-VNKIALLSTNKAVVSLSNGVSVLTSKV
 - X-NKIALLSTNKAVVSLSNGVSVLTSKVI
 - X-KIALLSTNKAVVSLSNGVSVLTSKVLD
 - X-IALLSTNKAVVSLSNGVSVLTSKVLDI
 - X-ALLSTNKAVVSLSNGVSVLTSKVLDLK
 - X-VAVSKVLHLEGEVNKIALLSTNKAVVS
- 15 X-AVSKVLHLEGEVNKIALLSTNKAVVSI
 - X-VSKVLHLEGEVNKIALLSTNKAVVSLS
 - X-SKVLHLEGEVNKIALLSTNKAVVSLSN
 - X-KVLHLEGEVNKIALLSTNKAVVSLSNO
 - X-LEGEVNKIALLSTNKAVVSLSNGVSVI
 - X-GEVNKIALLSTNKAVVSLSNGVSVLTS

X-CBEISTERTDACTALCARIAKLEAKELLESSDQI-Z	
X-CEPPISTER DVGTULCUAIAKLEAKELLESSDQ-Z	
X-DEGABLELERIDAGTALEGARIERKELLESSD-Z	
X-IDICEPISIERLDVGTVLGNAIAKLEAKELLESS-Z	
X-IDICBBICIES DACEMICATIVALE DI CONTROL DE C	
X-HKIDICBEICLEBIDACEMICAVIVALEVANICE C	
X-HAIDICABISIERIDACEMICAVIVALEVEITE S	
X-1.HPIDIGPPISI.FPI DUCTNII CNAIANI FAVELL-R	2 O
Anti-measles virus peptides	
bitana purin nofneom-ital	
X-FLEENITALLEEAQIQQEKUMYELQKLUSWDVFGN-Z	
X-DEFERITATIFEE OIGOEKHAKET ÖKT NEMDALG-Z	
X-ADEFEENILYTTEEVÕIÕÕEKNUKETÕKINAMAL-S	
X-KADELEENITALLEEAQIQQEKMMYELQKLUSMDV-Z	
	ST
X-KKADELEENITALLEERQIQQEKUMYELQKLUSWD-Z	
X-EKKADELEENITALLEEAQIQQEKUMYELQKLUSW-Z	
X-MERKYDFLEENITALLEEAQIQQEKUMYELQKLUS-Z	
X-EMERKADFLEENITALLEEAQIQQEKUMYELQKLN-Z	
X-QEWERKVDFLEENITALLEEAQIQQEKUMYELQKL-Z	
X-MÖEMEKKADEFEENITAFFEEPÖIGGEKNMKEFGK-Z	
Anti-simian immunodeficiency virus peptides	OT
X-YIKDINKYAĞƏAĞƏZIĞNГІAYIKƏAĞDAANKEIA-S	
X-FKEYIKDINKYNÖZNÖZZICNFINYIKZNÖDKNNK-S	
X-KFKEYIKDINKYAĞƏAĞƏƏICHFIAYIKƏAĞDAAN-S	
X-2DIEKTKEYIKDLNKYNÖ2NÖ22ICNFINYIK2NÖ-Z	
X-RSDIEKIKEPIKDTNKAVQSVQSSIGNLIVAIKSV-Z	
X-YEDIEKIKEYIKDINKYNÖZNÖZZIGNINYIKZ-Z	5
X-ÖYKEDIEKIKEYIKDINKYNÖENÖEZIGNINYIK-Z	
X-KÖYKEDIEKIKEYIKDLNKYNÖZNÖZZICNINYI-Z	
X-YKÖYKEDIEKIKEYIKDLNKYNÖZNÖZZICNINY-Z	
X-EYKÖYKEDIEKIKEYIKDINKYNÖZNÖZZICNIN-Z	
X-VEAKQARSDIEKLKEAIRDTNKAVQSVQSSIGNL-Z	
X-IVEAKQARSDIEKLKEAIRDTNKAVQSVQSSIGNL-Z	
X-AVALVEAKQARSDIEKLKEAIRDTNKAVQSVQSSI-Z	

X-PISLERLDVGTNLGNAIAKLEAKELLESSDQILR-Z

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"Z" may represent a carboxyl group; an amido T-butyloxycarbonyl group; a macromolecular of group including but not limited to lipid-fat conjugates, polyethylene glycol, or carbohyo

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5.4. SYNTHESIS OF PEPTIDES

Press, NY. Laboratory Manual, Vols. 1-3, Cold Spring Harb Sambrook, et al., 1989, Molecular Cloning, A those of ordinary skill in the art. See, for sug exbressed according to techniques well know of the invention may be synthesized, and/or cl. Here, the nucleotide sequences encoding the peptides may be made using recombinant DNA teci synthesized on a solid support or in solution. Sport peptides, for example, can be entirety. which is incorporated herein by reference in i and Molecular Principles, W.H. Freeman and Co. for example, Creighton, 1983, Proteins: or prepared by techniques well known in the ar The peptides of the invention may be synt

The peptides of the invention may alterna be synthesized such that one or more of the box which link the amino acid residues of the peptidonon-peptide bonds. These alternative non-pept bonds may be formed by utilizing reactions well to those in the art, and may include, but are limited to imino, ester, hydrazide, semicarbaz aso bonds, to name but a few. In yet another embodim nt of the invention, peptides comprising

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above.) Additionally, the hydrophobic groubutyloxycarbonyl, or an amido group may be the peptides' carboxy termini. (See "Z" in to IV, above.)

Further, the peptides of the invention synthesized such that their steric configural altered. For example, the D-isomer of one the amino acid residues of the peptide may rather than the usual L-isomer.

residues of the peptides of the invention:
substituted by one of the well known non-n
occurring amino acid residues. Alteration
these may serve to increase the stability,
bioavailability and/or inhibitory action o
peptides of the invention.

Any of the peptides described above madditionally, have a macromolecular carrie covalently attached to their amino and/or termini. Such macromolecular carrier grouinclude, for example, lipid-fatty acid con polyethylene glycol, carbohydrates or adding peptides. "X", in Tables I to IV, above, therefore additionally represent any of the macromolecular carrier groups covalently at the amino terminus of a peptide, with an a

in section 5.5.2, below. below, and assays for antiviral activity are de

5.5.1 ASSAYS FOR CELL FUSION EVENTS

capabilities. invention to test the peptides' antifusogenic conjunction, for example, with the peptides of those of skill in the art, and may be used in yaaska tor cell fusion events are well kno

but are not limited to, HIV, SIV, or respirator; that induces cell fusion. Such viruses may inc bresence of cells chronically infected with a v example, uninfected cells may be incubated in tl an observable level of syncytial formation. which, in the absence of any treatment would un Such an assay may comprise culturing ce Cell fusion assays are generally perform

wherein no peptid has been added. This range should include a control cu peptide, a range of peptide concentrations may : presence of a peptide to be assayed. For each For the assay, cells are incubated in the

After incubation for an appropriate period (24 known to those of ordinary skill in the art, ar Standard conditions for culturing cells, w

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syncytial virus.

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easily performed in vitro assays, such as the described below, which can test the peptides to inhibit syncytia formation, or their abilinhibit infection by cell-free virus. Using assays, such parameters as the relative ant activity of the peptides, exhibit against a strain of virus and/or the strain specific activity of the peptide can be determined.

A cell fusion assay may be utilized to peptides' ability to inhibit viral-induced, 10 HIV-induced, syncytia formation in vitro. assay may comprise culturing uninfected cel presence of cells chronically infected with syncytial-inducing virus and a peptide to b For each peptide, a range of peptide concen 15 may be tested. This range should include a culture wherein no peptide has been added. conditions for culturing, well known to tho ordinary skill in the art, are used. After for an appropriate period (24 hours at 37 C 20 example) the culture is examined microscopi the presence of multinucleated giant cells, indicative of cell fusion and syncytia form Well known stains, such as crystal violet s be used to facilitate syncytial visualizati 25 HIV as an example, such an assay would comp

in their entirety. These references are incorporated herein by ref (Willey, R. et al., 1988, J. Virol. 62:139-147) al., 1981, J. Virol. 38:239-248) and/or Willey described by, for example, Goff et al. (Goff, 1 may be tested using standard techniques such as OT as a measure of successful infection. The RT 8 brocedures, and tested for the present of RT ac cell-free supernatant is prepared, using standa appropriate period (e.q., 7 days) of culturing, peptide has been added. After incubation for a used, in addition to a control culture wher in As above, a range of peptide concentrations may conditions well known to those in the art are t in the presence of the peptide to be tested. (concentration (i.e., TCIDs) of virus and CD-4+

skill in the art may be utilized for assaying retroviral activity. See, for example, Pringle (Pringle, C.R. et al., 1985, J. Medical Virolog virus and parainfluenza virus activity assay virus activity activity activity virus virus activity activity activity virus vir

review of such techniques. These references an

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Additionally, anti-RSV activity can be vivo via well known mouse models. For example can be administered intranasally to mice of inbred strains. Virus replicates in lungs of strains, but the highest titers are obtained C57L/N and DBA/2N mice. Infection of BALB/oproduces an asymptomatic bronchiolitis charable lymphocytic infiltrates and pulmonary virus of 10⁴ to 10⁵ pfu/g of lung tissue (Taylor, (1984, Infect. Immun. 43:649-655).

Cotton rat models of RSV are also well Virus replicates to high titer in the nose a of the cotton rat but produces few if any sinflammation.

5.6. USES OF THE PEPTIDES OF THE INVI

The peptides of the invention may be used to identify agents which modulate intracellular processes involved coiled coil peptide structures. Further, supeptides may be used to identify agents which antifusogenic, antiviral or intracellular materials. Still further, the peptides of the invention may be utilized as organism or vitype/subtype-specific diagnostic tools.

The antifusogenic capability of the pe

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atructure with a cell membrane. Among the intracellular disorders involving, for exalthe invention are disorders involving, for exalthe invention are disorders involving, for exalthe invention.

With respect to antiviral activity, the v. whose transmission may be inhibited by the pep' the invention include, but are not limited to a invention include, but are not limited to a trains of the viruses listed above, in Tabl s strains of the viruses listed above, in Tabl s strains of the viruses listed above, in Tabl s strains of the viruses listed to a supplied that the property of the viruses of the viruses listed to a supplied the viruses listed to a supplied the viruses of the viruses listed to a supplied the viruses listed the viruses listed to a supplied the viruses listed the viruses listed to a supplied the viruses listed to a supplied the viruses listed to a supplied the viruses listed to a supplied the viruses listed to a supplied the viruses listed to a supplied the viruses listed to a supplied the viruses listed to a supplied the vi

These viruses include, for example, human retroviruses, particularly HIV-1 and HIV-2 and human T-lymphocyte viruses (HTLV-I and HIV-2 and by the peptides of the invention include, but i limited to bovine leukosis virus, feline sarcon limited to bovine leukosis virus, feline sarcon limited to bovine leukosis virus, sarcon viruses, simian immunodeficiency, sarchukemia viruses, simian immunodeficiency, sarchukemia viruses, simian immunodeficiency, sarchukemia viruses, simian immunodeficiency, sarchukemia viruses, simian immunodeficiency, sarchukemia viruses, simian immunodeficiency, sarchukemia viruses, simian immunodeficiency, sarchukemia viruses, simian immunodeficiency, sarchukemia viruses, simian immunodeficiency, sarchukemia viruses, simian immunodeficiency, sarchukemia viruses, simian immunodeficiency, sarchukemia viruses, simian immunodeficiency, sarchukemia viruses, simian immunodeficiency, sarchukemia viruses, simian immunodeficiency, sarchukemia viruses, simian immunodeficiency, sarchukemia viruses, simian immunodeficiency, sarchukemia viruses, simian immunodeficiency, sarchukemia viruses, sum sar

Mon retroviral viruses whose transmission incinhibited by the peptides of the invention inciput are not limited to human respiratory syncyl virus, canine distemper virus, newcastle diseas virus, human parainfluenza virus, influenza virus virus, human parainfluenza virus, influenza virus viruses, and simian Mason-Pfizer viruses.

are required for normal activity of the virus the peptides of the invention may also be ut components in assays for the identification compounds that interfere with such protein-pointeractions and may, therefore, act as antiagents. These assays are discussed, below, in 5.5.1.

As demonstrated in the Example presente Section 6, the antiviral activity of the pep the invention may show a pronounced type and 10 specificity, i.e., specific peptides may be in inhibiting the activity of only specific This feature of the invention presents many advantages. One such advantage, for example the field of diagnostics, wherein one can us 15 antiviral specificity of the peptide of the to ascertain the identity of a viral isolate respect to HIV, one may easily determine whe viral isolate consists of an HIV-1 or HIV-2 For example, uninfected CD-4+ cells may be c 20 with an isolate which has been identified as containing HIV the DP178 (SEQ ID:1) peptide, which the retroviral activity of cell superr be assayed, using, for example, the technique d scribed above in Section 5.2. Those isola 25 retroviral activity is completely or nearly

conjunction with the DP107/DP178 analog of inte described, above, for DP178, may be used in peptide sequence is found. A diagnostic proced

As demonstrated in the Example presented i

5.5.1. SCREENING ASSAYS

antifusogenic, antiviral or cellular modulatory DP107/DP178 protein-protein interactions may ac DP107, bind DP178, and/or act to disrupt normal normal viral infectivity. Thus, compounds whic maintenance of such interactions is necessary f interactions. As is also demonstrated, th protein gp41 form non-covalent protein-protein Section 8, below, DP107 and DP178 portions of t

Compounds which may be tested for an abili utilized as part of these screens for compounds above, in Sections 5.1 through 5.3 may also be DP107 analog or DP178 analog peptides described described, but it is to be understood that any peptides will be used as components of the assa for ease and clarity of discussion, DP107 and D identification of such compounds. Note that, w agents. Described below are assays for the

represent antifusogenic, antiviral or intracell interactions, and which therefore, potentially bind DP107, DP178, and/or disrupt DP107/DP178

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potentially effective materials may be scre variety of ways, as described in this Secti

The compounds, antibodies, or other mo identified may be tested, for example, for to inhibit cell fusion or viral activity, u for example, assays such as those described Section 5.5.

Among the peptides which may be tested soluble peptides comprising DP107 and/or DF domains, and peptides comprising DP107 and/domains having one or more mutations within both of the domains, such as the M41-P pept described, below, in the Example presented 8, which contains a isoleucine to proline m within the DP178 sequence.

- In one embodiment of such screening me method for identifying a compound to be tes antiviral ability comprising:
- peptide comprising a DP107 peptide for a ti sufficient to allow binding of the compound DP107 peptide;
 - (b) removing non-bound compounds
 - (c) determining the presence of compound bound to the DP107 peptide,
- thereby identifying an agent to be tested 1

determining the presence of the

thereby identifying an agent to be tested for compound bound to the DP178 peptide,

antiviral ability.

system, either the DP107 or DP178 protein may 1 example, nylon or nitrocellulose. In such an : wells, petri dishes, or membranes composed of, example, agarose or plastic beads, microtiter | the DP178 peptide to a solid matrix, such as, : would include the attachment of either the DP1 binding or DP178-binding compounds is an assay that may be pursued in the isolation of such D One method utilizing these types of approx

test substance, which is not anchored, is labe! suchored onto a solid surface, and the compount

either directly or indirectly. In practice,

от covalent attachments. Non-covalent attachm anchored component may be immobilized by non-co microtiter plates are conveniently utilized.

with a solution of the protein and drying. pe secombifaped simply by coating the solid sur

The surfac s may be prepared in adva: surface. protein may be used to anchor the protein to the preferably a monoclonal antibody, specific for Alternatively, an immobilised antibody,.

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stored.

complexes were formed. Where the labeled control pre-labeled, an indirect label can be usedetect complexes anchored on the surface; end a labeled antibody specific for the compound antibody, in turn, may be directly labeled of indirectly labeled with a labeled anti-Ig as

a liquid phase, the reaction products separa unreacted components, and complexes detected using an immobilized antibody specific for 1 DP178, whichever is appropriate for the give or ab antibody specific for the compound, i test substance, in order to anchor any comp formed in solution, and a labeled antibody for the other member of the complex to detect to complexes.

By utilizing procedures such as this, numbers of types of molecules may be simult screened for DP107 or DP178-binding capabil thus potential antiviral activity.

Further, compounds may be screened for to inhibit the formation of or, alternative DP107/DP178 complexes. Such compounds may tested for antifusogenic, antiviral or inte modulatory capability. For ease of descrip and DP178 will be referred to as "binding p

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peptides.

In order to test a compound for disruptive actific reaction is conducted in the presence and a of the test compound, i.e., the test compound minitially included in the reaction mixture, or the atime subsequent to the addition of one of binding partners; controls are incubated without complexes between the binding partners is then detected. The formation of a complex in the control of the formation detected, the formation of a complex in the control of the formation detected, the formation of a compound indicates that the compound indicates that the compound indicates that the compound interferes with the interaction of the DP107 and interferes with the interaction of the DP107 and interferes with the interaction of the DP107 and interferes with the interaction of the DP107 and interferes with the interaction of the DP107 and interferes with the interaction of the DP107 and interferes with the interaction of the DP107 and interferes with the interaction of the DP107 and interaction is compound.

The assay for compounds that interfere with interfere with the same of the binding partners can be conditing the same of the binding partners can be conditing the same of the binding partners can be conditing the same of the binding partners and the same of the binding partners are same of the

in a heterogeneous or homogeneous format.

Heterogeneous assays involve anchoring one of the binding partners onto a solid phase and detection complexes anchored on the solid phase at the entire reaction is carried out in a liquid phase. In approach, the order of addition of reactants can varied to obtain different information about the compounds being tested. For example, test compounds being tested. For example, test compoind interfere with the interaction between the binding partners, e.g., by competition, can be binding partners, e.g., by competition, can be

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been formed. The various formats are describriefly below.

In a heterogeneous assay system, one is partner, e.g., either the DP107 or DP178 per anchored onto a solid surface, and its bind partner, which is not anchored, is labeled directly or indirectly. In practice, microplates are conveniently utilized. The anchoreds species may be immobilized by non-covalent attachments. Non-covalent attachment may accomplished simply by coating the solid solution of the protein and drying. Although a solution of the protein and drying. Although the solid solution of the protein to the solid. The surfaces may be prepared in advance and

In order to conduct the assay, the bipartner of the immobilized species is adde coated surface with or without the test coafter the reaction is complete, unreacted are removed (e.g., by washing) and any comformed will remain immobilized on the solithe detection of complexes anchored on the surface can be accomplished in a number of where the binding partner was pre-labeled, detection of label immobilized on the surfindicates that complexes were formed. Whe

identified. or which disrupt preformed complexes can be the liquid phase, test compounds which inhibit depending upon the order of addition of reactar partner to detect anchored complexes. sug s Jspeled sutibody specific for the other ? because to suchor any complexes formed in solmtusing an immobilized antibody specific for one unreacted components, and complexes detected; { compound, the reaction products separated from liquid phase in the presence or absence of the Alternatively, the reaction can be conduct

In an alternative scr ening assay, test co DP-178 protein-protein interaction can be ident In this way, test substances which disrupt DP-1 result in the generation of a signal above back binding partners from the preformed complex wil substance that competes with and displaces one approach for immunoassays). The addition of a Patent No. 4,109,496 by Rubenstein which utilis quenched due to complex formation (see, e.g., l labeled, but the signal generated by the label prepared in which one of the binding partners preformed complex of the DP107 and DP178 peptic homogeneous assay can be used. In this approac In an alternate embodiment of the invention

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compounds for the disruption of the complexe by these two peptides by immunometrically v DP178/M41\Delta178 complexes via the human recomplexed, as described, below, in the Example in Section 8. M41\Delta178 is a maltose binding protein containing a gp41 region having its domain deleted, and is described, below, in Example presented in Section 8.

Utilizing such an assay, M41\Delta178 may b immobilized onto solid supports such as mic 10 A series of dilutions of a test com wells. then be added to each M41\Delta178-containing we presence of a constant concentration of DP-After incubation, at, for example peptide. temperature for one hour, unbound DP-178 an 15 compound are removed from the wells and wel incubated with the DP178/M41 Δ 178-specific F antibody. After incubation and washing, ur is removed from the plates and bound Fab-d quantitated. A no-inhibitor control should 20 conducted. Test compounds showing an abili disrupt DP178/M41\Delta178 complex formation are by their concentration-dependent decrease i of Fab-d binding.

A variation of such an assay may be understand perform a rapid, high-throughput binding as

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binding to M41A178 is then quantitated by meas the fraction of DP178 that is bound as ¹¹³I-DP1 calculating the total amount bound using a val apecific activity (dpm/µg peptide) determined labeled DP178 preparation. Specific binding the labeled DP178 preparation in the microtite binding, in addition, excess unlabeled DP17 containing, in addition, excess unlabeled DP17 containing, in addition, excess unlabeled DP17 (nonspecifics).

5.5 PHARMACEUTICAL FORMULATIONS, DOSAG AND MODES OF ADMINISTRATION

The peptides of the invention may be admi using techniques well known to those in the ar as Preferably, agents are formulated and administ systemically. Techniques for formulation and administration may be found in "Remington's administration and schemaceutical Sciences", 18th ed., 1990, Mack Pharmaceutical Sciences", 18th ed., 1990, Mack Pharmaceutical Sciences", Suitable routes membrishing Co., Easton, PA. Suitable routes membrishing Co., Easton, PA. Suitable routes membrishing Co., Easton, PA. Suitable routes membrishing Co., Easton, PA. Suitable routes membrishing Co., Easton, PA. Suitable routes membrishing Co., Easton, PA.

administration; parenteral delivery, including intramuscular, subcutan ous, intramedullary infraventions, as well as, intrathecal, direct intraventricular, intravenous, intraperitoneal stantranasal, or intraocular injections, just to intranasal, or intraocular injections, just to anomy of the inventi

include oral, rectal, transmucosal, or intesti

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agents is preferred, techniques well known ordinary skill in the art may be utilized. example, such agents may be encapsulated in liposomes, then administered as described a Liposomes are spherical lipid bilayers with interiors. All molecules present in an aqu solution at the time of liposome formation incorporated into the aqueous interior. The contents are both protected from the extern microenvironment and, because liposomes fus membranes, are effectively delivered into the cytoplasm. Additionally, due to their hydres when small molecules are to be administered intracellular administration may be achieve Nucleotide sequences encoding the pept

invention which are to be intracellularly a may be expressed in cells of interest, using techniques well known to those of skill in For example, expression vectors derived from such as retroviruses, vaccinia viruses, ade associated viruses, herpes viruses, or boys papilloma viruses, may be used for delivery expression of such nucleotide sequences into targeted cell population. Methods for the construction of such vectors and expression are well known. Se, for example, Sambrook

Effective dosages of the peptides of the post immune response directed against such pept ancy frestments do not rely upon the generation HIV-containing blood products. The successful in health care settings wherein workers are exp transmission exists, such as, for example, accisud other settings where the likelihood of HIV brevention of virus transmission from mother to the peptides may include, but are not limited t to an HIV virus. Examples of such prophylactic

circulating levels of about 1 to about 10 ng per prove efficacious <u>in vivo</u> at doses required to presented below in section 6, DP178, for example bioavailability, and toxicity. Given the data address such parameters as biological half-life brocedures well known to those in the art which invention to be administered may be determined .

in a patient. Toxicity and therapeutic efficac; amelioration of symptoms or a prolongation of si amount of the compound sufficient to result in A therapeutically effective dose refers to peptide.

(the dose lethal to 50% of the population) and experimental animals, e.q., for determining the pharmaceutical procedures in cell cultures or such compounds can be determined by standard

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little or no toxicity. The dosage may vary this range depending upon the dosage form e the route of administration utilized. compound used in the method of the inventio therapeutically effective dose can be estim initially from cell culture assays. A dose formulated in animal models to achieve a ci plasma concentration range that includes th (e.g., the concentration of the test compou achieves a half-maximal inhibition of the f event, such as a half-maximal inhibition of infection relative to the amount of the eve absence of the test compound) as determined culture. Such information can be used to m accurately determine useful doses in humans 15 in plasma may be measured, for example, by performance liquid chromatography (HPLC).

The peptides of the invention may, fur the role of a prophylactic vaccine, whereir raises antibodies against the peptides of t invention, which then serve to neutralize F by, for example, inhibiting further HIV inf

Administration of the peptides of the as a prophylactic vaccine, therefore, would administering to a host a concentration of effective in raising an immune response whi ...eeisiamt ta mantumalisa UTW

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response. Such adjuvants may include, but are limited to mineral gels such as aluminum hydro: surface active substances such as lysolecithin pluronic polyols, polyanions; other peptides; emulsions; and potentially useful human adjuvants BCG and Corynebacterium parvum. Many m those used to introduce the vaccine formulations described here. These methods include but are limited to oral, intradermal, intramuscular, intraperitoneal, intravenous, subcutaneous, and intranasal routes.

Alternatively, an effective concentration polyclonal or monoclonal antibodies raised aga peptides of the invention may be administered host so that no uninfected cells become infect HIV. The exact concentration of such antibodivary according to each specific antibody prepabut may be determined using standard technique known to those of ordinary skill in the art.

Administration of the antibodies may be accompusing a variety of techniques, including, but limited to those described in this section.

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For all such treatments described above, exact formulation, route of administration and can be chosen by the individual physician in v the patient's condition. (See e.g. Fingl et a

will vary with the severity of the conditic treated and the route of administration. I perhaps dose frequency, will also vary accorthe age, body weight, and response of the i patient. A program comparable to that disc may be used in veterinary medicine.

Use of pharmaceutically acceptable car formulate the compounds herein disclosed for practice of the invention into dosages suit systemic administration is within the scope 10 invention. With proper choice of carrier a manufacturing practice, the compositions of present invention, in particular, those for solutions, may be administered parenterally by intravenous injection. The compounds ca 15 formulated readily using pharmaceutically a carriers well known in the art into dosage! for oral administration. Such carriers en compounds of the invention to be formulated tablets, pills, capsules, liquids, gels, sy 20 slurries, suspensions and the like, for ora by a patient to be treated.

Pharmaceutical compositions suitable: the present invention include compositions active ingredients are contained in an effeamount to achieve its intended purpose. De

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for oral administration may be in the form of dragees, capsules, or solutions.

The pharmaceutical compositions of the prinvention may be manufactured in a manner that itself known, e.g., by means of conventional m dissolving, granulating, dragee-making, leviga emulsifying, encapsulating, entrapping or lyop processes.

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Pharmaceutical formulations for parentera administration include aqueous solutions of th 10 compounds in water-soluble form. Additionally suspensions of the active compounds may be pre appropriate oily injection suspensions. Suita lipophilic solvents or vehicles include fatty such as sesame oil, or synthetic fatty acid es 15 such as ethyl oleate or triglycerides, or lipc Aqueous injection suspensions may contain subs which increase the viscosity of the suspension as sodium carboxymethyl cellulose, sorbitol, c Optionally, the suspension may also 20 suitable stabilizers or agents which increase solubility of the compounds to allow for the preparation of highly concentrated solutions.

Pharmaceutical preparations for oral use obtained by combining the active compounds wit excipient, optionally grinding a resulting mix

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added, such as the cross-linked polyvinyl p agar, or alginic acid or a salt thereof suc alginate.

Dragee cores are provided with suitable For this purpose, concentrated sugar solutions used, which may optionally contain gum arab polyvinyl pyrrolidone, carbopol gel, polyet glycol, and/or titanium dioxide, lacquer so and suitable organic solvents or solvent mit Dyestuffs or pigments may be added to the tragee coatings for identification or to challenge to the different combinations of active compound design and suitable organic solvents or solvent mit by the suitable organic solvents or solvents or solvent mit by the suitable organic solvents or solv

pharmaceutical preparations which can orally include push-fit capsules made of gewell as soft, sealed capsules made of gelat plasticizer, such as glycerol or sorbitol. push-fit capsules can contain the active ir in admixture with filler such as lactose, k as starches, and/or lubricants such as talc magnesium stearate and, optionally, stabili soft capsules, the active compounds may be or suspended in suitable liquids, such as f liquid paraffin, or liquid polyethylen gly addition, stabilizers may be added.

6. EXAMPLE: DP178 (SEQ ID:1) IS A I INHIBITOR OF HIV-1 INFECTION

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is highly specific for HIV-1. Additionally, a synthetic peptide, DP-185 (SEQ ID:3), represent HIV-1-derived DP178 homolog is also found to b! HIV-1-mediated syncytia formation.

6.1. MATERIALS AND METHODS

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6.1.1. <u>PEPTIDE SYNTHESIS</u>

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Peptides were synthesized using Fast Moc chemistry on an Applied Biosystems Model 431A | 10 synthesizer. Generally, unless otherwise not (peptides contained amidated carboxy termini and acetylated amino termini. Amidated peptides we prepared using Rink resin (Advanced Chemtech) t peptides containing free carboxy termini were 15 synthesized on Wang (p-alkoxy-benzyl-alcohol) 1 (Bachem). First residues were double coupled 1 appropriate resin and subsequent residues were coupled. Each coupling step was followed by a anhydride capping. Peptides were cleaved from 20 resin by treatment with trifluoracetic acid (T) (10ml), H_2O (0.5ml), thioanisole (0.5ml), ethan (0.25ml), and crystalline phenol (0.75g). cation was carried out by revers phase HPLC. Approximately 50mg samples of crude peptide we: 25 chromatographed on a Waters Delta Pak C18 colu

6.1.2. **VIRUS**

The HIV-1, virus was obtained from R. (Popovic, M. et al., 1984, Science 224:497 propagated in CEM cells cultured in RPMI 1 containing 10% fetal calf serum. Supernat infected CEM cells was passed through a 0. and the infectious titer estimated in a microinfectivity assay using the AA5 cell support virus replication. For this purpo 10 serial diluted virus was added to 75μ l AA5 concentration of 2 x 105/ml in a 96-well m: plate. Each virus dilution was tested in Cells were cultured for eight days by addi fresh medium every other day. On day 8 po 15 infection, supernatant samples were tested replication as evidenced by reverse transc activity released to the supernatant. The calculated according to the Reed and Muenc (Reed, L.J. et al., 1938, Am. J. Hyg. 27:4 20 The titer of the HIV-1 and HIV-1 mn stocks these studies, as measured on the AA5 cell approximately 1.4 x 106 and 3.8 x 104 TCIDs resp ctively.

6.1.3. CELL FUSION ASSAY

Approximately 7×10^4 Molt cells were

at a 40x magnification which allowed visualizat the entire well in a single field.

Synthetic peptides were incubated at 37 C either 247 TCID₅₀ (for experiment depicted in FI or 62 TCID₅₀ (for experiment depicted in FIG.3) of HIV-1_{LAI} virus or 25 TCID₅₀ units of HIV-2_{NHZ} a CD4⁺ cells at peptide concentrations of 0, 0.04 4.0, and 40μg/ml for 7 days. The resulting rev transcriptase (RT) activity in counts per minut determined using the assay described, below, in Section 6.1.5. See, Reed, L.J. et al., 1938, A Hyg. 27: 493-497 for an explanation of TCID₅₀ calculations.

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The micro-reverse transcriptase (RT) assay adapted from Goff et al. (Goff, S. et al., 1981 Virol. 38:239-248) and Willey et al. (Willey, R al., 1988, J. Virol. 62:139-147). Supernatants virus/cell cultures are adjusted to 1% Triton-X 10µl sample of supernatant was added to 50µl of cocktail in a 96-well U-bottom microtitre plate the samples incubated at 37 C for 90 min. The cocktail contained 75mM KCl, 2mM dithiothreitol

paper, with partial vacuum applied. Each w minifold was washed four times with 200µl 2 full vacuum. The membrane was removed from minifold and washed 2 more times in a pyr x an excess of 2xSSC. Finally, the membrane on absorbent paper, placed on Whatman #3 pacovered with Saran wrap, and exposed to fil at -70°C.

6.2. RESULTS

6.2.1. PEPTIDE INHIBITION OF INFECT INDUCED SYNCYTIA FORMATION

The initial screen for antiviral activ peptides' ability to block syncytium format by overnight co-cultivation of uninfected 1 with chronically HIV-1 infected CEM cells. 15 results of several such experiments are pre herein. In the first of these experiments DP178 (SEQ ID:1) peptide concentrations bef 10µg/ml and 12.5ng/ml were tested for block cell fusion process. For these experiment: 20 chronically infected with either HIV-1, AI, F 1 or HIV-1 virus were cocultivated over The results (FIG uninfected Molt 4 cells. that DP178 (SEQ ID:1) afforded complete pro against each of the HIV-1 isolates down to 25 concentration of DP178 (SEO ID:1) used. F

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ID:1) is primary sequence-specific and not rel non-specific peptide/protein interactions. Th endpoint (i.e., the lowest effective inhibitor concentration) of DP178 inhibitory action is w the range of 1-10 ng/ml.

The next series of experiments involved to preparation and testing of a DP178 (SEQ ID:1) for its ability to inhibit HIV-1-induced syncy formation. As shown in FIG. 1, the sequence of (SEQ ID:3) is slightly different from DP178 (S in that its primary sequence is taken from the isolate and contains several amino acid differ relative to DP178 (SEQ ID:1) near the N termin shown in FIG. 4, DP-185 (SEQ ID:3), exhibits inhibitory activity even at 312.5ng/ml, the 1c concentration tested.

The next series of experiments involved a comparison of DP178 (SEQ ID:1) HIV-1 and HIV-2 inhibitory activity. As shown in FIG. 5, DP17 ID:1) blocked HIV-1-mediated syncytia formatic peptide concentrations below lng/ml. DP178 (Sfailed, however, to block HIV-2 mediated syncy formation at concentrations as high as 10µg/ml striking 4 log selectivity of DP178 (SEQ ID:1) inhibitor of HIV-1-mediated cell fusion demons an unexpected HIV-1 specificity in the action

6.2.2. PEPTIDE INHIBITION OF INFECT CELL-FREE VIRUS

DP178 (SEQ ID:1) was next tested for i to block CD-4+ CEM cell infection by cell f The results, shown in FIG. 2, ar virus. experiment in which DP178 (SEQ ID:1) was as its ability to block infection of CEM cells HIV-1, isolate. Included in the experim n three control peptides, DP-116 (SEQ ID:9). ID:8), and DP-118 (SEQ ID:10). DP-116 (SEC represents a peptide previously shown to be 10 using this assay, and DP-125 (SEQ ID:8: Wil al., 1992, Proc. Natl. Acad, Sci. USA 89:10 DP-118 (SEQ ID:10) are peptides which have been shown to be active in this assay. Eac concentration (0, 0.04, 0.4, 4, and $40\mu g/ml$ 15 peptide was incubated with 247 TCIDso units virus and CEM cells. After 7 days of cultu free supernatant was tested for the presenc activity as a measure of successful infecti results, shown in FIG. 2, demonstrate that 20 ID:1) inhibited the de novo infection proce by the HIV-1 viral isolate at concentration 90ng/ml (IC50=90ng/ml). In contrast, the t control peptides, DP-125 (SEQ: ID:8) and DF 25 ID:10), had over 60-fold higher IC50 concer approximately 5µg/ml.

In a separate experiment, the HIV-1 ar inhibitory action of DP178 (SEQ ID:1) was to see that HIV-1 are HIV-2

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as a HIV-1 inhibitor than a HIV-2 inhibitor. If inding is consistent with the results of the 1 inhibition assays described, above, in Section and further supports a significant level of selectivity (i.e., for HIV-1 over HIV-2).

7. EXAMPLE: THE HIV-1 INHIBITOR,
DP178 (SEO ID:1) IS NON-CYTOTOXIC

In this Example, the 36 amino acid synthether peptide inhibitor DP178 (SEQ ID:1) is shown to cytotoxic to cells in culture, even at the high peptide concentrations (40µg/ml) tested.

7.1. MATERIALS AND METHODS

Cell proliferation and toxicity assay:

15 Approximately 3.8x10⁵ CEM cells for each peptic concentration were incubated for 3 days at 37 flasks. Peptides tested were DP178 (SEQ ID:1) 116 (SEQ ID:9), as described in FIG. 1. Pepti synthesized as described, above, in Section 6.

20 concentrations of each peptide used were 0, 2. and 40μg/ml. Cell counts were taken at incubatimes of 0, 24, 48, and 72 hours.

7.2. RESULTS

25 Wh ther the potent HIV-1 inhibitor DP178

TD-11 exhibited any cytotoxic effects was asse

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The results of the cytotoxicity study that DP178 (SEQ ID:1) exhibits no cytotoxic cells in culture. As can be seen, below, i XXIV, even the proliferation and viability characteristics of cells cultured for 3 day 5 presence of the highest concentration of DI ID:1) tested (40µg/ml) do not significantly from the DP-116 (SEQ ID:9) or the no-p ptic The cell proliferation data is also represe graphic form in FIG. 6. As was demonstrate 10 Working Example presented above in Section (SEQ ID:1) completely inhibits HIV-1 mediat formation at peptide concentrations between 10ng/ml, and completely inhibits cell-fr e infection at concentrations of at least 901 15 Thus, this study demonstrates that even at concentrations greater than 3 log higher th inhibitory dose, DP178 (SEQ ID:1) exhibits cytotoxic effects.

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TABLE XXIV

% Viability
at time (hour

5	<u>Peptide</u>	Peptide Concentration µg/ml	0	24	48
	DP178 (SEQ ID:1)	40	98	97	95
10	10.17	10	98	97	98
		2.5	98	93	96
	DP116 (SEQ ID:9)	40	98	95	98
15		10	98	95	93
		2.5	98	96	98
20	No Peptide	0	98	97	99

8. EXAMPLE: THE INTERACTION OF DP178 AND
Soluble recombinant forms of gp41 used in
25 example described below provide evidence that 1
DP178 peptide associates with a distal site on

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due to their ability to form complexes with and interfere with its fusogenic process.

MATERIALS AND METHODS

8.1.1. CONSTRUCTION OF FUSION PF AND GP41 MUTANTS

Construction of fusion proteins and mu in FIG. 7 was accomplished as follows: the sequence corresponding to the extracellular gp41 (540-686) was cloned into the Xmn I si 10 expression vector pMal-p2 (New England Bio] The gp41 sequence was amplified from (Malim et al., 1988, Nature 355: 181-183) 1 polymerase chain reaction (PCR) with upstre 5'-ATGACGCTGACGGTACAGGCC-3' (primer A) and 15 primer 5'-TGACTAAGCTTAATACCACAGCCAATTTGTTA' M41-P was constructed by using the T7. in vitro mutagenesis kit from United States Biochemicals (USB) following the supplier: The mutagenic primer (5'instructions. 20 GGAGCTGCTTGGGGCCCCAGAC-3') introduces an I mutation in M41 at position 578. $M41\Delta107$, the DP-107 region has been deleted, was man deletion mutagenic primer 5'-CCAAATCCCCAGGAGCTGCTCGAGCTGCACTATACCAGAC-3

following the USB T7-Gen mutagenesis proto-

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were checked by restriction enzyme analysis an confirmed by DNA sequencing.

8.1.2. PURIFICATION AND CHARACTERIZ OF FUSION PROTEINS

- The fusion proteins were purified accordi 5 the protocol described in the manufacturer's h of protein fusion and purification systems fro England Biolabs (NEB). Fusion proteins (10 ng analyzed by electrophoresis on 8% SDS polyacry gels. Western blotting analysis was performed 10 described by Sambrook et al., 1989, Molecular A Laboratory Manual, 2d Ed, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, Ch. pp. 64-75. An HIV-1 positive serum diluted 10 or a human Fab derived from repertoire cloning 15 used to react with the fusion proteins. The s antibody was HRP-conjugated goat antihuman Fak ECL Western blotting detection system (Amersha used to detect the bound antibody. A detailed protocol for this detection system was provide 20 Rainbow molecular weight marker manufacturer. (Amersham) were used to estimate the size of 1 proteins.
- 25 8.1.3. <u>CELL FUSION ASSAYS FOR ANTI-HIV AC</u>

 Cell fusion assays were performed as prev

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not show cytotoxicity at the concentrations shown in FIG. 8.

Inhibition of HIV-1 induced cell-cell activity was carried out in the presence of DP178 and various concentrations of M41 Δ 178 P Δ 178 as indicated in FIG. 9. There was no syncytia in the presence of 10 nM DP178. Nor fusion protein was added in the control

8.1.4. ELISA ANALYSIS OF DP178 F TO THE LEUCINE ZIPPER MOT

The amino acid sequence of DP178 used YTSLIHSLIEESQNQQEKNEQELLELDKWASLWNWF. linked immunoassay (ELISA), M41\Delta178 or M41- μ g/ml) in 0.1M NaHCO₃, pH 8.6, were coated Linbro ELISA plates (Flow Lab, Inc.) overn: 15 well was washed three times with distilled blocked with 3% bovine serum albumin (BSA) hours. After blocking, peptides with 0.5% (40 mM Tris-HCl pH7.5, 150 mM NaCl, 0.05% ' were added to the ELISA plates and incubate 20 temperature for 1 hour. After washing thre with TBST, Fab-d was added at a concentrat ng/ml with 0.5% BSA in TBST. The plates w three times with TBST after incubation at : 25 temperature for 1 hour. Horse radish pero conjugated goat antihuman Fab antiserum at

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(Molecular Design) at 490 nm. Results are show FIG. 10.

8.2. RESULTS

8.2.1. THE EXPRESSION AND CHARACTERI OF THE ECTODOMAIN OF qp41

As a step toward understanding the roles c two helical regions in gp41 structure and funct the ectodomain of gp41 was expressed as a malto binding fusion protein (M41) (FIG. 7). The fus peptide sequence at the N-terminal of gp41 was 10 from this recombinant protein and its derivative improve solubility. The maltose binding protei facilitated purification of the fusion prot ins relatively mild, non-denaturing conditions. the M41 soluble recombinant gp41 was not glycos 15 lacked several regions of the transmembrane pro (i.e., the fusion peptide, the membrane spannir the cytoplasmic domains), and was expressed in absence of gp120, it was not expected to pr cis reflect the structure of native gp41 on HIV-1 1 20 Nevertheless, purified M41 folded in a manner t preserved certain discontinuous epitopes as ev: by reactivity with human monoclonal antibodies, 126-6, and 50-69, previously shown to bind conformational epitopes on native gp41 express 25

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eliminated reactivity with Fab-d. These reindicate that both helical regions, separatamino acids in the primary sequence, are remaintain the Fab-d epitope.

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8.2.2. ANTI-HIV ACTIVITY OF THE RECOMBINANT ECTODOMAIN OF

The wild type M41 fusion protein was 1 anti-HIV-1 activity. As explained, supra,

10 peptides corresponding to the leucine zipporand the C-terminal putative helix (DP178) 1 anti-HIV activity. Despite inclusion of box regions, the recombinant M41 protein did not HIV-1 induced membrane fusion at concentration high as 50 µM (Table XXV, below).

TABLE XXV							
DISRUPTION OF	THE	LEUCINE ZI	PPER				
GP41 FREES	THE	ANTI-HIV M	OTIF				

20		DP107	DP178	<u>M41</u>	M41-P
	Cell fusion (IC ₉₀)	1 μΜ	1 nM	> 50 μM	83 nM
25	Fab-D binding (k _D)	-	-	3.5x10°	2.5x10

HIV infectiv-

concentration of purified recombinant fusion protein in RPMI 164 10% fetal bovine serum and antibiotics in a 96-well microtiter pla CEM4 cells at 6 x 10⁵ cells/ml were added to each well, and culti incubated at 37°C in a humidified CO₂ incubator. Cells were cult days by the addition of fresh medium every 2 to 3 days. On days postinfection, supernatant samples were assayed for reverse transc activity, as described below, to monitor viral replication. The 50 culture infectious dose (TCID₅₀) was calculated for each condition to the formula of Reed & Muench, 1937, Am. J. Hyg. 27:493-49 activity was determined by a modification of the published method al., 1981, J. Virol. 38:239-248 and Willey et al., 1988, J. Virol. as described in Chen et al., 1993, AIDS Res. Human Retroviruse 1086.

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Surprisingly, a single amino acid substitu proline in place of isoleucine in the middle of leucine zipper motif, yielded a fusion protein which did exhibit antiviral activity (Table XXV 15 Fig. 8). As seen in Table XXV, M41-P blocked s formation by 90% at approximately 85 nM and neutralized HIV-1_{ms} infection by 90% at approxi 70 nM concentrations. The anti-HIV-1 activity P appeared to be mediated by the C-terminal hel 20 sequence since deletion of that region from M41 yielded an inactive fusion protein, M41-PΔ178 (This interpretation was reinforced by experiments demonstrating that a truncated fusi protein lacking the DP178 sequence, M41\D178, at 25 the potent anti-fusion activity of the DP178 pe tweeting_domandant manna

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the DP178 region, making it unavailable for activity.

A specific association between these is also indicated by other human monoclona studies. For example, Fab-d failed to bin DP178 peptide or the fusion protein M41 Δ 17 epitope was reconstituted by simply mixing reagents together (FIG. 10). Again, the p mutation in the leucine zipper domain of t protein, M41-P Δ 178, failed to reconstitute in similar mixing experiments.

9. EXAMPLE: METHOD FOR COMPUTER-AS IDENTIFICATION OF DP10 AND DP178-LIKE SEQUENC

well described in the literature and contarepeat positioning for each amino acid. (nomenclature labels each of seven amino acid heptad repeat A through G, with amino acid tending to be hydrophobic positions. Amin and G tend to be charged. These four positions and G form the amphipathic backbone simplification alpha-helix. The backbones of amphipathic helices interact with each other directions of the content

deducing the most likely possibilities for hept positioning of the amino acids of HIV-1 Bru DP-which is known to have coiled-coil structure, a 1 Bru DP178, which is still structurally undefi The analysis of each of the sequences is contai FIG. 12. For example, the motif for GCN4 was d as follows:

- The only amino acids (using standard singl letter amino acid codes) found in the A or positions of GCN4 were [LMNV].
- 2. All amino acids were found at B, C, E, F, positions except {CFGIMPTW}.
 - 3. The PESEARCH motif would, therefore, be wr as follows:
- [LMNV]-{CFGIMPTW}(2)-[LMNV]-{CFGIMPTW}(3)-[LMNV]-{CFGIMPTW}(2)-[LMNV]-{CFGIMPTW}(3)-[LMNV]-{CFGIMPTW}(2)-[LMNV]-{CFGIMPTW}(3)-[LMNV]-{CFGIMPTW}(2)-[LMNV]-{CFGIMPTW}(3)
- position either L, M, N, or V must occur; at position either L, M, N, or V must occur; at positions and C (the next two positions) accept everythexcept C, F, G, I, M, P, T, or W; at the D positions I and G (the next 3 positions) accept everything C, F, G, I, M, P, T, or W." This statement is contained four times in a 28-mer motif and five

sequence alignments for both DP107 and DP13 includes motif designs based on 28-mer, 35-full-length peptides. Notice that only sladifferences occur in the motifs as the peptilengthened. Generally, lengthening the bases results in a less stringent motif. This is useful in broadening the possibilities for DP107-or DP-178-like primary amino acid seareferred to in this document as "hits".

In addition to making highly specific 10 each type peptide sequence to be search d, possible to make "hybrid" motifs. made by "crossing" two or more very string to make a new search algorithm which will only both "parent" motif sequences but als 15 peptide sequences which have similarities other, or both "parents". For example, in "parent" sequence of GCN4 is crossed with possible "parent" motifs of DP-107. Now t motif must contain all of the amino acids 20 A and D positions of both parents, and exc the amino acids not found in either parent other positions. The resulting hybrid fro GCN4 or [LMNV] {CFGIMPTW} and DP107 (28-mer first L in the D position) or [ILQT] {CDFIN 25 [ILMNQTV]{CFIMPT}. Notice that now only t hybrid motifs exist which cover both frami

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Hybridizations can be performed on any combination of two or more motifs. FIG. 17 summarizes several three-motif hybridizations including GCN4, DP107 (both frames), and DP178 both frames). Notice that the resulting motifs now becoming much more similar to each other. fact, the first and third hybrid motifs are act subsets of the second and fourth hybrid motifs respectively. This means that the first and the hybrid motifs are slightly more stringent than second and fourth. It should also be noted that only minor changes in these four motifs, or by hybridizing them, a single motif could be obta which would find all of the sequences. However should be remembered that stringency is also re Finally, the most broad-spectrum and least-stri hybrid motif is described in FIG. 18 which summ the hybridization of GCN4, DP107 (both frames), (both frames), c-Fos, c-Jun, c-Myc, and Flu loc

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fact that DP-178 is located only approximately amino acids upstream of the transmembrane spans region of gp41 and just C-terminal to a proline separates DP107 and DP178. It has been postulated that DP178 may be an amphipathic helix when mer associated, and that the proline might aid in initiation of the helix formation. The same

release 11.0). Of these, 1092 are viral e glycoprotein sequences (library file PVIRU Tables V through XIV contain lists of prot names and motif hit locations for all the searched.

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10. EXAMPLE: COMPUTER-ASSISTED IDENTIFICA OF DP107 AND DP178-LIKE SEQU IN HUMAN IMMUNODEFICIENCY VI

FIG. 20 represents search results for isolate gp41 (PC/Gene protein sequence PEN 10 Notice that the hybrid motif which crosses DP-178 (named 107x178x4; the same motif as FIG. 16 found three hits including amino & 599, 636-688, and 796-823. These areas in plus eight N-terminal and four C-terminal 15 DP178 plus seven N-terminal and ten C-term acids; and an area inside the transmembras (cytoplasmic). FIG. 20 also contains the obtained from searching with the motif name for which the key is found in FIG. 17 ({C| 20 This motif also found thre {CFP}x5). DP107 (amino acids 510-599), DP178 (615-7 cytoplasmic region (772-841). These hits hits found by the motif 107x178x4 with co additional sequences on both the amino an 25 termini. This is not surprising in that

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at the very C-terminus of gp120, just upstream (cleavage site (P7LZIPC and P12LZIPC); and 735-76 the cytoplasmic domain of gp41 (P23LZIPC). These results are found in Tables VIII, IX, and X undersame sequence name as mentioned above. Notice the only area of HIV-1 BRU which is predicted by Lupas algorithm to contain a coiled-coil region from amino acids 635-670. This begins eight amicacids N-terminal to the start and ends eight amicacids N-terminal to the end of DP178. DP107, do the fact that it is a known coiled coil, is not predicted to contain a coiled-coil region using Lupas method.

11. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION
OF DP107-LIKE AND DP178-LIKE
SEQUENCES IN HUMAN RESPIRATORY
SYNCYTIAL VIRUS

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Respiratory Syncytial Virus (RSV; Strain A2) fu glycoprotein F1 (PC/Gene protein sequence name HRSVA). Motif 107x178x4 finds three hits inclu amino acids 152-202, 213-243, and 488-515. The arrangement of these hits is similar to what is in HIV-1 except that the motif finds two region similarities to DP-178, on just downstream of would be called the DP107 r gion or amino acids

12. EXAMPLE: COMPUTER-ASSISTED IDENTIFICAT DP107-LIKE AND DP178-LIKE SEQ IN SIMIAN IMMUNODEFICIENCY VI

Motif hits for Simian immunodeficienc (AGM3 isolate; PC/Gene protein sequence na PENV SIVAG) are shown in FIG. 22. Motif 1 5 finds three hits including amino acids 566 624, and 703-730. The first two hits only amino acids between them and could probabl combined into one hit from 566-624 which w represent a DP107-like hit. Amino acids 7 10 would then represent a DP178-like hit. finds three hits including amino acids 556 like), 651-699 (DP178-like), and 808-852 W represents the transmembrane spanning regi also has one region from 655-692 with a hi 15 propensity to form a coiled coil as predic Lupas algorithm. Both 107x178x4 and ALLMO find the same region. SIV does not have a motif hits in gp41.

- The identification of DP178/DP107 and second SIV isolate (MM251) is demonstrated Example presented, below, in Section 19.
- 13. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION DP107-LIKE AND DP178 LIKE SIN CANINE DISTEMPER VIRUS

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interest including: amino acids 228-297, which completely overlaps both the Lupas prediction a DP107-like 107x178x4 hit; residues 340-381, whi overlaps the second 107x178x4 hit; and amino ac 568-602, which is DP178-like in that it is loca just N-terminal to the transmembrane region. I overlaps another region (residues 570-602) pred by the Lupas method to have a high propensity t a coiled coil. Several PLZIP motifs successful identified areas of interest including P6 and F which highlight residues 336-357 and 336-361 respectively; P1 and P12LZIPC which find residue 5 and 562-592 respectively.

14. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION DP107-LIKE AND DP178-LIKE SEQUENCE IN NEWCASTLE DISEASE VIRUS

FIG. 24 shows the motif hits found in Newconsease Virus (strain Australia-Victoria/32; PC protein sequence name PVGLF_NDVA). Motif 107x1 finds two areas including a DP107-like hit at acids 151-178 and a DP178-like hit at residues 512. ALLMOTI5 finds three areas including res: 117-182, 231-272, and 426-512. The hits from a include a region which is predicted by the Lupa method to have a high coiled-coil propensity (a

(FIG. 25). In addition, the two motifs have like hit just slightly C-terminal at amino 241. Both motifs also have DP178-like hits transmembrane region including amino acids 462-512 respectively. Several PLZIP motif also observed including 283-303 (P5LZIPC), (P12LZIPC), 453-474 (P6LZIPC), and 453-481 The Lupas algorithm predicts that amino acimay have a propensity to form a coiled-c in

16. EXAMPLE: COMPUTER-ASSISTED IDENTIFICA'
DP107-LIKE AND DP178-LIKE SEINFLUENZA A VIRUS

FIG. 26 illustrates the Lupas predict coiled coil in Influenza A Virus (strain A at residues 379-436, as well as the motif 15 107x178x4 at amino acids 387-453, and for residues 380-456. Residues 383-471 (38-12 were shown by Carr and Kim to be an extend coil when under acidic pH (Carr and Kim, 1 73: 823-832). The Lupas algorithm predict 20 coil at residues 379-436. All three metho successfully predicted the region shown to have coiled-coil structure; however, ALLMC predicted the greatest portion of the 88 I str tch. 25

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that several of the identified peptides exhibit antiviral capability. Additionally, it is show several of these peptides exhibit a substantial helical character.

17.1 MATERIALS AND METHODS

Structural analyses: The CD spectra were measured in a 10mM sodium phosphate, 150mM sod: chloride, pH 7.0, buffer at approximately 10mM concentrations, using a 1 cm pathlength cell of Jobin/Yvon Autodichrograph Mark V CD spectrophotometer. Peptides were synthesized according to the methods described, above, in 6.1. Peptide concentrations were determined finishing Edlehoch's method (1967, Biochemistry 6:

Anti-RSV antiviral activity assays: The utilized herein tested the ability of the pept disrupt the ability of HEp2 cells acutely infewith RSV (i.e., cells which are infected with multiplicity of infection of greater than 2) t and cause syncytial formation on a monolayer of uninfected an uninfected line of Hep-2 cells. lower the observed level of fusion, the greate antiviral activity of the peptide was d termin be.

Uninfected confluent monolayers of Hep-2

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washed with DPBS (Dulbecco's Phosphate Buff w/o calcium or magnesium; Bio Whittaker Cat 512F) and cell monolayers were removed with (1:5000; Gibco Life Technologies Cat. No. 1 The cells were spun 10 minutes and resusper FBS. Cell counts were performed using a hemacytometer. Persistent cells were add c uninfected Hep-2 cells.

The antiviral assay was conducted by, removing all media from the wells containing uninfected Hep-2 cells, then adding peptide dilutions described below) in 3% EMEM, and RSV-infected Hep2 cells per well. Wells we incubated at 37°C for 48 hours.

checked for fusion centers, media was removed wells, followed by addition, to each will, crystal Violet stain or XTT. With respect Violet, approximately 50µl 0.25% Crystal Vin methanol were added to each well. The rinsed immediately, to remove excess stain allowed to dry. The number of syncytia pethen counted, using a dissecting microscop

With respect to XTT (2,3-bis[2-Methox sulfophenyl]-2H-tetrazolium-5-carboxyanili salt), 50µl XTT (1mg/ml in RPMI buff red w HPPES pH 7.2-7.4. plus 5% DMSO) were adde

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2) peptides T-120 to T-141 and T-576, as shown 1 27B, and peptides T-12, T-13, T-15, T-19, T-28 1 30, T-66, T-69, T-70 and T-576, as shown in FIG. and

3) peptides T-67 and T-104 to T-119 and T-384, a shown in FIG. 28A, and peptides T-71, T-613 to T-662 to T-676 and T-730, as shown in FIG. 28B.

The peptides of group 1 represent portions RSV F2 protein DP178/107-like region. The peptigroup 2 represent portions of the RSV F1 protein DP107-like region. The peptides of groups 3 reportions of the RSV F1 protein DP178-like region

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Each peptide was tested at 2-fold serial dilutions ranging from $100\mu g/ml$ to approximatel 100ng/ml. For each of the assays, a well conta no peptide was also used. The IC₅₀ data for each peptide represents the average of several experimental conducted utilizing that peptide.

17.2 RESULTS

The data summarized in FIGS. 27A-B and 28A represent antiviral and structural information obtained from peptides derived from the RSV F2 DP178/DP107-like F2 region (FIG. 27A-B), the RS DP-107-like region (FIG. 27C-D) and the RSV DP1 F2 region (FIG. 28A-B).

131, T-135 and T-137 to T-139, as dem nstructure low IC₅₀ values. In addition, CD and 27A, 27C) reveals that many of the peptide some detectable level of helical structure

The results summarized in FIG. 28A-B
that a number of DP178-like purified pepti
a range of potent anti-viral activity. Th
include, for example, T-67, T-104, T-105 a
T-119, as listed in FIG. 28A, and T-665 to
T-671 to T-673, as listed in FIG. 28B. In
some of the DP178-like peptides exhibited
of helicity.

Thus, the computer assisted searches hereinabove, successfully identified viral domains that represent highly promising an antiviral compounds.

18. EXAMPLE: POTENTIAL HUMAN PARAINFLUEN TYPE 3 DP178/DP107 ANALOGS: ANTIVIRAL CHARACTERIZATION

In the Example presented herein, human parainfluenza virus type 3 (HPIV3) peptide by utilizing the computer-assisted search described in the Examples presented in Section 15, above, were tested for anti-HPIV3 act:

Additionally, circular dichroism (CD) structure analyses were conducted on the peptides, analyses

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spectra were measured in a 10mM sodium phosphat 150mM sodium chloride, pH 7.0, buffer at approx 10mM concentrations, using a 1 cm pathlength ce Jobin/Yvon Autodichrograph Mark V CD

spectrophotometer. Peptide concentrations were determined from A_{280} using Edlehoch's method (19) Biochemistry <u>6</u>:1948).

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Anti-HPIV3 antiviral activity assays: The utilized herein tested the ability of the pepti disrupt the ability of Hep2 cells chronically i with HPIV3 to fuse and cause syncytial formatic monolayer of an uninfected line of CV-1W cells. more potent the lower the observed level of fus the greater the antiviral activity of the pepti

Uninfected confluent monolayers of CV-1W c
were grown in microtiter wells in 3% EMEM (Eag)
Minimum Essential Medium w/o L-glutamine [Bio
Whittaker Cat. No. 12-125F], with fetal bovine
[FBS; which had been heat inactivated for 30 mi
at 56°C; Bio Whittaker Cat. No. 14-501F) supple
at 3%, antibiotics/antimycotics (Gibco BRL Life
Technologies Cat. No. 15040-017) added at 1%, a
glutamine added at 1%.

cells, cultures of chronically infected Hep2 co were washed with DPBS (Dulbecco's Phosphate Bu:

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dilutions described below) in 3% EMEM, and chronically HPIV3-infected Hep2 cells per were then incubated at 37°C for 24 hours.

on day 2, after cells in control well checked for fusion centers, media was removells, followed by addition, to each well, approximately 50µl 0.25% Crystal Violet st methanol. Wells were rinsed immediately, excess stain and were then allowed to dry. of syncytia per well were then counted, us dissecting microscope.

Alternatively, instead of Crystal Vicanalysis, cells were assayed with XTT, as avove, in Section 17.1.

Peptides: The peptides characterized study presented herein were:

- peptides 157 to 188, as shown in FIG peptides T-38 to T-40, T-42 to T-46 shown in FIG. 29B. These peptides a from the DP107 region of the HPIV3 F protein (represented by HPF3 107, as FIG. 29A); and
- 2) Peptides 189 to 210, as shown in FIG 269, T-626, T-383 and T-577 to T-579 FIG. 30B. These peptides are primar from the DP178 region of the HPIV3 F protein (represented by HPF3 178, as

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500ng/ml. For each of the assays, a well cont no peptide was also used.

18.2 RESULTS

The data summarized in FIGS. 29A-B and 30 represent antiviral and structural information obtained from peptides derived from the HPIV3 protein DP107-like region (FIG. 29A-B) and th fusion protein DP178-like region (FIG. 30A-B).

As shown in FIG. 29A-B, a number of the H
DP107-like peptides exhibited potent levels of
antiviral activity. These peptides include, f
example, peptides T-40, T-172 to T-175, T-178,
and T-185.

that a number of the DP178-like peptides teste exhibit a range of anti-viral activity. These peptides include, for example, peptides 194 to evidenced by their low IC50 values. In fact, peptides 201 to 205 exhibit IC50 values in the nanogram/range. In addition, many of the DP178-like peexhibited some level of helicity.

Thus, the computer assisted searches deschereinabove, have successfully identified virapeptide domains that represent highly promising HPIV3 antiviral compounds.

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amino acid residues 156-219 and 245-286. Etherefore, identify similar regions.

Interestingly, the first SIV peptide r (i.e., from amino acid residue 156 to approamino acid residue 219) correlates with a I region, while the second region identified approximately amino acid residue 245 to approximately amino acid residue 245 to approximately amino acid residue 289) correlates with the region of HIV. In fact, an alignment of SI MM251 and HIV isolate BRU, followed by a set the best peptide matches for HIV DP107 and reveals that the best matches are found will peptide regions identified by the 107x178x4 ALLMOTI5 search motifs.

region at amino acid residues 242-282 is protected the Lupas program. This is similar to the in HIV in which the coiled-coil is predicted Lupas program to be in the DP178 rather the DP107 region. It is possible, therefore, be similar to HIV in that it may contain a structure in the DP107 region, despite such structure being missed by the Lupas algorithic Likewise, it may be that the region corresponded in SIV may exhibit an undefinitive tructure, despite the Lupas program's presented in the

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20. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION DP178/DP107 ANALOGS IN EPSTEIN-VIRUS

The results presented herein describe the identification of DP178/DP107 analogs within different Epstein-Barr Virus proteins. Epsteis a human herpes virus which is the causative of, for example, infectious mononucleosis (IM also associated with nasopharyngeal carcinomas Burkitt's lymphoma and other diseases. The v predominantly exists in the latent form and is activated by a variety of stimuli.

FIG. 32 depicts the search motif results Epstein-Barr Virus (Strain B95-8; PC/Gene® pr sequence PVGLB_EBV) glycoprotein gp110 precur (gp115). The 107x178x4 motif identified two of interest, namely the regions covered by am residues 95-122 and 631-658. One PZIP region identified at amino acid residue 732-752 which likely a cytoplasmic region of the protein. algorithm predicts a coiled-coil structure for

acids 657-684. No ALLMOTI5 regions were iden FIG. 33 depicts the search motif results Zebra (or EB1) trans-activator protein (BZLF1 above-identified Epstein-Barr virus. This pra a transcription factor which represents the periodical mediator of viral reactivation. It is a member of the periodical reactivation.

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at amino acid residues 193-220, as shown in The Lupas program predicted no coiled-coil

21. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION DP178/DP107 ANALOGS IN MEASI

FIG. 34 illustrates the motif search in the fusion protein F1 of measles virus, stimed Edmonston (PC Gene® protein sequence PVGLF successfully identifying DP178/DP107 analogous

The 107x178x4 motif identifies a sing.

10 amino acid residues 228-262. The ALLMOTI5

motif identifies three regions, including a
residues 116-184, 228-269 and 452-500. The
containing proline residues followed by a
zipper-like sequence were found beginning
15 residues 214, 286 and 451.

The Lupas program identified two regipredicted had potential for coiled-coil st which include amino acid residues 141-172

20 22. EXAMPLE: COMPUTER-ASSISTED IDENTIFIC DP178/DP107 ANALOGS IN HEPA VIRUS

FIG. 35 depicts the results of a PZIP search conducted on the Hepatitis B virus
Two regions of interest within the major s
antigen precursor S protein were identifie
first lies just C-terminal to the proposed

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putative DP178/DP107 analog regions. The pept synthesized according to standard Fmoc chemist Rinkamide MBHA resins to provide for carboxy t blockade (Chang, C.D. and Meinhofer, J., 1978, Pept. Protein Res. 11:246-249; Fields, G.B. an R.L., 1990, Int. J. Pept. Protein Res. 35:161-Follwing complete synthesis, the peptide amino terminus is blocked through automated acetylat the peptide is cleaved with trifluoroacetic ac and the appropriate scavengers (King, D.S. et 1990, Int. J. Pept. Res. 36:255-266). After c the peptide is precipitated with ether and dri vacuum for 24 hours.

by utilizing standard assays to determine the peptide concentration required to cause an acc (e.g., 90%) decrease in the amount of viral pr formed by cells exposed to an HBV viral inocul Candidate antivial peptides are further charac in model systems such as wood chuck tissue cul animal sytems, prior to testing on humans.

23. EXAMPLE: COMPUTER-ASSISTED IDENTIFICATION DP178/DP107 ANALOGS IN SIMIAN PRIZER MONKEY VIRUS

The results depicted herein illustrate the results of search motifs conducted on the Simi

24. EXAMPLE: COMPUTER-ASSISTED IDENTIFIC DP178/DP107 ANALOGS IN BACT: PROTEINS

The results presented herein demonstration of DP178/DP107 analogs conto sequences present in proteins of a varibacterial species.

Pseudomonas aeruginosa fimbrial protein (Pregions were identified by motifs 107x178x

ALLMOTIS. The regions located at amino ac 30-67 and 80-144 were identified by the 10 motif. The regions at amino acid residues 80-125 were identified by the ALLMOTIS.

Pseudomonas gonorrhoeae fimbrial protein (
single region was identified by both the I
the ALLMOTIS motifs. The region located a
residues 66-97 was identified by the 107x1
The region located at amino acid residues
identified by the ALLMOTIS search motif.
coil regions were predicted by the Lupas I

FIG. 39 depicts the search motif resulted by Influenza fimbrial protein (Pilsingle region was identified by both the the ALLMOTI5 motifs. The region located residues 102-129 was identified by the 10 may region located at amino acid:

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region located at amino acid residues 102-148 identified by the ALLMOTI5 search motif. No coil regions were predicted by the Lupas progr

FIG. 41 summarizes the motif search result conducted on the Staphylococcus aureus enterot Type E protein. These results demonstrate the successful identification of DP178/DP107 analocorresponding to peptide sequences within this protein, as described below.

acid residues 22-27. The 107x178x4 motif ider two regions, with the first at amino acid residues and the second at 88-115. A P12LZIPC motif identified two regions, at amino acid residues and 230-250.

The Lupas program predicted a region with propensity for coiling at amino acid residues. This sequence is completely contained within tregion identified by both ALLMOTIS and 107x178 motifs.

FIG. 42 depicts the search motif results conducted on a second Staphylococcus aureus to enterotoxin A. Two regions were identified by ALLMOTI5 motif, at amino acid residues 22-70 acid residues 164-205. The 107x178x4 motif for regions, the first at amino acid residues 26-1 the second at amino acid residues 165-192. A

55-115, and the second residing at amino a 216-254. The 107x178x4 motif identified a region at amino acid residues 78-105. No regions were predicted by the Lupas pr gra

5 25. EXAMPLE: COMPUTER-ASSISTED IDENTIFIC DP178/DP107 ANALOGS WITHIN HUMAN PROTEINS

The results presented herein demonstr identification of DP178/DP107 analogs corr peptide sequences present within several d human proteins.

FIG. 44 illustrates the search motif conducted on the human c-fos oncoprotein. ALLMOTI5 motif identified a single region acid residues 155-193. The 107x178x4 motione region at amino acid residues 162-193. program predicted a region at amino acid residues 162-193. to have coiled-coil structure.

conducted on the human lupus KU autoantige pro. The ALLMOTI5 motif identified a sinc amino acid residues 229-280. The 107x1781 identified one region at amino acid residue The Lupas program predicted a region at an residues 232-267 to have coiled-coil structure.

FIG. 46 illustrates the search motif

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26. EXAMPLE: POTENTIAL MEASLES VIRUS DP178/C
ANALOGS: CD AND ANTIVIRAL
CHARACTERIZATION

In the Example presented herein, measles virus DP178-like peptides identified by utiliz computer-assisted search motifs described in t Examples presented in Sections 9 and 21, above tested for anti-MeV activity. Additionally, dichroism (CD) structural analyses are conduct the peptides, as discussed below. It is demonsthat several of the identified peptides exhibit antiviral capability. Additionally, it is shown of the these peptides exhibit a substantical character.

26.1 MATERIALS AND METHODS

Structural analyses: The CD spectra were measured in a 10mM sodium phosphate, 150mM sodium chloride, pH 7.0, buffer at approximately 10mM concentrations, using a 1 cm pathlength cell c Jobin/Yvon Autodichrograph Mark V CD spectrophotometer. Peptide concentrations were determined from A₂₈₀ using Edlehoch's method (1 Biochemistry 6:1948).

Anti-M V antiviral activity syncytial rec 25 assay: The assay utilized herein tested the a of the peptides to disrupt the ability of Vero

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[FBS; which had been heat inactivated for : at 56°C; Bio Whittaker Cat. No. 14-501F) su at 10%, antibiotics/antimycotics (Bio White No. 17-602E) added at 1%, and glutamine add

addition to the uninfected cells, cultures infected Vero cells were washed twice with Whittaker Cat. No. 10-543F) and cell monol removed with trypsin (Bio Whittaker Cat. No. 10 once cells detached, media was added, any clumps of cells were dispersed, and hemacy counts were performed.

The antiviral assay was conducted by, removing all media from the wells containi uninfected Vero cells, then adding peptide dilutions described below) in 10% FBS EMEN acutely MeV-infected Vero cells per well. then incubated at 37°C for a maximum of 18

on day 2, after cells in control well checked for fusion centers, media was removells, followed by addition, to each well, approximately 50µl 0.25% Crystal Violet simethanol. Wells were rinsed twice with wind immediately, to remove excess stain and wallowed to dry. The number of syncytia potential counted, using a dissecting microscopy Anti-MeV antiviral activity plaque removed.

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The antiviral assay was conducted by, fir removing all media from the wells containing uninfected Vero cells, then adding peptides (a dilutions described below) in 10% FBS EMEM, ar stock virus at a final concentration of 30 pla forming units (PFU) per well. Wells were ther incubated at 37°C for a minimum of 36 hours an maximum of 48 hours.

on day 2, after cells in control wells we checked for fusion centers, media was removed wells, followed by addition, to each well, of approximately 50µl 0.25% Crystal Violet stain methanol. Wells were rinsed twice with water immediately, to remove excess stain and were t allowed to dry. The number of syncytia per we then counted, using a dissecting microscope.

Peptides: The peptides characterized in study presented herein were peptides T-252A0 t 256A0, T-257B1/C1, and T-258B1 to T-265B0, and to T-268A0, as shown in FIG. 47. These peptid represent a walk through the DP178-like region MeV fusion protein.

Each peptide was tested at 2-fold serial dilutions ranging from $100\mu g/ml$ to approximate 100ng/ml. For each of the assays, a well cont no peptide was also used.

The IC₅₀ values for such peptides were determined in FIG. 47, and ranged from 1.35 μ g/ml 257B1/C1) to 0.072 μ g/ml (T-265B1). None of like peptides showed, by CD analysis, a det level of helicity.

Thus, the computer assisted searches d hereinabove, as in for example, the Example in Section 9, for example, successfully ide viral peptide domains that represent highly anti-MeV antiviral compounds.

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27. EXAMPLE: POTENTIAL SIV DP178/DP107 AN ANTIVIRAL CHARACTERIZATION

In the Example presented herein, simia immunodeficiency virus (SIV) DP178-like per identified by utilizing the computer-assist motifs described in the Examples presented 9, 12 and 19, above, were tested for anti-S activity. It is demonstrated that several identified peptides exhibit potent antivira capability.

27.1 MATERIALS AND METHODS

Anti-SIV antiviral assays: The assay herein were as reported in Langolis t al. 25 A.J. et al., 1991, AIDS Research and Human

Retroviruses 7:713-720).

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27.2 RESULTS

The data summarized in FIG. 48 represents antiviral information obtained via "peptide wa: through the DP178-like region of the SIV TM pro

As shown in FIG. 48, peptides T-391 to T-4 tested and exhibited a potent antiviral activit crude peptides.

Thus, the computer assisted searches describered hereinabove, as in for example, the Example present in Section 9, for example, successfully identificated peptide domains that represent highly presentions.

28. EXAMPLE: ANTI-VIRAL ACTIVITY OF DP107 ANI 178 PEPTIDE TRUNCATIONS AND MUTI

a study of the antiviral activity of DP107 and truncations and mutations. It is demonstrated several of these DP107 and DP178 modified pept: exhibit substantial antiviral activity.

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28.1 MATERIALS AND METHODS

Anti-HIV assays: The antiviral assays per were as those described, above, in Section 6.1. Assays utilized HIV-1/IIIb and/or HIV-2 NIHZ is Purified peptides were used, unless otherwise 1 FIGS. 49A-C.

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acid sequence. Further, certain peptides have had amino- and/or certainal groups either added or as indicated in the figures; and FIG. 50. presents peptides which truncations of DP107 and/or the certain of the certain of the are unblocked or biotinylated, as in the figure.

which vary from the DP178 sequenc

Blocked peptides contained an acyl N-1 an amido C-terminus.

28.2 RESULTS

Anti-HIV antiviral data was obtained of group 1 DP178-derived peptides listed in Fine full-length, non-mutant DP178 peptide in FIG. 49A-C as T20) results shown are for

In FIG. 49A, a number of the DP178 tr exhibited a high level of antiviral activi evidenced by their low IC₅₀ values. These example, test peptides T-50, T-624, T-636 645 to T-650, T-652 to T-654 and T-656. Trepresents a test peptide which contains a mutation, as indicated by the residue's shackground. The HIV-1-derived test peptid

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activity (IC₅₀= 3µg/ml). A number of additional peptides also exhibited a high level of antivial activity. These included, for example, T-61/T-217 to T-221, T-235, T-381, T-677, T-377, T-590378, T-591, T-271 to T-272, T-611, T-222 to T-7-60/T-224. Certain of the antiviral peptides point mutations and/or amino acid residue additional which vary from the DP178 amino acid sequence.

In FIG. 49C, point mutations and/or amino carboxy-terminal modifications are introduced. DP178 amino acid sequence itself. As shown in figure, the majority of the test peptides list exhibit potent antiviral activity.

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IG. 50 as T21) were also produced and tested, in FIG. 50. FIG. 50 also presents data concerblocked and unblocked peptides which contain additional amino acid residues from the gp41 rewhich the DP107 sequence resides. Most of the peptides showed antiviral activity, as evidence their low IC50 values.

Thus, the results presented in this Secti demonstrate that not only do the full length D DP178 peptides exhibit potent antiviral activitruncations and/or mutant versions of these pecan also possess substantial antiviral charact

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29.1 MATERIALS AND METHODS

Electrophoretic Mobility Shift Assays Briefly, an EBV Zebra protein was synthesia utilizing SP6 RNA polymerase in vitro trans and wheat germ in vitro translation systems Corporation recommendations; Butler, E.T. & Chamberlain, M.J., 1984, J. Biol. Chem. 25 Pelham, H.R.B. and Jackson, R.J., 1976, Eui Biochem. 67:247). The in vitro translated protein was then preincubated with increas: of peptide up to 250 ng/ml prior to the add 10,000 to 20,000 c.p.m. of a 32P-labeled Zel element DNA fragment. After a 20 minute i: the presence of the response element, the : analyzed on a 4% non-denaturing polyacryla: followed by autoradiography, utilizing sta shift procedures. The ability of a test p prevent Zebra homodimer DNA binding was as peptide's ability to abolish the response migration retardation characteristic of a bound nucleic acid molecule.

Peptides: The peptides characterized study represent peptide walks through the containing, and flanked on both sides by, DP178/DP107 analog region identified in th presented in Section 20, above, and shown FIG. 33. Specifically, the peptide walks

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29.2 RESULTS

The EBV Zebra protein transcription facto contains a DP178/DP107 analog region, as demon in the Example presented, above, in Section 20 protein appears to be the primary factor respo for the reactivation capability of the virus. method by which the DNA-binding function of th virus may be abolished may, therefore, repr s effective antiviral technique. In order to id potential anti-EBV DP178/DP107 peptides, there peptides derived from the region identified in 20, above, were tested for their ability to in Zebra protein DNA binding.

The test peptides' ability to inhibit Zeb protein DNA binding was assayed via the EMSA a described, above, in Section 28.1. The data summarized in FIG. 51A-B presents the results assays of the listed EBV test peptides. These peptides represent one amino acid "walks" thro region containing, and flanked on both sides b DP178/DP107 analog region identified in the Ex presented in Section 20, above, and shown as s FIG. 33. As shown in FIG. 51A-B, the region f which these peptides are derived lies from EBV protein amino acid residue 173 to 246. the test peptides which were assayed exhibited ability to inhibit Zebra protein homodimer DNA

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of the invention, and functionally equivaler and components are within the scope of the interest and components are within the scope of the interest addition to those shown and described her in become apparent to those skilled in the art foregoing description and accompanying draw: modifications are intended to fall within the appended claims.

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WHAT IS CLAIMED IS:

- An isolated peptide recognized by an ALLMOTI5, 107x178x4 or a PLZIP sequence search
 - 2. The peptide of Claim 1 wherein the percorresponds to a peptide present in a virus.
- 3. The peptide of Claim 2 in which the '
 HIV-1 or HIV-2.
 - 4. The peptide of Claim 2 in which the a respiratory syncytial virus.
- 5. The peptide of Claim 2 in which the a human parainfluenza virus.
- 6. The peptide of Claim 2 in which the an influenza virus.
 - 7. The peptide of Claim 2 in which the a hepatitis B virus.
- 8. The peptide of Claim 2 wherein the van Epstein-Barr virus.

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- 11. The method of Claim 9 wherein the respiratory syncytial virus.
- 12. The method of Claim 9 wherein the human parainfluenza virus.
- 13. The method of Claim 9 wherein th an influenza virus.
- 14. The method of Claim 9 in which to a hepatitis B virus.
 - 15. The method of Claim 9 wherein th an Epstein-Barr virus.

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7872-020 (SHEET 63)

LOARILAVERYLKDQQQ

LEANISKSLEQAQIQQEKNMYELQKLNSWDIFGNWF LEANISQSLEQAQIQQEKNMYELQKLNSWDVFTNWL

SSESFTLLEGMNNMKLQLAEGMLEQINEKHYLEDIS

QQL L DVVKRQQEMLRL TVMCTKNLQARVTA I EKYLKDQ

CGGNNLLRAIEAQQHLLQLTVWG1KQLQARILAVERYLKDQ

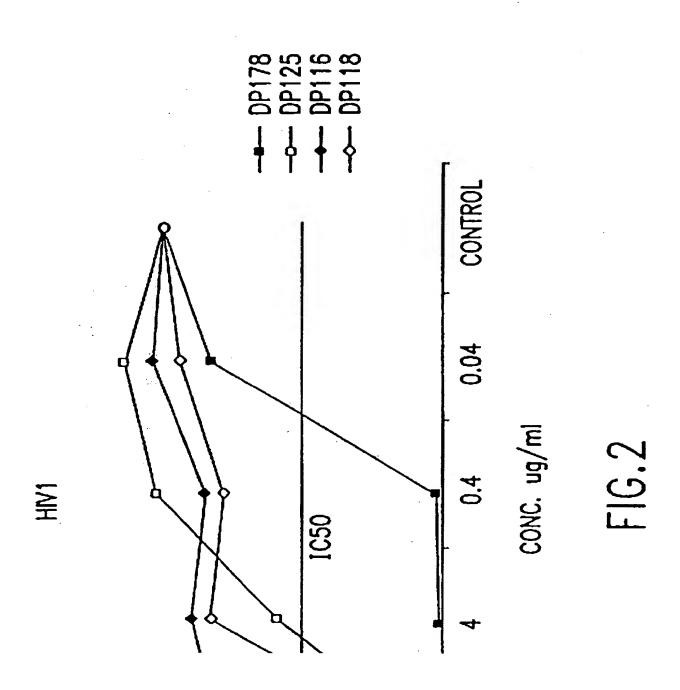
YTSL I HSL I EESONQOEKNEOELLELDKWASLWNWF YTNTIYNLLEESONQOEKNEOELLELDKWASLWNMF EQ 10:1)

£0 10:3)

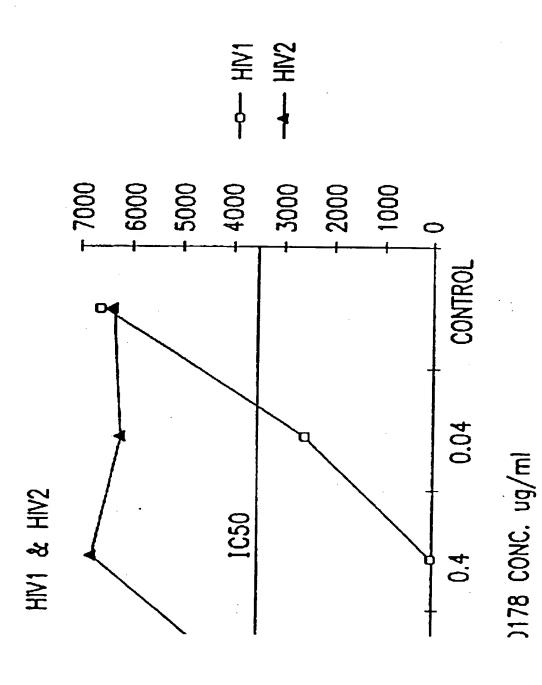
YTGIIYNLLEESONQQEKNEOELLELDKWANLWNWF

YTSL IYSLLEKSQTQQEKNEQELLELDKWASLWNWF

7872-020 (SHEET 2 OF 63)



7872-020 (SHEET 3 OF 63)



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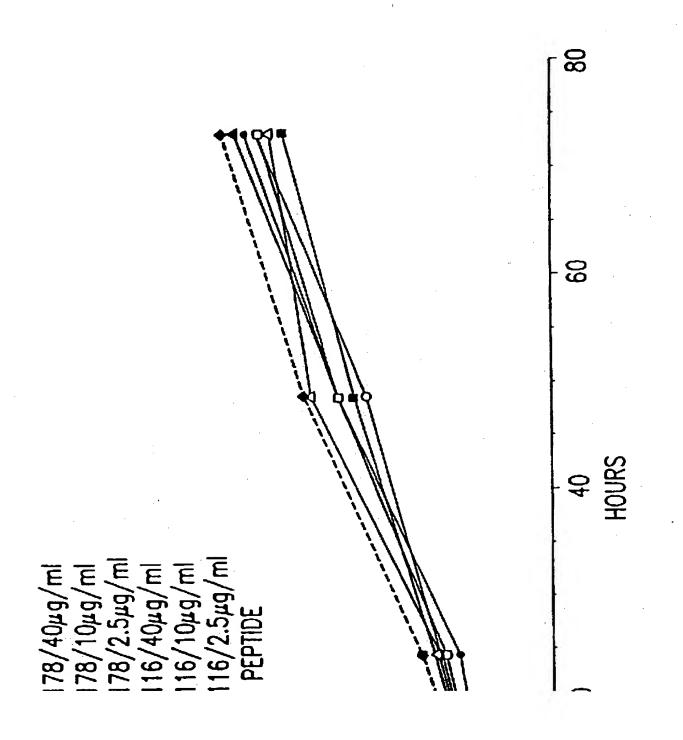
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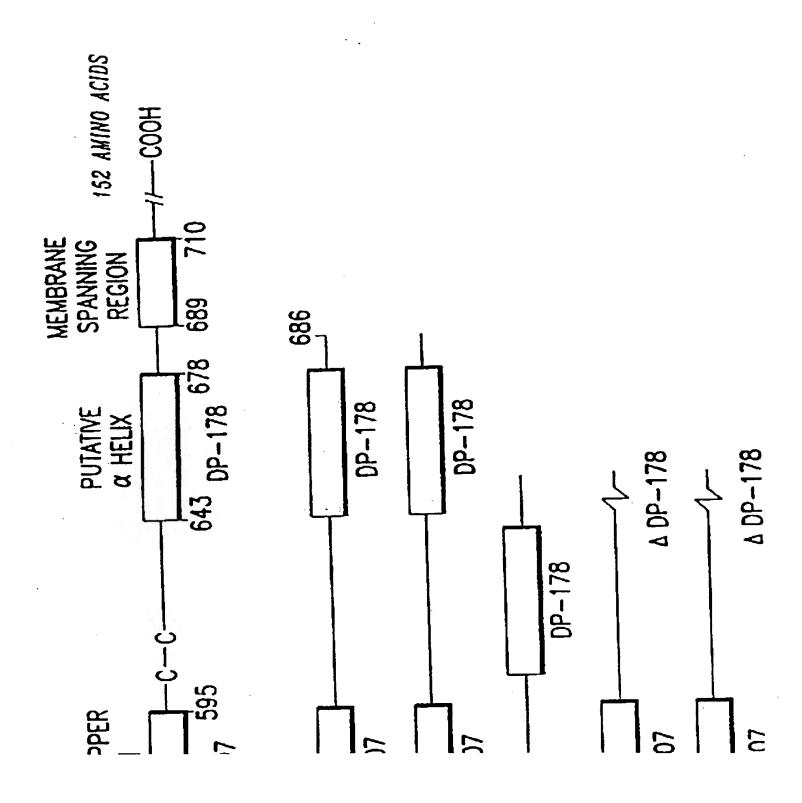
7872-020 (SHEET 4 OF 63)

Number	of Syn	cytia,	/well	conce	ntratio	n in μg/i	ml (micro	grams/ml)
00170	10			0.2	0.1	0.05	0.025	0.0125
<u>DP178</u>	10	5		0.2	<u> </u>	0.03	0.025	0.0123
Syncylia	_	•	^	•	^	•	•	•
HIVILAI	0	0	0	0	0	0	0	0
HIVIMN	0	0	0	0	0	ND	ND	ND
HIVIRF	0	0	0	0	0	ND	ND	ND
HIVISF2	0	0	0	0	0	ND	ND	ND
DP125	10	5	1	0.2	0.1	0.05	0.025	0.0125
Syncylia								
HIVILAL	0	0	54	69	80	75	79	82
HIVIMN	0	0	30	36	ND	ND	ND	ND
HIVIRF	0	0	67	63	ND	ND	ND	ND
HIV1SF2	0	0	9	66	ИD	ND	ND	ND
	_	·	-					
0P116	10	5	1	0.2	0.1	0.05	0.025	0.0125
Syncylio								
HIVILAI	7 5	ND D	ND	ND	ND	ND	ND	ND
HIVISF2	81	ND						
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	Number	of	Syncyt	io/well:	conce	ntration	in ng/ml	(nanc
DP178	20	10	5	2.5	1.25	0.625	0.3125	Cı
Syncylia HIV1	0	0	0	0	0	14	20	
DP116	20	10	5	2.5	1.25	0.625	0.3125	Cı
Syncylia HIV1	ND	48	ND	ND	ND	ND	ND	
				HIV	2			
·	Number	of	Syncyl	io/well	: conce	ntration	in μg/ml	(mic
DP178	20	10	5	2.5	1.25	0.625	0.3125	<u>C</u>
Syncylio HIV2	5 በ	54	55	57	63	77	78	

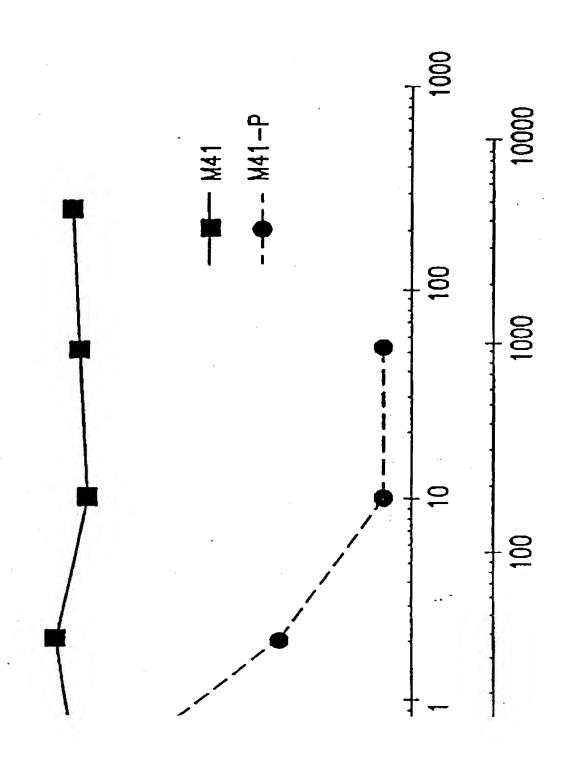
7872-020 (SHEET 6 OF 63)



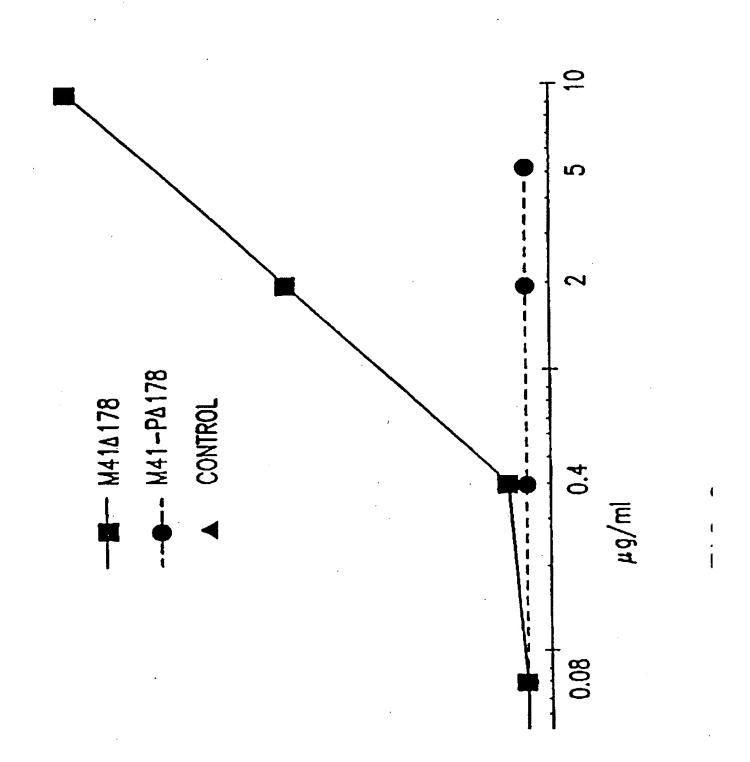
7872-020 (SHEET 7 OF 63)



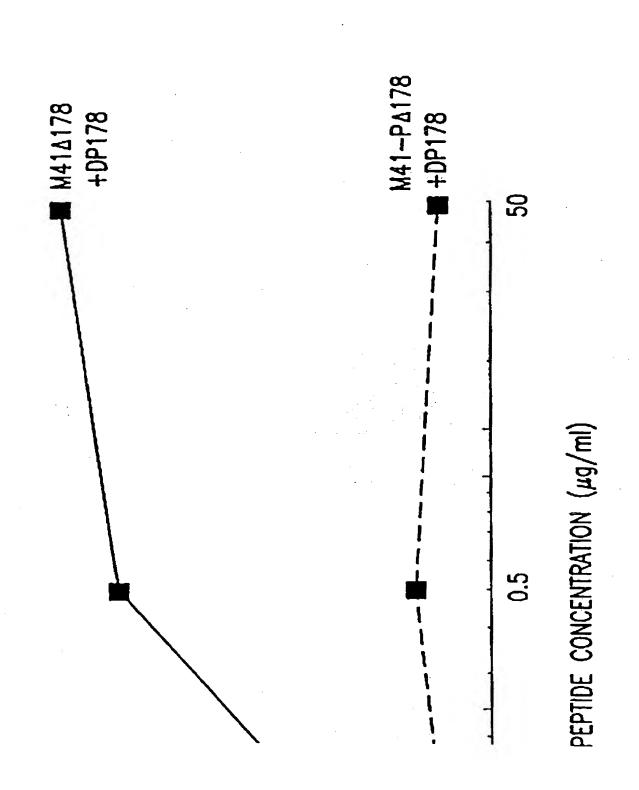
7872-020 (SHEET & OF 63)



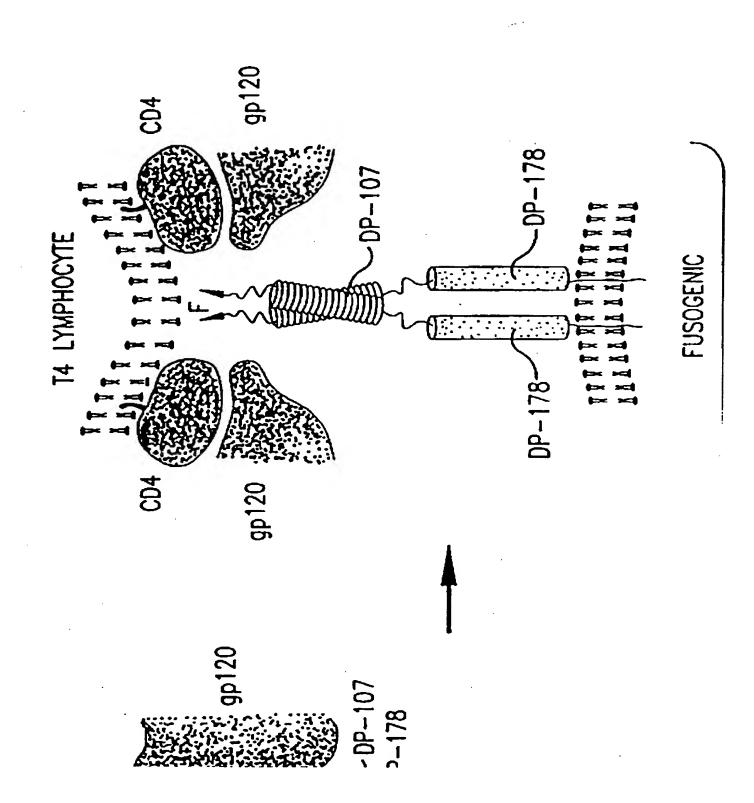
7872-020 (SHEET 9 OF 63)



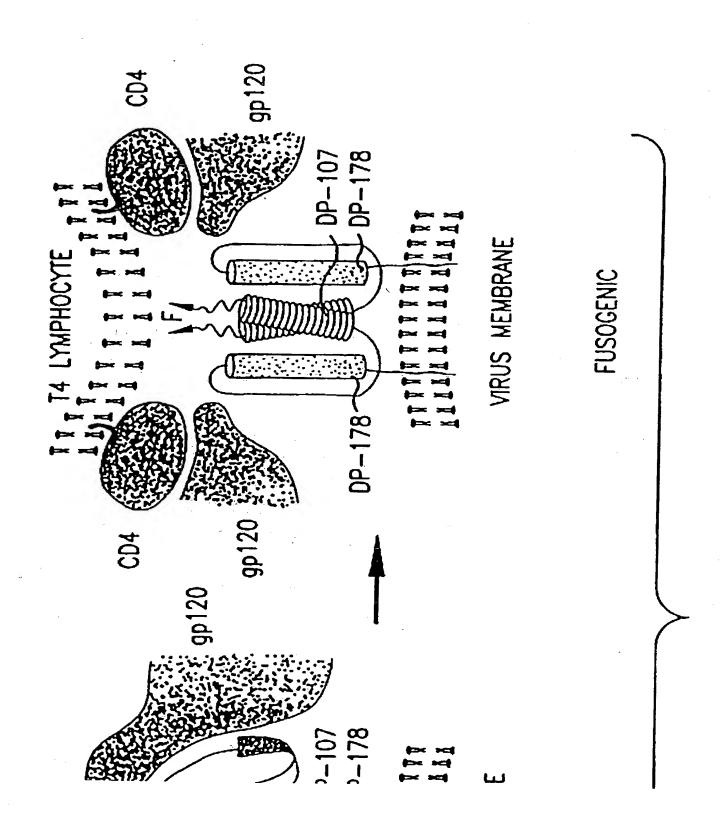
7872-020 (SHEET 10 OF 63)



7872-020 (SHEET II OF 63)



7872-020 (SHEET 12 OF 63)



7872-020 (SHEET 13 OF 63)

Molifs		[LMNV] (CFG IMPTW)	[IKLT] {CFGHIMPRWM}	[AILNV] (COFGHILPWIY)	[ELR] {ACFGAPVMY}	[FILTV] {ACFLMPTVW}
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FIG. 12

7872-020 (SHEET 14 OF 63)

Motifs		[ILQT] {CFIMPSTY} [ILQTV] {CDFIMPST} [ILQTV] {CDFIMPST}	[EKLNOV] {CDFKNPSVY} [EKLNOV] {CFKNPS} [EKLNOV] {CFKNPS}	[EKLOY] {ACFGWPRWMY} [EKLOWY] {CFGWPRVY} [EFKLOWY] {CFGWPRVY}	[EILNOSY] {ACFGMPRYMY} [EILNOSMY] {CFGMPRYY} [EFILNOSMY] {CFGMPRYY}
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7872-020 (SHEET 14 OF 63)

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FIG. 1.

7872-020 (SHEET 15 OF 63)

	Hybrid Molif		[ILMADIV] {CF MPT}	[ILMADIV] (CFIMPT)	[ILMAOTV] (CF [APT]	[EKLMOV] {CFMP}	[EKLANOV] SCFMP!	[EKLMNOV] [CFMP]
	Porent Motif	[LMNV] {CFGIMPTW}	[ILOT] {CF IMPSTY}	[ILOTY] (COF IMPST]	[1LOTV] {CDF IMPST}	[EKLNOY] {CDFKWPSVY}	[EKLNOV] (CFKAPS)	(CFKAPS)
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				AVERYL	A V E R Y L K D		VERYL	VERYLKOO
	6			LAVERYL	LAVERYLXD		AVERYL	A VERYLKOO
	6			ILAVERYL	IL AVERYLX D		LAVERYL	LAVERYLKOO
			8	RILAVERYL	R Y E R Y L X D		I L A V E R Y L	ILAVERYLKOO
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FIG. 14

7872-020 (SHEET 15 OF 63)

	Hybrid Molil		[ILMADIV] (CFINPT)	[ILMADIV] {CF IMPT}	(ILMOTV) {CFIMPT}	[EKLIANOV] {CFMP}	[EKLANOV] {CFMP}	[EKLIMOV] {CFIRP}
	Parent Hotil	[LMNV] {CFGIMPTH}	[1101] {CF INPSTY}	[1101V] [COF [MPST]	[11014] [COF 11,PPST]	[EKLNOV] [CDFKAPSYY]	[EKLNOV] (GFKNPS)	[EKLNOV] {CFKNPS}
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	Sequence	CON4 (gand yeast)	D-107 (env hylbru)[1=0	DP-107 (env. hv1bru)[1=0	DP-107 (env_hv1bru)[1=0 N N L	(P-10) (eny hyllyru)[24)	DP-107 (env.hvlbru)(2=0 NN L L	OP-107 (env_hv1bru)L2=0

FIG. 12

7872-020 (SHEET 16 OF 63)

Hybrid Holif	•	[LMN] {GFGIMPTM}	[EKLOY] {ACFGAPRYMY} [EKLMADYN'] {CFGAPM} {EKLOHY] {CFGAPRYY} [EKLMADYHY] CFGAP} {EFKLOHY] {CFGAPRYY} [EFKLMADYMY] {CFGAP}	EILNOSY] {ACFGAPRYNY} [EILMAGSYY] {CFGAPH} EILNOSMY] {CFGAPRYY} [EILMAGSYNY} {CFGAP} EFILNOSMY] {CFGAPRYY} [EFILMAGSYNY] {CFGAP}
Parent Holif	•	[LIMAN]	[EKLOY] [EKLOHY]	
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	Sequence	XXV (gen4 yeast)	DP-178 (env_hvlbru)Y1=A DP-178 (env_hvlbru)Y1=A DP-178 (env_hvlbru)Y1=A	09-178 (env_hv1bru)Y1=0 09-178 (env_hv1bru)Y1=0 09-178 (env_hv1bru)Y1=0

FIG. 15

7872-020	(SHEET	17	OF	63)
Hybrid Molif [EFIKLNOSTVMY] (GMP)				
Parent Malii [ILOTV] {COFIMPS] [EKLNOV] [OFIAPS] [EFKLOMY] [OFIAPRY] [EFILNOSMY] {CGAPRYY]	[FILTV] {ACTLAPTWI]		•	
Sequence OP-107 (env_hv1bru)L1=0 NNLL R A 1 E A Q Q H L L Q L 1 V W G 1 K Q L Q A R 1 L A V E R Y L K D Q OP-178 (env_hv1bru)Y1=0 NN L L R A 1 E E S Q N Q Q E K N E O E L L E L D K W A S L W N W F OP-178 (env_hv1bru)Y1=0 Y T S L I H S L I E E S Q N Q O E K N E O E L L E L D K W A S L W N W F	FLU LOOP 36 I E KIT IN E KIF IN OI I E K E F S E V E G R I I O D L E K Y		FIG.16	

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M D A D D	Hybrid Hotif			[EFINDIANDIVAN] [CFLP]	[EFILMORSTVMY] {GFLP}	[efklimowm] [grip]	(CELIVITANDAMA) (CELIVITA				
M	Porent Wolif			[EFKLOM] [COLPRY]	(35) (37) (37) (37)	82_					
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FIG. 1.

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	Sequence	GCN4 (gen4 yeast)	OP-107 (env_hv1bru)L1=0	DP-107 (env_hv16ru)L2=0	DP-178 (env_hvlbru)Y1=A	DP-178 (env_hvlbru)Y1=0	C-FOS (fos_human)	C-JUN (top1_humon)	C-MC (myo_humon)	FLU 1009 36 1 E K T N E K F

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FIG. 18

7872-020 (SHEET 20 OF 63)

•

FIG. 19

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Fusion

YALLMOTI5Y

Peptide

+107x178x4+

v......Flgflg A AGSTMGARSM TLTVQARQ **↑LLSGIYQQQ** *DP107-NNL*

LRAIEAOOHL LOLTYWGIKO LOARILAYER YLKDO-DP107 QLLG * I WGC

4107x178x4 4 1

VALLMOTISY

LVS Coilcd-Coil

SGKLICT TAVP ▼WNASWS NKSLEQIWNN MTWM *E ◆ WDREINN DP178-

YTSLIHSL IEESONOOEK NEOELLELDK* WASLWNWF-DP178 NI

◆Transmembrane Region ◆

TNWLWYIK * + IF IMIYGGLYGL RIYFAYLSIY NRVRQGYS * PL

+P23LZIPC+

SFOTHLPTPR GPDR *PEGIEE EGGERDRDRS IRLVNGSLAL IWDDLRSL* CL

YALLMOTISY

4107x178x4 4

F ▼SYHRLRDLL LIVTRIVELL GRRGW ▲EALKY WWNLLQYWSQ

ELKNSAYSLL NAT A ALAVAEG TDRVIEVVQG A CRAIRHIPR

RIRQGLERIL L

FIG. 20

7872-020 (SHEET 22 OF 63)

Fusion -

∀ALLMOTI5∀

Peptide

★107x178x4◆

v.....FLGFL

LGVGSAIAS GVA *YSKYLHL EGEVNICKSA

+PI&12LZIPC+

LLSTNKAYYS LSNGVSYLTS KYLDLKNYID KQ++ LL +PIVNKQ

+107x178x4+

SC ASISNIETY I+ EFOQIONNELLEITREFSYNAGA VITTYVSTMLINSELLSL

+P1&12LZIPC+

♥ALLMOTI5♥

INDM →PI →TNDQ KKLMSNNVQI V→ RQQSYSI→ MS IIKEEVLAYV

VQ▼ LPLYGVID TPCWKLHTSP LCTTNTKEGS NICLTRTDRG WYCDNAGSVS

FFPQAETCKV QSNRVFCDTM NSLTLPSEIN LCNVDIFNPK

YDCKIMTSKT DVSSSVITSL GAIVSCYGKT KCTASNKNRG

IIKTFSNGCDYVSNKGMDTV SVGNTLYYVN KQEGKSLYVK G

+P7, 12, & 23LZIPC+

4107x178x44

∀ALLMOTI5∀

EPINFYDPLVF +PSDE +FDASISOVNEKINOSLAF *I+ RKSDELL+

+Transmembrane Region +

HNYNA + GK STIN + IMITTI IIVIIVILLS LIAVGLLLY + C+

KARSTPVTLS KDQLSGINNI AFSN

7872-020 (SHEET 23 OF 63)

Fusion

Peptide __FLGFLG **VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5 VALLMOTI5**

♥AAGTA MGAAA ◆TALTYOSQHLLAGILQQOKNLLAAY

+107x178x4+ EAQ+ QQM +LKLTIWGVKNLNARYTALEKYLEDQARLN+ AWG+ CA

LVS Coiled-Coil

∀ALLMOTI5∀ 4107x178x44

WKQVCHTTVP WQWNNRTPDW *NNMT *WLE *WERQISYLEGNIT

4107x178x44

TOLEEARAQEEKNLD+ AYOKLSS* WSDFWSW+ FDF +SKWLN +ILK

*Transmembrane Region *
IGFLDVLGIIGLRLLYTY + YS * CIARVRQGYS PLSPQIHIHP WKGQPDNAEG

PGEGGDKRKN SSEPWQKESG TAEWKSNWCK RLTNWCSISS IWLYNS

∀ALLMOTI5∀

▼CLTL LVHLRSAFQY IQYGLGELKA AAQEAVVALA RLAQNAGYQIWL▼

ACRSAYRA IINSPRRVRQ GLEGILN

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Fusion

.....EAG

4107x178x44

Peptide VALLMOTI5 V

LVS Coilcd-Coil

▼VYL AGVALGVATA AQITAGIALHQ **▲*SNLNAQAIQ**

SLRTSLEOSNKAIEEIREATOETYIA* VOGYODY* VNNEL* VP

∀ALLMOTI5∀

★107x178x4★

+P6 & 12LZIPC+

AMQHMSCELVGQRLGLRLLRYYTELLSIFGPSLRD &PISA &VEISIOALIYAL

GGEHKILEKLGYSGSD → MIAILESRGIKTKI → THVDLPGKF IILSISY

+P1 & 12LZIPC+

+PTLSEVKGVIVHRLEAV+ SYNIGSQEWYTTVPRYIATNGYLISNFDESSCVFVS

ESAICSQNSL YPMSPLLQQC IRGDTSSCAR TLVSGTMGNK FILSKGNIVA

NCASILCKCY STSTIINQSP DKLLTFIASD TCPLVEIDGA TIQVGGRQYP

LVS Coiled-Coil

∀ALLMOTI5 ∀

4P12 & 23LZIPC4

DMVYEGKVAL G +PAISLD +RL+DYGTNLGNALKKLDDAKVLI+

+Transmembrane Region +

DSS÷ NOILETVRRS→+ SFN +FGSLLSYPILSCTAL ALLLLIYCC+

K RRYQQTLKQH TKVDPAFKPD LTGTSKSYVR SL

7872-020 (SHEET 25 OF 63)

Fusion VALLMOTISY

Peptide ◆107x178x4◆

▼......FIGAI IGSVALGVA TAAQITAASA LIQANQNAAN ◆ILRLIŒSITA

TIEAVHEYTDGLSQLAYA → VG KM → QQFVNDQFNNTAQELDCIKITQQV

♥ALLMOTIS♥
GVELNLYLTELTTV FGPQITSPAL ▼TQLTIQALYNAGGNMDYLLTKLGVG

+P1 & 12LZIPC+
NNQLSSLIGSGLIT GN♥ +PILYDSQT QLLGIQVTLP SVGNLNNMRATYLET

LSVST TKGFASALVP KVVTQVGSVI EELDTSYCIE TDLDLYCTRI VTFPMSPGIY

SCLNGNTSAC MYSKTEGALT TPYMTLKGSV IANCKMTTCR CADPPGIISQ

∀ALLMOTI5∀ ◆107x178x4◆

NYGEAVSLID RHSCN ♣♥VLSLD GITLRLSGEF DATYQKNISI LDSQVIVTG

LVS Coiled-Coil

N LDISTELGNY NNSISNALDK LEESNSKLDK VNVKLTSTSA +LIT* YIA

membrane Region +
LTAISLVCGIJSLV → LACYLMY + KQKAQQKTLLWLGNNTLGQMRATTKM

7872-020 (SHEET 26 OF 63)

Fusion

♥ALLMOTI5♥

Peptide

★107x178x4★ *LVS Coiled-Coil*

...FFGGV

◆IG ◆TIALG •YATSAQITAAYALYEAKQARSDIEKLKE

AIRDTNKAVOSVOSSIGNLIVAIKSVQ* DYVNKE** IVPSIARLGCEAAG

YALLMOTISY

↑107x178x4↑

LQLGIALTQH *YSELTNIFGDNIGSLQEKGIKLQGIASLYRTNITEY*

+P5 & 12LZIPC+

IFTTSTVDKYDIYDLLFTESIKVRVIDVDLNDYSITLQVRL +PLLTRLLNTQIYR

VDSISYNI+ QNREWYI+ PLPSHIMTKGAFLGGADVKECIEAFSSYIC

PSDPGFVLNHEMESCLSGNISOCPRTVVKSDIVPRYAFVNGGVVANCITT

TCTCNGIGNRINQPPDQGVKIITHKECNTIGINGMLFNINKEGTLAFYTP

YALLMOTI5Y

+107x178x4+

+P6 & 23LZIPC+

NDITLNNSVALD *PIDI *SIELN *KAKSDLEESKEWI* RRSNOKL*

◆Transmembrane Region ◆

DSIGNWHOSSTT +IIIV → LIM IIILFIINVT II → ILAVKYY → R

IQKKNRVDQN DKPYVL1NK

7872-020 (SHEET 27 OF 63)

Fusion Peptide

....GLFGAI AGFIENGWEGMIDGWYGFRHQNSEGTG

4107x178x44

VALLMOTISY

LYS Coilcd-Coil

*Q *AADLKST *QAAIDQINGKLNRYIEKTNEKFHQIEKEESEYEGRIQ

DLEKYVEDTKIDL* WSYNAELLVALENOHII* DLT▼ DSEMNKLFEKTR

RQLRENAEEMGNGCFKIYHKCDNACIESIRNGTYDHDVYRDEALNNRFQIKG

VELKSGYKDWILWISFAISCFLLCVVLLGFIMWACQRGNIRCNICI

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7872-020 (SHEET 38 OF 63)

Fusion

♥ALLMOTI5♥

Peptide

4107x178x44

.....RNKRGVFVLGFLGFLATAGSAMGAAS ** XXXXAQSRTLLAGIVQQQQQ

LLDVVKRQQELLRLTVWGTKNLQTRVTAIEKYLKDQAQL*NAWG* CAF

♥ALLMOTI5♥

*LVS Predicted Coiled -Coil

RQVCHTTVPWPNASLTPDW *NND ▼TWQEWERKVDFLEENITALLEEAQIQQ

↑107x178x4↑

IYIVMLAKLRQGYRPVFSSPPSYFQXTHTQQDPALPTREGKEGDGGEGGGNSSWP

WQIEYIHF

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MTRRRVLSVVVLLAALACRLGAQTPEQPAPPATTVQPTATRQQTSFPFRVCELSSHGDLFRFSSD

IQCPSFGTRENHTEGLLMVFKDNIIPYSF ★KYRSYTKIVTNILIYNGWYADSVTNRHE ↓
EKFSVDSY ETDQMDTIYQ CYNAVKMTKD GLTRVYVDRD GVNITVNLKP TGGLANGVRR
YASQTELYDA PGWLIWTYRT RTTVNCLITD MMAKSNSPFD FFVTTTGQTV EMSPFYDGKN
KETFHERADS FHVRTNYKIV DYDNRGTNPQ GERRAFLDKG TYTLSWKLEN RTAYCPLQHW
QTFDSTIATE TGKSIHFVTD EGTSSFVTNT TVGIELPDAF KCIEEQVNKT HEKYEAVQD
RYTKGQEAIT YFITSGGLLL AWLPLTPRSL ATVKNLTELT TPTSSPPSSP SPPAPSAARG
STPAAVLRRR RRDAGNATTP VPPTAPGKSL GTLNNPATVQ IQFAYDSLRR QINRMLGDLA
RAWCLEQKRQ NMVLRELTKI NPTTVMSSIY GKAVAAKRLG DVISVSQCVP VNQATVTLRK
SMRVPGSETM CYSRPLVSFS FINDTKTYEG QLGTDNEIFL TKKMTEVCQA TSQYYFQSGN

\$\frac{107x178x4}{2}\$
EIHVYNDYHH FKTIELDGIA TLQTFISLNT \$\frac{107x178x4}{2}\$
\$\tag{SLIENIDFASLELYSRDEORASNVFD} *\LE_{\text{A}}\$

'LVS Predicted Coiled Coil* TM Potential
GIFREYNFQAQNIAGLRKDLDNAVSN* GRNQ FVDGLGELMDSLGSVG QSITN

+P12LZIPC →

TM Potential
LVSTVGGLFSSLVSGFISF FK N +PFGGMLILVLVAGVVILVISL+ TRRTRQMS

QQPVQMLYPG IDELAQQHAS GEGPGINPIS KTELQAIMLA LHEQNQEQKR AAQRAAGPSV

ASRALQAARDRFPGLRRRRY HDPETAAALL GEAETEF

F1G. 32

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MMDPNSTSED VKFTPDPYQV PFVQAFDQAT RVYQDLGGPS QAPLPCVLWP VLPEPLPQGQ

LTAYHVSTAP TGSWFSAPQP APENAYQAYA APQLFPVSDI TQNQQTNQAG GEAPQPGDNS

TVQTAAAVVF ACPGANQGQQ LADIGVPQPA PVAAPARRTR KPQQPESLEE CDSELEI

@DNA Binding@

4107x178x4 4 +Dimerization+

@KRY KNRVASRKCRAK ♠FK@ Q

+LLOHYREVAAAKSSENDRLRLLLKO

MCPSLDVD+ SI IPRTPDVLHE DLLNF

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Fusion

Peptide ♥ALLMOTIS♥ *LVS Coiled-Coil*

FAG VVLAGAALGVATAAQITAGIALHQSML*NSQAIDNLRASLETTN

QAIEAIRQAGQEMI*LAVQGVQDYINN* ELIPSMNQLSCDLIGQKLGLKLLRYYT

+P23LZIPC+

+P6,12LZIPC+

4107x178x4 4

♥ALLMOTI5♥

EILSLFGPSLRD +PISA *VEISIOALSYALGGDINKV+ LEKLGYSGGDL+

÷P1,12LZIPC

LGILES A RGIKARI → THVDTESYFIVLSIAY +PTLSEIKGVIVHRLEGV+ SY

NIGSQEWYTTVPKYVATQGYLISNFDESSCTFMPEGTVCSQNALYPMSPLLQECL

RGSTKSCARTLVSGSFGNRFILSQGNLIANCASILCKCYTTGTIINQDPDKILTYIAA

∻P23LZIPC÷

♣P12LZIPC ♣

VALLMOTI5

LVS Coiled-Coil

DHCPVVEVNGVTIQVGSRRYPDAVYLHRIDLGP →P ▼IS*LERLDVGTNLGN

◆Transmembrane Region◆

AIAKLEDAKELL+ ESSDOI+L+ RSMK +GLSSTSIVYILI♥ AVCLGGLIGIP

ALICCC ◆ RGRCNKKGEQVGMSRPGLKPDLTGTSKSYVRSL

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Pre S1 and Pre S2
MGQNLSTSNPLGFFPDHQLDPAFRANTANPDWDFNPNKDTWPDANKVGAGAFG
LGFTPPHGGLLGWSPQAQGILQTLPANPPPASTNRQSGRQPTPLSPPLRNTHPQAM
QWNSTTFHQTLQDPRVRGLYFPAGGSSSGTVNPVLTTASPLSSIFSRIGDPALN

Major Surface Antigen (HBs)

Fusion Peptide

♣P12 & 23LZIPC♣

MENITSG FLG +PLL VLQAGFFLLTRILTI+ PQSLDSWWTSLNFLGGTTVCLG

*P12 & 23LZIPC *
QNSQSPTSNHSPTSCPPTC *PGYRWMCLRRFIIFLFILLLCLIFLLVLLDYQGML *
PVCPLIPGSSTTSTGPCRTCMTTAQGTSMYPSCCCTKPSDGNCTCIPIPSSWAFGKF

*Transmembrane Region *
LWEWASARFSWLS *LLVPFVQWFVGLSPTVWLSVI * WMMWYWGPSL

- ◆Transmembrane Region ◆
- *YSILSPFLPLLPIFFCLWVYI *

7872-020 (SHEET 43 OF 63)

Fusion

♥ALLMOTI5♥

★107x178x4★

Peptide

*LVS Coiled Coil

AIQLIPLFVG LGI ◆TTAVSTGAAGLGVS AIT *QYTKLSHQLISDV

QAISSTIQDLQDQVDSLAEVVLQ* NRRGLDLLTAE* QGGI♥

CLALQEKCCFYANKSGIVRDKIKNLQDDLERRRRQLIDNPFWTSFHG

FLPYVMPLLGPLLCLLLVLSFGPIIFNKLMTFIKHQIESIQAKPIQVHYH

Transmembrane Region

RLEQEDSGGSYLTLT......????????????????????????

F16 36

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MKAQKGFTLI ELMIVVAIIG ILAAIAIPQ

- **↑107x178x4↑**
- **♥ALLMOTI5♥**
- **♦♥YODYTARTOYTRAYSEVSALKTAAESAILEGKEIYSSA♦** T**♥**

PK DTQYDIGFT

- **↑107x178x4 ↑**
- **♥ALLMOTI5♥**
- **♦♥ESTLLDGSGKSQIQVTDNQDGTVELVATLGKSSGS**♠AIKGAVITVSR♥

KNDGV WNCKITKTPT AWKPNYAPAN CPKS

7872-020 (SHEET 45 OF 63)

MNTLQKGFTL IELMIVIAIV GILAAVALPA YQDYTARAQV

SEAILLAEGQ KSAVTEYYLN HGIWP

- **↑107x178x4**◆
- **♥ALLMOTI5♥**
- **♦♥KDNTSAGVASSSSIKGKYVKEVKVENGVVTAT**◆

MNSSNVNKEIQGKKLSLWAKRQDGSVKW▼

FCGQP VTRNAKDDTV TADATGNDGK IDTKHLPSTC RDNFDAS

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MKKTLLGSLI LLAFAGNVQA DINTETSGKV TFFGKVVENT

CKVKTEHKNL SVVLNDVGKN SLSTKVNTAM PTPFTITLON

CDPTTANGTA NKANKVGLYF Y

- **↑107x178x4↑**
- **♥ALLMOTI5♥**
- **♦♥SWKNVDKENNFTLKNEQTTADYATNVNI**

QLMESNGTKAISVVGKETE •

DF MHTNNNGVAL NQTHPNNAHI SGSTQLTTGT NELPLHFIAQ

YYATNKATAG KVQSSVDFQI AYE

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MNKKLLMNFF IVSPLLLATT ATDFTPVP

- **4107x178x44**
- **♥ALLMOTI5♥**
- **♦♥LSSNOIIKTAKASTNDNIKDLLDWYSSGSDTFTNS♦♥**

EVLDNSL GSMRIKNTDG SISLIIFPSP YYSPAFTKGE KV

- **↑107x178x4↑**
- **♦DLNTKRTKKSOHTSEGTYIHFQISGYT♦**

N TEKLPTPIEL PLKVKVHGKD SPLKYG

- P12LZIPC →
- **+PKFDKKQLAISTLDFEIRHQLTQI +**

HGLYRSSDKT GGYWKITMND GSTYQSDLSK KFEYNTEKPP

INIDEIKTIE AEIN

7872-020 (SHEET 48 OF 63)

♥ALLMOTI5♥

MKKTAFILLL FLALTLTTSP L ▼VNG

★107x178x4★

- *LVS Predicted Coiled-Coil*
 - S & EKSEEINEKDLRKKSELQRNALSNLRQIY* YYNEKAITENKESDD &

QFLENTLL♥ FKG FFTGHPW

- **4107x178x4 4**
- ***YNDLLVDLGSKDATNKYKGKKVDLYGAY**

YGYQCAGGTPNKTACMYGGVTLHDN NRLTEEKKVP INLWIDGKQTTV

- *P12LZIPC*
- *PIDKVKTSKKEVTVQELDL* QARHYLHGK FGLYNSDSFGGKVQ

+P12LZIPC+

RGLIVF HSSEGSTVSY DLFDAQGQY +P DTLLRIYRDN KTINSENLHI+

DLYLYTT

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7872-020 (SHEET Y OF 63)

♥ALLMOTI5**♥**

MKKTAFTLLL FIALTLTTSP L

♥VNGS

★107x178x4★

♠EKSEEINEKDLRKKSELOGTALGNLKOIYYYNEKAKTENKESHD♠ Q♥

FLOHTILFKG FFTDHSWYND LLVDFDSKDI VDKYKGKKVDLYGAYY

GYQC AGGTPNKTAC MYGGVTLHDN NRLTEEKKVPINLWLDGKQNTV

↑107x178x4↑

♥ALLMOTI5♥

+P12LZIPC+

♣P ♥L ♠ETVKTNKKNVTVOELDLOARRYL♣ **QEKYNLYN**♠

SDVFDGKVQR♥ GLIVF HTSTE

+P23LZIPC+

PSVNYDLFGAQGQYSNTLLRIYRDNKTINSENMHI DIYLYTS

F1G. 42

7872-020 (SHEET 50 OF 63)

MKNITFIFFILLASPLYANGDRLYRADSRPPDEIKRFRSLMPRGNEYFDRGT

- **♥ALLMOTI5♥**
- **♥QMNINLYDHARGTQTGFVRYDDGYV**
- 4107x178x44
- **♦STSLSLRSAHLAGQYILSGYSLTIYIVI ♦** ANMFNVNDVISVY **♥**

SP HPYEQEVSAL GGIPYSQIYG WYRVNFGVID ERLHRNREYR

DRYYRNLNIA PAEDGYRLAG FPPDHQAWRE EPWIHHAPQG

CGDSSRTITG DTCNE

- **♥ALLMOTI5♥**
- **▼ETQNLSTIYLREYQSKVKRQIFSDYQSEVDIYNRIRDEL▼**

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MMFSGFNADY EASSSRCSSA SPAGDSLSYY HSPADSFSSM

GSPVNAQDFC TDLAVSSANF IPTVTAISTS PDLQWLVQPA

LVSSVAPSQT RAPHPFGVPA PSAGAYSRAG VVKTMTGGRA

LVS Predicted Coiled-Coil

QSIGRRGKVE QLSPEEEEKR RIRRE *RNKMA AAK

↑107x178x4◆

♥ALLMOTI5♥

♥CRNRRREL ♠TDTLOAETDQLEDEKSALOTEIANLLKEKEKL ♥

EFILAAH R* PACKIPDDL GFPEEMSVAS LDLTGGLPEV

ATPESEEAFT LPLLNDPEPK PSVEPVKSIS SMELKTEPFD

DFLFPASSRP SGSETARSVP DMDLSGSFYA LPLLNDPEPK

PSVEPVKSIS SMELKTEPFD DFLFPASSRP SGSETARSVP

DMDLSGSFYA GSSSNEPSSD SLSSPTLLAL

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SGWESYYKTEGDEEAEEQEENLEASGDYKYSGRDSLIFLVDASKA
MFESQSEDELTPFDMSIQCIQSVYISKIISSDRDLLAVVFYGTEKDKNS
VNFKNIYVLQELDNPGAKRILELDQFKGQQGQKRFQDMMGHGSDY
SLSEVLWVCANLFSDVQFKMSHKRIMLFTNEDNPHGNDSAKASRAR
TKAGDLRDTGIFLDLMHLKKPGGFDISLFYRDIISIAEDED

↑107x178x4↑

♥ALLMOTI5♥

LVS Predicted Coiled-Coil

▼LRVH *FEE ★SSKLEDLLRKVRAKETRKRALSRLKLKLNKDIV* ISV

GIYNLVQKAL♥ KPPPIKLYRETN♠ EPVKTKTRTFNTSTGGLLLPSDTKR

SQIYGSRQIILEKEETEELKRFDDPGLMLMGFKPLVLLKKHHLRPSLFVYPE ESLVIGSSTLFSALLIKCLEKEVAALCRYTPRRNIPPYFVALVPQEEELDDQK IQVTPPGFQLVFLPFADDKRKMPFTEKIMATPEQVGKMKAIVEKLRFTYRS DSFENPVLQQHFRNLEALALDLME

- +P12LZIPC+
- *PEQAVDLTLPKVEAMNKRL* GSLVDEFKELVYPPDYNPEGKVTKR
 KHDNEGSGSKRPKVEYSEEELKTHISKGTLGKFTVPMLKEACRAYGLKSG
 LKKQELLEALTKHFQD

PCT/US95/16733

7872-020 (SHEET 53 OF 63)

GGGALSPQHSAVTQGSIIKNKEGMDAKS

- 4107x178x44
- **♥ALLMOTI5♥**
- ▼◆LTAWSRTLVTFKDVFVDFTREEWKLLDT AQQIVYRNV
 MLENYKNLVSLGYQLT VKPDVILRLEKGEEPWLVEREIHQETHPD
 SETAFEIKSSVSSRSIFKDKQSCDIKMEGMARNDLWYLSLEEVWKCR
 DQLDKYQENPERHLRHQLIHTGEKPYECKECGKSFSRSSHLIGHQKT
 HTGEEPYECKECGKSFSWFSHLVTHQRTHTGDKLYTCNQCGKSFVH
 SSRLIRHQRTHTGHKPYECPECGKSFRQSTHLILHQRTHVRVRPYECN
 ECGKSYSQRSHLVVHHRIHTGLKPFECKDCGKCFSRSSHLYSHQRTH
 TGEKPYECHDCGKSFSQSSALIVHQRIHTGEKPYECCQCGKAFIRKN
 DLIKHQRIHVGAETYKCNQCGIIFSQNS
- +P23LZIPC+
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L-V-L-Q-A-G-F-F-L-LT-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T-T-V
V-L-Q-A-G-F-F-L-LT-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-M-F-L-G-G-T-T-V-C-L
L-Q-A-G-F-F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-M-F-L-G-G-T-T-V-C-L
-A-G-F-F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T-T-V-C-L-G-Q
A-G-F-F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T-T-V-C-L-G-Q-N-S-Q-F-F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T-T-V-C-L-G-Q-N-S-Q-R-F-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T-T-V-C-L-G-Q-N-S-Q-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T-T-V-C-L-G-Q-N-S-Q-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T-T-V-C-L-G-Q-N-S-Q-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T-T-V-C-L-G-Q-N-S-Q-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T-T-V-C-L-G-Q-N-S-Q-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T-T-V-C-L-G-Q-N-S-Q-L-L-T-R-I-L-T-I-P-Q-S-L-D-S-W-W-T-S-L-N-F-L-G-G-T-T-V-C-L-G-Q-N-S-Q-R-S-Q-N-S-Q-

FIG. 52 A

23PGY-RWMCLR-RF41F1F1LF1L-1-CL1F1L-V-L-DY-Q-GM-LP-V-CP-L-IP-G-S-S-T-S-T-G-R-T-CM-T-1291

Domain II:

63)

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I-F-L-L-V-L-L-D-Y-Q-A-M-L-P-V-C-P-L-I-P-Q-8-8-T-8-T-Q-P-C-R-T-C-H-T-T
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P-0-Y-X-X-M-C-L-X-X-X-X-I-I-Y-
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INTERNATIONAL SEARCH REPORT

International application No. PCT/US95/16733

l	ASSIFICATION OF SUBJECT MATTER		
	:C07K 7/04,14/025, 14/16; C12N 9/94, 9/96, 9/98 :530/324; 424/184.1	i, 9/99	
According	to International Patent Classification (IPC) or to bot	h national classification and IPC	
	LDS SEARCHED		
ž –	documentation searched (classification system follow		
U.S. :	530/324, 325, 326, 327, 328, 329; 424/184.1, 185.	.1, 186.1, 187.1, 188.1	
Documenta	tion searched other than minimum documentation to t	he extent that such documents are included	d in the fields searched
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	data base consulted during the international search (c	name of data base and, where practicable	, search terms used)
MEDLIN	IE, AIDSLINE, APS		
C. DOC	CUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where a	ppropriate, of the relevant passages	Relevant to claim No.
X	PROCEEDINGS OF THE NATIONAL		1-3, 9, and 10
~~~	OF THE UNITED STATES OF AME	RICA, Volume 89, Number	
Y	21, issued November 1992, Wild Inhibitor of Human Immunodefi	et al, "A Synthetic Peptide	4-8 and 11-15
	Correlation Between Solution Stru		
	pages 10537-41, see entire docu		
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X Furth	er documents are listed in the continuation of Box C		
	cini categories of cited documents: ************************************	date and not in conflict with the applica	restional filing data or priority tion but ched to understand the
to b	e of particular relovance	principle or theory underlying the inventor.  'X' decument of particular relevance; the	
	for document published on or after the international filing date  unusual Which may throw doubts on priority chance) or which is	"X" document of particular relevance; the considered novel or cannot be consider when the document is taken alone	red to involve an inventive step
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O' dec	uncer referring to an oral disciours, use, exhibition or other	considered to invelve an inventive combined with one or more other such being obvious to a person skilled in th	documents, such combination
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	actual completion of the international search	Date of mailing of the international sea	rch report
28 MARC	H 1996	09 APR 1996	·
Name and m	ailing address of the ISA/US	Authorized officer	Frus for
Box PCT	D.C. 20231	JEFFREY STUCKER	11/0000 101
	o. (703) 305-3230	Telephone No. (703) 308-0196	

#### INTERNATIONAL SEARCH REPORT

International application No. PCT/US95/16733

C (Continua	tion). DOCUMENTS CONSIDERED TO BE RELEVANT	
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No
X Y	PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, Volume 91, Number 26, issued December 1994, Wild et al, "Propensity for a Leucine Zipper-Like Domain of Human Immunodeficiency Virus Type 1 gp41 to Form Oligomers Correlates With a Role in Virus-Induced Fusion Rather Than Assembly of the Glycoprotein Complex", pages 12676-80, see entire document.	1-3, 9 and 10 
Y	PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, Volume 81, Number 24, issued December 1984, Collins et al, "Nucleotide Sequence of the Gene Encoding the Fusion (F) Glycoprotein of Human Respiratory Syncytial Virus", pages 7683-87, see pages 7683 and 7685.	1 and 4  9 and 11
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